

## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 1843.35 seconds  
(without alignments)  
10908.879 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 415  
Sequence: 1 aagctttacagttactcagc.....tggggccaaggacactagt 415

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_on:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pt:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_ey:\*

13: gb\_un:\*

14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	415	100.0	415	6	BD232417
C 2	415	100.0	415	6	BD232417 Antibodie
3	415	100.0	415	6	BD232449 Antibodie
C 4	415	100.0	415	6	AX010600 Sequence
5	310.6	74.8	1658	10	BC031470 Sequence
6	310.4	74.8	453	6	AR302238 Sequence
7	310.4	74.8	453	6	AR560594 Sequence
8	310.4	74.8	453	6	AX080317 Sequence
9	301.4	72.6	1774	6	BD137123
10	295.6	71.2	405	10	MMU05819
11	295.2	71.1	477	10	AB050074
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13	289.8	69.8	396	10	MMU223543
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15	288	69.4	314	10	MUSIGHRU
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24	278.6	67.1	414	10	MUSIGHAA2	M59222 Mouse Ig he
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41	269	64.8	351	10	AY090913	AY090913 Mus muscu
42	268.8	64.8	351	10	MMU73591	U73591 Mus musculu
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#### ALIGNMENTS

RESULT 1  
BD232417  
LOCUS  
DEFINITION  
ACCSSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD232417  
Antibodies against CD23, derivatives thereof and therapeutic  
utilization of the same.  
BD232417  
JP 2002514421-1 GI:33042187  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and  
Shearin,J.  
Antibodies against CD23, derivatives thereof and therapeutic  
utilization of the same  
Patent: JP 2002514421-A 1 21-MAY-2002;  
GLAXO GROUP LTD  
OS Mus musculus (mouse)  
PN JP 2002514421-A/1  
PD 21-MAY-2002  
PF 07-MAY-1999 JP 2000548470  
PR 09-MAY-1998 GB 9809839.5  
PI JEAN YVES MARCEL PAUL BONNEFOY, SCOTT JAMES CROWE, JONATHAN PI  
HENRY ELLIS,  
PI NICHOLAS TIMOTHY RAPSON JEAN SHEARIN  
PC CL2N15/02.A61K39/395,C07K16/28,CL2N15/00  
CC Antibodies against CD23, derivatives thereof and therapeutic  
utilization  
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PH Key Location/Qualifiers  
FT CDS Location/Qualifiers  
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 utilization of the same.  
 ACCESSION BD232449  
 VERSION BD232449.1 GI:33042219  
 KEYWORDS JP 2002514421-A/33.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 415)  
 REFERENCE Bonnefoy, J.Y.M.P., Crowe, S.J., Ellis, J.H., Rapson, N.T. and  
 Shearin, J.  
 AUTHORS Antibodies against CD23, derivatives thereof and therapeutic  
 TITLE utilization of the same  
 JOURNAL Patent: JP 2002514421-A 33 21-MAY-2002;  
 GLAXO GROUP LTD  
 COMMENT OS Mus musculus (mouse)  
 PN JP 2002514421-A/33  
 PD 21-MAY-2002  
 PF 07-MAY-1999 JP 2000548470  
 PR 09-MAY-1998 GB 9809839.5  
 PI JEAN YVES MARCEL PAUL BONNEFOY, SCOTT JAMES CROWE, JONATHAN PI  
 HENRY ELLIS,  
 PI NICHOLAS TIMOTHY RAPSON, JEAN SHEARIN  
 PC C12N15/02, A61K39/395, C07K16/28, C12N15/00  
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 CC of the same  
 CC Key  
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 FT Location/Qualifiers  
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Query Match 100.0%; Score 415; DB 6; Length 415;

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 ACCESSION AX010600  
 VERSION AX010600.1 GI:9997411  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1  
 REFERENCE Bonnefoy, J.Y., Crowe, S.J., Rapson, N.T., Ellis, J.H. and Shearin, J.  
 AUTHORS Antibodies to cd23, derivatives thereof, and their therapeutic uses  
 TITLE Patent: WO 9958679-A 1 18-NOV-1999;  
 JOURNAL BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON  
 NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY  
 (GB); SHEARIN JEAN (US)  
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Query Match 100.0%; Score 415; DB 6; Length 415;

Best Local Similarity 100.0%; Pred. No. 4.6e-112;  
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DEFINITION Sequence 46 from Patent WO9958679.
ACCESSION AX010643
VERSION AX010643.1 GI:9997452
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)

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1. Bonney, J.Y., Crowe, S.J., Rapson, N.T., Ellis, J.H. and Shearin, J.
   Antibodies to cd23, derivatives thereof, and their therapeutic uses
   Patent: WO 9958679-A 46 18-NOV-1999; and their therapeutic uses
   BONNEY JOAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON
   NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY
   (GB); SHEARIN JEAN (US)
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RESULT 5
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DEFINITION Mus musculus cDNA clone MGC:25748 IMAGE:3991558, complete cds.
ACCESSION BC031470
VERSION BC031470.1 GI:21594582
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)

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1. (bases 1 to 1658)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
Schurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
JOURNAL MEDLINE
12477932
2 (bases 1 to 1658)
Strausberg, R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAX Plate: 30 Row: h Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
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source

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DB 152 TGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTTTGAGTGGCTTCTGAT 211

QY 188 GTCTTGGTCCGCTCTCCAGAGAGGGCTTGGTGGTGGCTGAAATAGATTGAA 247  
DB 212 GAATGGTCCGCTCTCCAGAGAGGGCTTGGTGGTGGCTGAAATAGATTGAG 271

QY 248 ATCTGATAATTAACAACATTAATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAG 307  
DB 272 ATCTGATAATTAACAACATTAATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAG 331

QY 308 AGATGATTCAAAGTCGTCTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGG 367  
DB 332 AGATGATTCAAAGTCGTCTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGG 391

QY 368 AGTTATTACTGTACAGATTTTCATAGACT 396  
DB 392 AATTATTACTGCACAAATGCTATGACT 420

RESULT 6  
AR302238  
LOCUS AR302238 453 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 14 from patent US 6541212.  
ACCESSION AR302238  
VERSION AR302238.1 GI:31690457  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 453)  
AUTHORS Reiter,R.E. and Witte,O.N.  
TITLE Methods for detecting prostate stem cell antigen protein  
JOURNAL Patent: US 6541212-A 14 01-APR-2003;  
FEATURES Location/Qualifiers  
source 1. .453  
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ORIGIN  
Query Match 74.8%; Score 310.4; DB 6; Length 453;  
Best Local Similarity 92.6%; Pred. No. 5.4e-81;  
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 35 CATGATTTTGGGCTGATTTTTTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGTAA 94  
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QY 95 GCTTGAAGGATCTGAGGAGGCTTGGTGAACCTGGAGATCCATGAACCTCTCTGTGT 154  
DB 66 GCTTGAAGGATCTGAGGAGGCTTGGTGAACCTGGAGATCCATGAACCTCTCTGTGT 125

QY 155 ACCCTCTGATTTACTTTTCAGTGGCTTCTGGATGCTTGGTCCGACAGTCTCCAGAGAA 214  
DB 126 ACCCTCTGATTTACTTTTCAGTGAATTAATCTGGATGATTTGGTCCGACAGTCTCCAGAGAA 185

QY 215 GGGGCTTGAAGTGGTGTGTAATTTAGATTTGAAATCTGATAATATGCAACATTTATGC 274  
DB 186 GGGGCTTGAAGTGGTGTGTAATTTAGATTTGAAATCTGATAATATGCAACATTTATGC 245

QY 275 GGAGTCTGTAAGGAGGATTCACCATCTCAGAGATGATTTCCAAAAGTCGTCTTACCT 334  
DB 246 GGAGTCTGTAAGGAGGATTCACCATCTCAGAGATGATTTCCAAAAGTCGTCTTACCT 305

QY 335 GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386  
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RESULT 7  
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LOCUS AR560594 453 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 14 from patent US 6756036.  
ACCESSION AR560594  
VERSION AR560594.1 GI:53972904  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 453)  
AUTHORS Reiter,R.E. and Witte,O.N.  
TITLE Methods for treating cancer using PSA antibodies and fragments thereof  
JOURNAL Patent: US 6756036-A 14 29-JUN-2004;  
FEATURES Location/Qualifiers  
source 1. .453  
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QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCAATAG---ACTGGGGCCAAAGGGA 408
Db 323 GAGCTGAAGACACTGGCATTTATTACTGTACGATTACGATGCTTACTTGGGGCCAAAGGGA 382
QY 409 CACTAGT 415
Db 383 CTCTGGT 389

RESULT 10
MMU05819
LOCUS Mus musculus BALB/c Ig mu heavy chain V-JH2 region mRNA, partial
DEFINITION cds.
ACCESSION U05819
VERSION U05819.1 GI:456279
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 405)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL 1 (bases 1 to 405)
AUTHORS Yong,T.J., Chan,S. and Ren,E.
TITLE Identification of a new VH J606 family member utilized in the
JOURNAL murine immune response to Hepatitis B surface antigen
REFERENCE 2 (bases 1 to 405)
AUTHORS Ren,E.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1994) Be-Chee Ren, Microbiology and W.H.O.
Immunology Center, National University of Singapore, Faculty of
Medicine, Singapore, 0511, Republic of Singapore
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Best Local Similarity 92.8%; Pred. No. 1.3e-76;
Matches 310; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 53 TTTTATTATGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGAGTCTGGAGG 112
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QY 173 CAGTGGCTACTGATGTCTTTGGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTTC 232
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QY 293 GTTCACCATCTCAAGAGATGATTCCAAAGTGTCTCTACCTGCAAAATGAACAGCTTAAAG 352
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QY 353 AGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 324 AACTGAAGACACTGGAAATTTATTACTGTACGGCT 357

RESULT 11
AB050074
LOCUS Mus musculus VH10G1 mRNA for anti-dsRNA (RDV-RNA) antibody, partial
DEFINITION cds.
ACCESSION AB050074
VERSION AB050074.1 GI:19909923
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 477)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL 1 (bases 1 to 477)
AUTHORS Kitagawa,Y., Matsumoto,T., Okuhara,E. and Shikata,E.
TITLE Immunogenicity of rice dwarf virus ribonucleic acid
JOURNAL Tohoku J. Exp. Med. 122 (4), 337-343 (1977)
MEDLINE 78034786
PUBMED 918970
REFERENCE 2
AUTHORS Kitagawa,Y.
TITLE anti-dsRNA (RDV-RNA) Ab VH region-VH10G1
JOURNAL Published Only in Database (2002)
REFERENCE 3 (bases 1 to 477)
AUTHORS Kitagawa,Y.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural
University, Biotechnology Institute; minami 2-2, Ogata, Akita
010-0444, Japan (E-mail:kitagawa@agri.akita-pu.ac.jp,
URL:www.akita-pu.ac.jp/, Tel:81-185-45-2026(ex.400),
Fax:81-185-45-2678)
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QY 113 AGCTTGGTGCAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTTT 172
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QY 233 TGAATTAGATTGAATCTGAATTAATTATGCAACACATTTATCGGAGTCTGTGAAGGAA 292
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QY 293 GTTCACCATCTCAAGAGATGATTCCAAAAGTCTCTCTACCTGCAATGAACAGCTTAAG 352
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QY 353 AGCTGAAGCAGTGGAGTTTATTACTGTACAGA 385
DB 324 GGCTGAAGACACTGGAATTTATTACTGCTCAGA 356

RESULT 14
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LOCUS
DEFINITION
Mouse Ig active H-chain (GAC1) mRNA linear ROD 27-APR-1993
68.2D8, partial cds.
ACCESSION M32044.1 GI:195969
VERSION M32044.1
KEYWORDS V-region; immunoglobulin heavy chain; processed gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 314)
AUTHORS Jarvis,C.D., Cannon,L.E. and Stavnezer,J.
TITLE Mouse antibody response to group A streptococcal carbohydrate
JOURNAL J. Immunol. 143 (12), 4213-4220 (1989)
MEDLINE 90079033
PUBMED 2512352
COMMENT Original source text: Mouse (strain A/J), cDNA to mRNA, anti-GAC
hybridoma 68.2D8.
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Best Local Similarity 95.2%; Pred. No. 1.2e-74;
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DB 2 GGGTCAGAGTGAAGTGAAGTTCGAGGAGTCTCGAGGAGGCTTGGTCAACCTGGAGGAT 61
QY 136 CCATGAACCTCTCTGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGGATCTTTGGG 195
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DB 62 CCATGAACCTCTCTGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGGATCTTTGGG 121
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DB 242 CCAAAAGTCTCTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTATT 301
QY 376 ACTGTACAGATTT 388
DB 302 ACTGCACAGATCT 314

MUSIGHRT
LOCUS
DEFINITION
Mouse Ig active H-chain (GAC1) mRNA linear ROD 27-APR-1993
68.3D3, partial cds.
ACCESSION M32045
VERSION M32045.1 GI:195970
KEYWORDS V-region; immunoglobulin heavy chain; processed gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 314)
AUTHORS Jarvis,C.D., Cannon,L.E. and Stavnezer,J.
TITLE Mouse antibody response to group A streptococcal carbohydrate
JOURNAL J. Immunol. 143 (12), 4213-4220 (1989)
MEDLINE 90079033
PUBMED 2512352
COMMENT Original source text: Mouse (strain A/J), cDNA to mRNA, anti-GAC
hybridoma 68.3D3.
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DB 2 GGGTCAGAGTGAAGTGAAGTTCGAGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGAT 61
QY 136 CCATGAACCTCTCTGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGGATCTTTGGG 195
DB 62 CCATGAACCTCTCTGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGGATCTTTGGG 121
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QY 316 CCAAAAGTCTCTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTATT 375
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QY 376 ACTGTACAGATTT 388
DB 302 ACTGCACAGATCT 314

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%  
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8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	284	68.4	1526	3	BC011342
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9	273.4	65.9	597	1	AA472093
10	269.2	64.9	955	5	BUS24174
11	266	64.1	625	8	BH021344
12	247.4	59.6	615	2	BE288134
13	244.4	58.9	713	4	BG967386
14	236	56.9	642	7	CF110127
15	223	53.7	904	2	BF133700
16	221.4	53.3	352	5	BY219846
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21	207.8	50.1	766	7	CO573418
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25 207.4 50.0 898 5 BQ711108  
26 205 49.4 355 2 BF116408  
27 204.6 49.3 422 5 BX439233  
28 202.6 48.8 565 5 BQ711793  
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30 202 48.7 429 5 BX360630  
31 201 48.4 636 6 CD684919  
32 200.2 48.2 900 5 BQ952498  
33 199.6 48.1 934 2 BF181593  
34 199.4 48.0 527 6 CD699968  
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36 198.8 47.9 948 2 BF663384  
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#### ALIGNMENTS

RESULT 1  
LOCUS BF163883  
DEFINITION 601772396F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3991558 5', mRNA linear EST 30-OCT-2000  
ACCESSION BF163883  
VERSION BF163883.1 GI:11044161  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 914)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: L1AM9204 row: p column: 23  
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Stem cell origin."  
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/clone\_lib="NCI\_CGAP\_Lu29"  
/notes="Organ: lung; Vector: pCMV-SPORT6; Site\_1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

#### FEATURES

source  
71.5%; Score 296.8; DB 2; Length 914;  
Best Local Similarity 90.8%; Pred. No. 5.4e-76;  
Matches 327; Conservative 0; Mismatches 32; Indels 1; Gaps 1;



DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MCC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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   Technologies. Note: This is a NCI CGAP Library."

RESULT 4	
LOCUS	BF119726
DEFINITION	548 bp mRNA linear EST 24-OCT-2000 601758583F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3992829 5', mRNA sequence.
ACCESSION	BF119726
VERSION	BF119726.1 GI:10958675
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 548)
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs@email.nih.gov">cgapbs@email.nih.gov</a> Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM9208 row: e column: 22  
 High quality sequence stop: 539.

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112	QY	GAGGCTTGGTGCAACTGGAGATCCATGAATACTCTCTGTGTGATGCTCTCGATTACTTT	171	
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232	QY	CTGAAATTAGATTGAAATCTGATAATTATGCAACACATTTATGCGGAGTCTGTGAAAGGGA	291	
204	Db	CTGAAATTAGATTGAAATCTAATAATTATGCAACACATTTATGCGGAGTCTGTGAAAGGGA	263	
292	QY	AGTTCAACATCTCAAGAGATGATTCCAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAA	351	
264	Db	GGTTCAACATCTCAAGAGATGATTCCAAAGTAGTGTCTACTCTGCAAAATGAACACTTAA	323	
352	QY	GAGCTGAAGACAGTGGAGTTTATTACTGTA-----CAGATTTCATAGACTGGGGCCAAAGG	406	
324	Db	GNGTTGAAGACNCTGGCATTTATTACTGTACCAAGCTGGGTTGCTTACTGGGGCCNAGG	383	
407	QY	GACACTAGT 415		
384	Db	GACTCTGGT 392		

## RESULT 5

BC011342	BC011342	1526 bp	mRNA	linear	HTC 13-FEB-2004
LOCUS	Mus musculus cDNA clone IMAGE:3992829, with apparent retained intron.				
DEFINITION	BC011342				
ACCESSION	BC011342.1	GI:15030173			
VERSION	HTC.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 1526)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,				

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketterman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kryzyski, M.I., Skalska, U., Smailus, D.E., Schnerf, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1526)

Direct Submission

Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabs-rc@mail.nih.gov](mailto:cgabs-rc@mail.nih.gov)

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: [angbcm.tmc.edu](mailto:angbcm.tmc.edu)

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegged, H., Kowitz, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 23 Row: n Column: 19

This clone has the following problem: retained intron.

#### FEATURES

Location/Qualifiers

1..1526

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="mix FVB/N, C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:3992829"

/tissue\_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."

/clone\_lib="NCI CGAP Mam5"

/lab\_host="DH10B"

/note="Vector: pCMV-SPORT6"

#### ORIGIN

Query Match 68.4%; Score 284; DB 3; Length 1526;  
Best Local Similarity 87.6%; Pred. No. 3.6e-72;  
Matches 324; Conservative 0; Mismatches 40; Indels 6; Gaps 1;

QY 52 TTTTCTTTTATGTTCTTTTAAAGGGGTCAGAGTGAAGCTTGAGGAGTCTGGAG 111  
DB 35 TATTCATAGTTTCTTTTAAAGGGTGCAGAGTGAAGTGTGAGTAGTCTGGAG 94

QY 112 GAGGCTTGTCGAACCTGGAGGATCCATGAACCTCTCTGTGAGCTCTGGATTACTT 171  
DB 95 GAGGCTTGTCGAACCTGGAGGATCCATGAACCTCTCTGTGAGCTCTGGATTACTT 154

QY 172 TCAGTGGCTACTGGATGTTCTTGGTCCGCGAGTCTCCAGAGAGGGCTTGAGTGGTTG 231  
DB 155 TCACCTAACTACTACATGAACCTGGTCCGCGAGTCTCCAGAGAGGGCTTGAGTGGTTG 214

QY 232 CTGAATAGTAGTTGAATCTGATATTATGCAACACATTATTCGCGAGTCTGTGAAGGGA 291  
DB 215 CTGAATAGTAGTTGAATCTGATATTATGCAACACATTATTCGCGAGTCTGTGAAGGGA 274  
QY 292 AGTTTCAACCTCTCAAGAGATGATTCCTCAAAAGTCGTCCTTACCTGCAAAATGAACAGCTTAA 351  
DB 275 GGTTCACCATCTCAAGAGATGATTCCTCAAAAGTAGTGTCTACCTGCAAAATGAACACTTAA 334  
QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTA-----CAGATTTCTAGACTGGGGCCAG 405  
DB 335 GAGTTGAAGACACTGGCATTTTATTACTGTACCAGGGCTGGGTTTCTTACTTGGGGCCAG 394  
QY 406 GCACACTAGT 415  
DB 395 GGACTCTGCT 404

#### RESULT 6

BB842247

LOCUS BB842247

DEFINITION BB842247 RIKEN full-length enriched, 6 days neonate spleen Mus musculus cDNA clone F430004H07 5', mRNA sequence.

ACCESSION BB842247

VERSION BB842247.1 GI:17042978

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 367)

AUTHORS Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sobabe, Y., Suzuki, H., Tagawa, A., Takahashi, P., Takaku-Akahita, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: [genome-res@gsc.riken.jp](mailto:genome-res@gsc.riken.jp), URL: <http://genome.gsc.riken.jp/>  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.  
e mouse tissues.  
Location/Qualifiers  
1..367  
/organism="Mus musculus"

#### FEATURES

Location/Qualifiers  
1..367  
/organism="Mus musculus"



ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 560)

NIH-MGC <http://mgs.nci.nih.gov/>. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D. Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLN9801 row: h column: 08

High quality sequence stop: 555.

Location/Qualifiers

1. .560

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:4219447"

/lab\_host="DH10B (T1 phage-resistant)"

/notes="Organ: colon; Vector: pCMV-SPORT6; Site: 1: Not I; Site 2: SalI. Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

FEATURES

source

1. .560

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:4219447"

/lab\_host="DH10B (T1 phage-resistant)"

/notes="Organ: colon; Vector: pCMV-SPORT6; Site: 1: Not I; Site 2: SalI. Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN

Query Match 66.6%; Score 276.2; DB 2; Length 560;

Best Local Similarity 90.0%; Pred. No. 5.4e-70;

Matches 307; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

52 TTTTATTTATGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGCTCGGAG 111

82 TATTATAGATTTTCTCTTAAAGGTGTCAGAGTGAAGTGAAGCTTGAGGCTCGGAG 141

112 GAGCTTGTGTCACCTCGAGGATCCATGAATCTCTCTGTAGCTCTCGGATTTACTT 171

142 GAGG-TTGGTGCACCTCGAGGATCCATGAATCTCTCTGTAGCTCTCGGATTTACTT 200

172 TCAGTGGCTACTGGATCTTTGGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 231

201 TTAGCAACTACTGGATGACCTGGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGATTG 260

232 CTGAATAGATTCGAATCTGATTAATATGCAACACATTTATGCGAGTCTGTGAAAGGGA 291

261 CTGAATTAATTAATGACATCTGATTAATTTTGAACACATTTATGCGAGTCTGTGATAGGA 320

292 AGTTTCAACATCTCAAGAGATGATTCCTCAAAAGTCTCTCTACCTGCAATGAACAGCTTAA 351

321 GTTTCACATCTCAAGAGATGATTCCTCAAAAGTCTCTCTACCTGCAATGAACAGCTTAA 380

352 GAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCTA 392.

381 GAGCTGAAGACACTGGCTTTTATTACTGTACGGGTCTACTA 421

RESULT 9

AA472093

LOCUS

DEFINITION

h10a05.r1 Soares mammary\_gland NbMMG Mus musculus cDNA clone IMAGE:875024 5', similar to gb:S65761 IG GAMMA-2 CHAIN C REGION (HUMAN); gb:L36938 Mus musculus germline immunoglobulin gamma constant region (MOUSE);, mRNA sequence.

ACCESSION

AA472093

VERSION

AA472093.1

GI:2200084

EST.

Mus musculus (house mouse)

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 597)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)

This clone is available royalty-free through LLNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

MGI:514504

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 440.

Location/Qualifiers

1. .597

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:875024"

/sex="male"

/tissue type="mammary gland"

/dev stage="4 weeks"

/lab\_host="DH10B"

/clone\_lib="Soares mammary\_gland NbMMG"

/note="Organ: mammary gland; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dt) primer [5', TGTTACCAATCTGAGTGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

FEATURES

source

1. .597

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:875024"

/sex="male"

/tissue type="mammary gland"

/dev stage="4 weeks"

/lab\_host="DH10B"

/clone\_lib="Soares mammary\_gland NbMMG"

/note="Organ: mammary gland; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dt) primer [5', TGTTACCAATCTGAGTGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 65.9%; Score 273.4; DB 1; Length 597;

Best Local Similarity 80.8%; Pred. No. 3.7e-69;

Matches 332; Conservative 0; Mismatches 76; Indels 3; Gaps 1;

8 ACAGTTACTCAGACACAGGACCTCACCATGATTTTGGCTGATTTTTTTTATTGTTCT 67

32 ACACAGATAGAACATCCACATGACTTGGGACTGAACTGTACTCATAGTTTCT 91

68 TTTTAAAGGGTCCAGAGTGAAGCTTGAGAGTCTGGAGGCTGGTGGCAACC 127

92 CTTTAAAGGGTCCAGAGTGAAGGAAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGGCAACC 151

128 TGGAGGATCCATGAACACTCTCTGTAGCTCTGATTTTACTTTTTCAGTGGCTTGGAT 187

152 TGGAGGATCCATAAAACTCTCTGTGTTCTCTGTTGATTCATTTTCAGTGACGCTGGAT 211

188 GTCTTGGGTCGCGAGCTCTCCAGAGAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAA 247

212 GGACTGGTCCGCGAGCTCTCCAGAGAGGGGACTTGGTGGTGGTTGCTGAAGATTAGACAA 271

248 ATCTGTAATATTATGCAACACATTTATCGGAGTCTGTGAAAGGGAGTTTCAACATCTCAAG 307

272 AGCTAGTAATATTATGCAACACATTTATCGTGGTTTGTGAGAGGAGGTTTCAACATCTCAAG 331

308 AGATGATTCACAAAGCTGCTCTCTACCTGCAAAATGAACAGCTTAAAGAGCTGAACAGCTGG 367



Db AGATGATTCCAAAATAGTGTCTACCTGCAAAATGAACACCTTAAAGTCTGAAGACACCGG 391

QY AGTTTATTACTGTAC---AGATTTTCATAGACTGGGGCCAAAGGCACCTAGT 415

Db CATTTATTCTGTACTAGTGGGACATAGACTGGGGCCAAAGGCCTTAGT 442

RESULT 10	BU524174	LOCUS	BU524174	955 bp	mRNA	linear	EST 13-SEP-2002
DEFINITION	AGENCOURT 10126522 NCI CGAP Co24						Mus musculus cDNA clone
							IMAGE:6530936 5', mRNA sequence.

ACCESSION	BU524174
VERSION	BU524174.1
KEYWORDS	GI:22834613
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 955)
JOURNAL	NIH-MGC <a href="http://mgc.mci.nih.gov/">http://mgc.mci.nih.gov/</a> .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph. D.

COMMENT	<p>Contact: Robert Strausberg, Ph.D.  Email: cgaaps-r@mail.nih.gov</p> <p>Tissue Procurement: The Cepko Laboratory</p> <p>CDNA Library Preparation: Life Technologies, Inc.</p> <p>CDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)</p> <p>DNA Sequencing by: Agencourt Bioscience Corporation</p> <p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a></p> <p>Plate: LLAM14133 row: h column: 08</p> <p>High quality sequence stop: 561.</p>
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FEATURES
source
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Location/Qualifiers
/organism="Mus musculus"
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/db_xref="taxon:10090"
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."

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Query Match	64.9%	Score 269.2;	DB 5;	Length 955;
Best Local Similarity	87.3%	Pred. No. 7.3e-68;		
Matches 295;	Conservative	0;	Mismatches 43;	Indels 0;
			Gaps	0;

52	QY	TTTTTTTTATGTTCTTTTAAAAAGGGGTCCAGAGTGAAGTGAAGCTTTGAGAGGAGTCTCGAG	111
53			
54			
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67			
68			
69			
70	DB	TATTCATAGTATTTTCTCTTAAAAAGGTCCAGAGTGAAGTGAAGCTTTGAGAGGAGTCTCGAG	129
71			
72			
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78			
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112	QY	GAGGCTTGGTGCACACCTGGAGGATCCATGAAACTCTCCTGTGTAGCTCTCGGATTTTAATT	171
113			
114			
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120			
121			
122			
123			
124			
125			
126			
127			
128			
129			
130	DB	GAGGCTTGGTGCACACCTGGAGGATCCAGGAAACTCTCCTGTGTGCTCTTGGATTCACTT	189
131			
132			
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169			
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171			
172	QY	TCAGTGCTACTGGATGTCCTTGGGTCCGCAGTCTCCAGAGAAAGGGCTTTGAGTGGGTG	231
173			
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Qy	352	GAGCTGAGACACGTGGAGTTTATTATCTGTACAGATTTC	389
Db	370	GAGCTGAAGACACTGGCAATTATTCTGTGCCAGGTTTC	407

RESULT	11
LOCUS	BH021344
DEFINITION	BH021344 625 bp DNA linear GSS 27-JUN-2001 CT77-463K16-SP6-R1734 CitbCJ7 mouse BAC library Mus musculus genomic clone CT77-463K16 similar to VhJ606 family gene, genomic survey sequence.
ACCESSION	BH021344
VERSION	BH021344.1
KEYWORDS	GI:14572403
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE	1 (bases 1 to 625) Chevallard, C., Mauhar, A., Herring, C.D. and Riblet, R. A 1.5 Mb 129 mouse BAC contig spanning the Ch and proximal Vh regions of the Igh* locus
JOURNAL	Unpublished (2001)
COMMENT	Other GSSs: CT77-463K16-T7-R1737 Contact: Riblet R

Genetics  
Torrey Pines Institute for Molecular Studies  
3550 General Atomics Ct., San Diego, CA 92121, USA  
Tel: 858 455 3762  
Fax: 858 455 3739  
Email: [rriblet@tpims.org](mailto:rriblet@tpims.org)  
Direct cycle sequence.  
Seq primer: SP6: CAGCTATGACCATGATTACG  
Class: BAC ends.

```

FEATURES
source
CLASS: BAC ends.
Location/Qualifiers
1. 625
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129S3/SvimJ"
/db_xref="taxon:10090"
/clone="CT7-463K16"
/cell_type="Embryonic stem cell line"
/cell_line="CJ7"
/lab_host="HS996 (modified DH10B)"
/clone_lib="ClbCJ7 mouse BAC library"
/notes="Vector: pBeloHAC1; Site_1: HindIII; Available from
Research Genetics (www.ResGen.com); note - strain of
origin actually 129S1/Sv, immediate ancestor of
129S3/SvimJ; for description of 129 substrains see Simpson
et al. (1997) Nature Genetics 16: 19-27 and
http://www.informatics.jax.org/mgihome/nomen/strain_129.sh
tml"

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ORIGIN		Cm1*	
Query Match	64.1%	Score 266;	DB 8; Length 625;
Best Local Similarity	94.8%	Pred. No. 5,6e-67;	
Matches 275;	Conservative	0; Mismatches 15;	Indels 0; Gaps 0;
Qy	93	AAGCTTGAGGAGCTGGAGGAGCGCTTGTCGAACCTGGAGGATCCATGAAACTCTCTCT	152
Db	1	AAGCTTGAGGAGCTGGAGGAGCGCTTGTCGAACCTGGAGGATCCATGAAACTCTCTCT	60
Qy	153	GTAGCCTCTGGATTTACTTTTCAGTGGCTACTGGATGTCTTGGGTCGGCCAGTCTCCAGAG	212
Db	61	GTGGCTCTGGATTCACATTTTCAGTAACTACTCGGATGAACCTGGGTCGGCCAGTCTCCAGAG	120
Qy	213	AAGGGCTTGAGTGGGTTGCTGAAATTCAGATTGAAATCTGATAATTATGCAACACATTAT	272
Db	121	AAGGGCTTGAGTGGGTTGCTGAAATTCAGATTGAAATCTAATAATTATGCAACACATTAT	180
Qy	273	GGGGAGCTCTGTGAAAGGGGAAGTTTCACCATCTCAAGAGATGATTCCAAAGAGTCGTCTCTAC	332

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Db 181 GCGAGCTCTGTGAAGGGAGTTTACCATCTCAAGAGATGATTCACAAAAGTAGTGTCTAC 240
QY 333 CTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTGAAGAGCTTAATTAAGTCTAC 382
Db 241 CTGCAATGAACAACTTAAGAGCTGAAGAGCTGAAGAGCTTAATTAAGTCTAC 290

RESULT 12
BE288134 615 bp mRNA linear EST 26-OCT-2000
LOCUS 601095304F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489841 5',
DEFINITION mRNA sequence.
ACCESSION BE288134
VERSION BE288134.1 GI:9167624
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 615)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8531 row: h column: 02
High quality sequence stop: 583.
Location/Qualifiers
FEATURES
source
1..615
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3489841"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN
Query Match 59.8%; Score 247.4; DB 2; Length 615;
Best Local Similarity 78.5%; Pred. No. 1.7e-61;
Matches 296; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 8 ACAGTTACTCAGCACACAGGACCTCACCATTGGATTTTGGCTCATTTTATTTTATTTCT 67
Db 19 AAGTGACACAGATCATTCATCAATGTTACTTGGAGCTGAGCTGTGATTCATGTTTCT 78
QY 68 TTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAAGAGCTTGAAGAGGCTTGGTGCAACC 127
Db 79 CTTTAAAGGTGTCAGTGTGAGGTGAAGTGAAGCTGAGATGAGCTGGAGGAGGCTTGGTGCAACC 138
QY 128 TGAGGATCCATGAAGTCTCTGTAGCTCTGAGCTTCACTTTTCACTTCACTTCACTTCACT 187
Db 139 TGGGAGGCCCATGAAGTCTCTGTGTGTCTGAGTTCATTTTGGTGAATCTGGAT 198
QY 188 GTCTTGGTCCGCGAGTCTCCAGAGAGGGGCTTGAAGTGGTGTGCTGAATTAAGATTGA 247
Db 199 GAAGTGGTCCGCGAGTCTCCAGAGAGGAGTGGAGTGGTATTCACAAATTAGAACA 258
QY 248 ATCTGATTAATTGCAACACATTATGCGGAGTCTGTGAAGAGGAGTTTCAACCATCTCAAG 307

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Db 259 ACCTTATAATTATGAACATATATTTCAGATTCTGTGAAGGCAGATTCCACCATCTCAAG 318
QY 308 AGATGATTCCTCAAAAGCTGCTTACTTCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGG 367
Db 319 AGATGATTCCTCAAAAGCTGCTTACTTCTGCAATGAACAACTTAAGACCTGAAGAGCATGG 378
QY 368 ACTTTATTACTGTACAG 384
Db 379 TATCTATTATTGTACAG 395

RESULT 13
BG967386 713 bp mRNA linear EST 12-JUN-2001
LOCUS 602833514F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988282 5',
DEFINITION mRNA sequence.
ACCESSION BG967386
VERSION BG967386.1 GI:14355023
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 713)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1000 row: k column: 03
High quality sequence stop: 703.
Location/Qualifiers
FEATURES
source
1..713
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4988282"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 Kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 58.9%; Score 244.4; DB 4; Length 713;
Best Local Similarity 85.3%; Pred. No. 1.3e-60;
Matches 285; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 52 TTTTATTATTCTTTCTTTTAAAGGGTCCAGAGTGAAGCTTGAAGGAGCTCTGGAG 111
Db 79 TATTCATAGTTTTTCTTTTAAAGGGTCCAGAGTGAAGCTTGAAGGAGCTCTGGAG 138
QY 112 GAGGCTTGTGTCAACTCTGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTTTACTT 171
Db 139 GAGGCTTGTGTCAACTCTGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTTTACTT 198
QY 172 TCAGTGGCTTACTTGGATGTTTGGGTCCGCGAGCTCTCCAGAGAGGGGCTTGAAGTGGGTTG 231
Db 199 TCACAACTACTTGGATGAAGTGGGTCCGCGAGCTCTCCAGAGAGGGGCTTGAAGTGGGTTG 258
QY 232 CTGAATTAAGATTGAATCTGATTAATGAACACATTATCGGAGTCTGTGGAAGGGA 291
Db 259 CTGAAGTTAGATTGAATCTAATTAATTATGCCACACATTATCGGAGTCTGTGGAAGGGA 318

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QY 292 AGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCGTCTCTACCTCCAAAT---GAACAGCT 348  
 |||||  
 Db 319 GGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCGTCTCTACCTCCAAATTTGAACCAACT 378  
 |||||  
 QY 349 TAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382  
 |||||  
 Db 379 TAAGAACTGGAAGACACTGGGTTTATATCTGTGC 412  
 |||||

RESULT 14  
 CFI10127 642 bp mRNA linear EST 23-JUL-2003  
 LOCUS Shultzomicao3378 Rat lung airway and parenchyma cDNA libraries  
 DEFINITION Rattus norvegicus cDNA clone Contig298 5', mRNA sequence.  
 CFI10127  
 ACCESSION CFI10127.1 GI:33165670  
 VERSION EST.  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 642)  
 REFERENCE Shultz, M.A., Zhang, L., Gu, Y.-Z., Baker, G.L., Fannuchi, M.V.,  
 AUTHORS Padua, A.M., Gurske, W.A., Morin, D., Penn, S.G., Jovanovich, S.B.,  
 Plopper, C.G. and Buckpitt, A.R.  
 TITLE Gene expression analysis in response to lung toxicants: I.  
 JOURNAL Sequencing and microarray development  
 COMMENT Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)  
 Contact: Shultz MA  
 Dept. of Molecular Biosciences, School of Veterinary Medicine  
 University of California, Davis  
 1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA  
 Tel: 530 752 0793  
 Fax: 530 752 4698  
 Email: mashultz@ucdavis.edu  
 Average Phred score is 20 or better. All poor quality data (Phred <  
 20) and vector/linker sequence has been removed.  
 High quality sequence stop: 642.

## FEATURES

Location/Qualifiers  
 1..642  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="Contig298"  
 /sex="male"  
 /tissue\_type="airway or parenchyma"  
 /dev\_stage="adult"  
 /clone\_lib="Rat lung airway and parenchyma cDNA libraries"  
 /note="Organ: lung; Vector: pGEM-11zf(-); Site 1: Eco RI;  
 Site 2: Not I; mRNA was isolated from microdissected rat  
 lung airways and parenchyma tissues."

## ORIGIN

Query Match 56.9%; Score 236; DB 7; Length 642;  
 Best Local Similarity 81.9%; Pred. No. 3.9e-58;  
 Matches 272; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
 QY 52 TTTTATTTATGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111  
 |||||  
 Db 99 TTTTATTTGTCATTTTAAAGGTGTCTTGTGTGAGGTGAAGTGAAGTGAAGTCTGGG 158  
 |||||  
 QY 112 GAGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 171  
 |||||  
 Db 159 GAGGTTTGGTACACCTGGAGTGTCCCTGAAACTCTCTGTGCAACCTCTGGATTCACTT 218  
 |||||  
 QY 172 TCAGTGGCTACTGATGTTCTTGGGTCCGCAAGTCTCCAGAGAGGGGCTTGAGGGTTG 231  
 |||||  
 Db 219 TCAGTAACCTACTGATGAATGGGTTCGACAGTCTCCAGGGAAGGGGTTAGAATTGGTTG 278  
 |||||  
 QY 232 CTGAAATTTAGATTGAAATCTGATAATTATGCAACATATTATGCGGAGTCTGTGAAAGGA 291  
 |||||

Db 279 CTGAAATTTAGAACCAACCTCTATAATTATGCAACATATATGGGAGTCTAGTGAAGGCA 338  
 |||||  
 QY 292 AGTTTCACCTCTCAAGAGATGATTCCTCAAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAA 351  
 |||||  
 Db 339 GATTTCACCTCTCAAGAGATGATTCCTCAAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAA 398  
 |||||  
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 383  
 |||||  
 Db 399 GATCTGAAGATACTGGCATTATTACTGTACA 430  
 |||||

RESULT 15  
 BFI33700 904 bp mRNA linear EST 24-OCT-2000  
 LOCUS 601778606F1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4006801 5',  
 DEFINITION mRNA sequence.  
 BFI33700  
 ACCESSION BFI33700.1 GI:10972740  
 VERSION EST.  
 KEYWORDS Mus musculus  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 904)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgabbs@mail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM9238 row: 1 column: 02  
 High quality sequence stop: 680.

## FEATURES

Location/Qualifiers  
 1..904  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="CZECH II"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4006801"  
 /tissue\_type="tumor, metastatic to mammary"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_Lu30"  
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; transgenic model WNT-1, expression driven by  
 MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo  
 dt. Library constructed by Life Technologies.  
 Investigator providing samples: Gilbert Smith, NIH"

## ORIGIN

Query Match 53.7%; Score 223; DB 2; Length 904;  
 Best Local Similarity 79.0%; Pred. No. 2.8e-54;  
 Matches 290; Conservative 0; Mismatches 75; Indels 2; Gaps 2;  
 QY 10 AGTTACTCAGCACACAGGACCTCACCATGGATTTTGGGCTGATTTTTTTTATTGTTCTTT 69  
 |||||  
 Db 2 AGTGACACAGACCATTCACCATGTACTTGGGACTGAGCTGTGATTATCATGGTTTTTCTCT 61  
 |||||  
 QY 70 TAAAGGGGTCCAGAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACCTG 129  
 |||||  
 Db 62 TAAAGGTGTCCAGTGTGAGGTGAAGCTGATCGTCTGGTGGAGGCTTGGTGCACCTG 121  
 |||||  
 QY 130 GAGGATCCATGAACCTCTCTGTGTAGCCCTCTGGATTACTTTTCAGTGGCTACTGGATGT 189  
 |||||  
 Db 122 GGAGGTCCATGAACCTCTCTGTGT-GCCTCTGGATTCTTTTAGTGACTA-TGGATGA 179  
 |||||  
 QY 190 CTTGGGTCCGCCAGTCTCCAGAGAGGGGCTTGAGTGGGTGTGTAATTTAGATTGAAAT 249  
 |||||



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 233.448 Seconds  
(without alignments)  
10523.523 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 415  
Sequence: 1 agcgttacgtactcagc.....tggggccaaggacactagt 415

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	415	100.0	415	3	Aaz34745 Mouse ant
2	310.4	74.8	453	4	Abk09984 Mouse hea
3	310.4	74.8	453	5	Aaf27975 Murine PS
4	301.4	72.6	1774	2	Aaz20419 Antibody
5	293.6	70.7	496	2	Aav71155 Coding st
6	293.6	70.7	497	2	Aaq08605 Br-3 Heav
7	293.6	70.7	497	2	Aat43437 MAb Br-3
8	293.6	70.7	497	8	Abx79231 DNA encod
9	289.4	69.7	480	2	Aaq85388 MAB.4197X
10	282.2	68.0	469	2	Aaq12060 Sequence
11	282.2	68.0	469	2	Aaq12016 Sequence
12	272	65.5	357	2	Aav22331 Nucleic a
13	271.6	65.4	856	5	Aac90472 Antibody
14	270.2	65.1	408	13	Aad59058 Anti-K88
15	269.8	65.0	1979	2	Aaq85386 Anti-cata
16	269.4	64.9	403	2	Aaq62750 Murine Br
17	269.4	64.9	403	2	Aaq62775 Murine Br
18	269.2	64.9	445	10	Adf53232 HAb18 rel
19	268.6	64.7	498	2	Aaq11969 Sequence
20	267.8	64.5	360	2	Aat58263 Lead bind

21	267.2	64.4	366	3	AAA38896
22	267.2	64.4	374	13	ADR59064
23	265.4	64.0	765	6	AAg97143
24	265.2	63.9	809	2	AAQ34841
25	265	63.9	350	2	AAQ31971
26	263.6	63.5	899	5	AAC90471
27	263	63.4	403	2	AAQ62791
28	262.4	63.2	768	6	AAg97139
29	262.4	63.2	1509	6	AAg97147
30	260.6	62.8	5227	2	AAT79537
31	260.2	62.7	789	12	ADG16988
32	259.2	62.5	348	8	ACD17061
33	259.2	62.5	348	8	ACD17060
34	259.2	62.5	348	8	ACC69834
35	259.2	62.5	348	8	ACC69835
36	259.2	62.5	348	12	ADQ90876
37	259.2	62.5	348	12	ADQ90877
38	259	62.4	342	3	AAA38900
39	258.2	62.2	351	12	ADG16990
40	256.6	61.8	357	2	AAT58262
41	256.6	61.8	810	8	ACD17048
42	256.6	61.8	810	8	ACD17049
43	256.6	61.8	810	8	ACC69823
44	256.6	61.8	810	8	ACC69822
45	256.6	61.8	810	12	ADQ90804

#### ALIGNMENTS

RESULT 1

AAZ34745

ID AAZ34745 standard; cDNA; 415 BP.

AC AAZ34745;

XX

DT 15-FEB-2000 (first entry)

XX

DE Mouse anti-CD23 MAb C11 heavy chain variable region cDNA.

XX

KW CD23; FCER1; IGE receptor; monoclonal antibody; C11; mouse;

KW monoclonal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX therapy; ds.

OS Mus musculus.

XX

FH Key Location/Qualifiers

CDS 3..413

FT /\*tag= a

XX

PN WO9958679-A1.

XX

PD 18-NOV-1999.

XX

PF Abx79231 DNA encod

XX

PR Aaq85388 MAB.4197X

XX

PR Aaq12060 Sequence

XX

PR Aaq12016 Sequence

XX

PA Aav22331 Nucleic a

XX

PA Aac90472 Antibody

XX

PI Aad59058 Anti-K88

XX

PI Aaq85386 Anti-cata

XX

XX Aaq62750 Murine Br

XX

DR Aaq62775 Murine Br

XX

DR Adf53232 HAb18 rel

XX

DR Aaq11969 Sequence

XX

PT Aat58263 Lead bind

XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,

PT diabetes, multiple sclerosis and psoriasis.

XX Claim 16; Fig 1; 81pp; English.

XX This DNA sequence encodes the heavy chain variable region (VH) of murine  
PS anti-CD23 (FCERII) monoclonal antibody C11. The invention provides  
PS altered antibodies, such as chimeric or humanised antibodies (see  
CC AAZ34747 and AAZ34748), which comprise sufficient of the amino acid  
CC sequences of the C11 light and heavy chain complementarity determining  
CC regions (see AY32254-59) to render them capable of binding to the CD23  
CC type II molecule expressed on haematopoietic cells. The antibodies are  
CC used to block soluble CD23 formation in human therapy, for the treatment  
CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
CC malignancies (claimed). They are also useful for studying interactions  
CC between CD23 and various ligands and determining the binding agents  
XX

XX Sequence 415 BP; 111 A; 76 C; 110 G; 118 T; 0 U; 0 Other;

Query Match 100.0%; Score 415; DB 3; Length 415;  
Best Local Similarity 100.0%; Pred. No. 1.3e-114;  
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTTTACAGTTTACTCAGCACAGGACCTCACCATGATTTTGGGCTGATTTTAA 60  
Db 1 AAGCTTTTACAGTTTACTCAGCACAGGACCTCACCATGATTTTGGGCTGATTTTAA 60  
QY 61 TTGTTCTTTTAAAGGGGTCACAGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTGG 120  
Db 61 TTGTTCTTTTAAAGGGGTCACAGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTGG 120  
QY 121 TGCACCTGGAGGATCCATGAATCTCCCTGCTGAGCTCTGATTTTACATTTTCAGTGGCT 180  
Db 121 TGCACCTGGAGGATCCATGAATCTCCCTGCTGAGCTCTGATTTTACATTTTCAGTGGCT 180  
QY 181 ACTGGATGCTTGGGTCGGCAGTCTCCAGAGAGGGGCTTGAGTGGGTTGCTGAATTA 240  
Db 181 ACTGGATGCTTGGGTCGGCAGTCTCCAGAGAGGGGCTTGAGTGGGTTGCTGAATTA 240  
QY 241 GATTGAATCTGATAATTATGCAACACATTTATGCGGAGTCTGTGAAGGGAAGTTTACCA 300  
Db 241 GATTGAATCTGATAATTATGCAACACATTTATGCGGAGTCTGTGAAGGGAAGTTTACCA 300  
QY 301 TCTCAAGAGATGATTCACAAAGTCTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAG 360  
Db 301 TCTCAAGAGATGATTCACAAAGTCTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAG 360  
QY 361 ACAGTGGAGTTTATTACTGTACAGATTTTATAGACTGGGCGCAAGGACACTAGT 415  
Db 361 ACAGTGGAGTTTATTACTGTACAGATTTTATAGACTGGGCGCAAGGACACTAGT 415

RESULT 2

ABK09984  
ID ABK09984 standard; DNA; 453 BP.

XX AC ABK09984;

XX 21-MAY-2002 (first entry)

XX Mouse heavy chain variable domain region of PSMA antibody 2H9 gene.

XX Mouse; prostate stem cell antigen; PSMA; gene; antibody; immunogen;  
KW prostate cancer; bladder cancer; pancreatic cancer; immunoconjugate;  
KW PSMA-associated cancer; heavy chain variable domain region; PSMA antigen;  
KW PSMA antibody 2H9; ds.

XX Mus sp.

XX Key Location/Qualifiers  
FH 1. .453  
FT /\*tag= a  
FT /partial  
FT /product= "Mouse PSMA antibody 2H9"  
FT /note= "This sequence lacks both a start and stop codon"  
FT misc\_feature 133. .162  
FT /\*tag= b  
FT /note= "Complementarity determining region 1 (CDR1)"  
FT misc\_feature 205. .261  
FT /\*tag= c  
FT /note= "Complementarity determining region 2 (CDR2)"  
FT misc\_feature 358. .375  
FT /\*tag= d  
FT /note= "Complementarity determining region 3 (CDR3)"  
PN US2001055751-A1.  
PD 27-DEC-2001.  
XX 03-MAY-2000; 2000US-00564329.  
XX 10-MAR-1997; 97US-0228816P.  
PR 12-JAN-1998; 98US-0071141P.  
PR 13-FEB-1998; 98US-0074675P.  
PR 10-MAR-1998; 98US-00038261.  
PR 02-DEC-1998; 98US-00203939.  
PR 21-DEC-1998; 98US-0113230P.  
PR 17-FEB-1999; 99US-00251835.  
PR 16-MAR-1999; 99US-0124658P.  
PR 25-MAY-1999; 99US-00318503.  
PR 20-JUL-1999; 99US-00359326.  
XX (REIT/) REITER R E.  
PA (WITT/) WITTE O N.  
PA (SAFF/) SAFFRAN D C.  
PA (JAKO/) JAKOBOVITS A.  
XX Reiter RE, Witte ON, Saffran DC, Jakobovits A;  
XX WPI; 2001-159478/16.  
DR P-PSDB; AAU76696.  
XX Antibodies binding to prostate stem cell antigen inhibit the growth of  
PT cancer cells and are used to detect and treat prostate, pancreatic or  
PT bladder cancers.  
XX Example 21; Fig 60; 127pp; English.

The present invention relates to new antibodies that specifically bind a novel prostate stem cell antigen (PSCA), which is widely over-expressed across all stages of prostate cancer. The antibodies of the invention are useful to kill tumour cells expressing PSCA and as PSCA expression is observed in prostate tumour cells and in other human cancers, particularly bladder and pancreatic carcinomas, the antibodies are useful therapeutically to treat these diseases. In particular, monoclonal antibodies can be administered to subjects suffering from PSCA-associated cancers, e.g. prostate, bladder or pancreatic cancer, to inhibit the cancer and prolong the subject's life. The antibodies can be combined with a therapeutic agent in immunoconjugates useful to treat subjects suffering from malignant diseases, characterised by cells having PSCA antigen on the cell surface e.g. cancers, by killing the cells. The antibodies and immunoconjugates may also be included with a carrier in pharmaceutical compositions useful to kill human cells expressing PSCA antigen on the cell surface. The antibodies are also useful diagnostically to detect cancers, especially prostate cancer, to isolate prostate cancer cells e.g. to enable culture growth to evaluate candidate therapeutic compounds, assist in identification of rare genes associated with prostate cancer, and to isolate and purify PSCA and PSCA homologues. The present nucleic acid sequence encodes the mouse heavy chain variable

CC domain region of the PSA monoclonal antibody 2H9 of the invention  
 XX  
 SQ Sequence 453 BP; 115 A; 93 C; 122 G; 123 T; 0 U; 0 Other;  
 Query Match 74.8%; Score 310.4; DB 4; Length 453;  
 Best Local Similarity 92.6%; Pred. No. 4.4e-83;  
 Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
 QY 35 CATGGATTGGGCTGATTTTTTTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGTAA 94  
 DB 6 CTTCCGGTTGAGCTGGGTTTTTATTTATTTGTTCTTTTAAAGGGTCCGAGTGAAGTAA 65  
 QY 95 GCTTGAGAGTCTGAGAGAGCTTTGTCGAACCTGGAGGATCCATGAATCTCTCTGTGT 154  
 DB 66 GCTTGAGAGTCTGAGAGAGCTGGGTGCAACCTGGAGGATCCATGAATCTCTCTGTGT 125  
 QY 155 AGCTCTGGATTACTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214  
 DB 126 AGCTCTGGATTACTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185  
 QY 215 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAATCTGATAATTATGCAACACATTATGC 274  
 DB 186 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAATCTGATAATTATGCAACACATTATGC 245  
 QY 275 GGAGTCTGTGAAGGGAGTTTCAACATCTCAAGAGATGATTTCCAAAAGTCTCTCTACCT 334  
 DB 246 GGAGTCTGTGAAGGGAGTTTCAACATCTCAAGAGATGATTTCCAAAAGTCTCTCTACCT 305  
 QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTGAAGAGCTGAAGAGCT 386  
 DB 306 GCAAAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTGAAGAGCTGAAGAGCT 357

RESULT 3  
 AAF27975  
 ID AAF27975 standard; DNA; 453 BP.  
 XX  
 AC AAF27975;  
 XX  
 DT 08-MAY-2001 (first entry)  
 XX  
 DE Murine PSA antibody 2H9 H chain V region coding sequence.  
 XX  
 KW Prostate stem cell antigen; PSA; human; mouse; prostate cancer;  
 KW diagnosis; treatment; chromosome 8q24.2; ds.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200105427-A1.  
 XX  
 PD 25-JAN-2001.  
 XX  
 PF 20-JUL-2000; 2000WO-US019967.  
 XX  
 PR 20-JUL-1999; 99US-00359326.  
 PR 03-MAY-2000; 2000US-00564329.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (UROC-) UROGENESIS.  
 XX  
 PI Reiter R, Witte O, Saffran DC, Jakobovits A;  
 XX  
 DR WPI; 2001-159478/16.  
 DR P-PSDB; AAB35292.  
 XX  
 XX Antibodies binding to prostate stem cell antigen inhibit the growth of  
 PT cancer cells and are used to detect and treat prostate, pancreatic or  
 PT bladder cancers.  
 XX  
 PS Example 21; Fig 60; 229pp; English.  
 XX  
 CC The present invention describes a method of treating cancer associated  
 CC with prostate stem cell antigen (PSCA) by administering an antibody which

CC selectively binds to PSCA and inhibits the growth of the cancer cells.  
 CC The PSCA gene is found on human chromosome 8q24.2. The invention provides  
 CC the human and murine PSCA protein and coding sequences, which can be used  
 CC not only in the treatment of, but also in detection and prognosis of  
 CC prostate cancer  
 XX  
 SQ Sequence 453 BP; 115 A; 93 C; 122 G; 123 T; 0 U; 0 Other;  
 Query Match 74.8%; Score 310.4; DB 5; Length 453;  
 Best Local Similarity 92.6%; Pred. No. 4.4e-83;  
 Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
 QY 35 CATGGATTGGGCTGATTTTTTTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGTAA 94  
 DB 6 CTTCCGGTTGAGCTGGGTTTTTATTTATTTGTTCTTTTAAAGGGTCCGAGTGAAGTAA 65  
 QY 95 GCTTGAGAGTCTGAGAGAGCTTTGTCGAACCTGGAGGATCCATGAATCTCTCTGTGT 154  
 DB 66 GCTTGAGAGTCTGAGAGAGCTGGGTGCAACCTGGAGGATCCATGAATCTCTCTGTGT 125  
 QY 155 AGCTCTGGATTACTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214  
 DB 126 AGCTCTGGATTACTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185  
 QY 215 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAATCTGATAATTATGCAACACATTATGC 274  
 DB 186 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAATCTGATAATTATGCAACACATTATGC 245  
 QY 275 GGAGTCTGTGAAGGGAGTTTCAACATCTCAAGAGATGATTTCCAAAAGTCTCTCTACCT 334  
 DB 246 GGAGTCTGTGAAGGGAGTTTCAACATCTCAAGAGATGATTTCCAAAAGTCTCTCTACCT 305  
 QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTGAAGAGCTGAAGAGCT 386  
 DB 306 GCAAAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTGAAGAGCTGAAGAGCT 357

RESULT 4  
 AAZ20419  
 ID AAZ20419 standard; cDNA; 1774 BP.  
 XX  
 AC AAZ20419;  
 XX  
 DT 19-NOV-1999 (first entry)  
 XX  
 DE Antibody ABX-CBL heavy chain coding sequence.  
 XX  
 KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 58..1770  
 FT /\*tag= a  
 XX  
 PN WO9945031-A2.  
 XX  
 PD 10-SEP-1999.  
 XX  
 PF 03-MAR-1999; 99WO-US004583.  
 XX  
 PR 03-MAR-1998; 98US-00034607.  
 PR 03-FEB-1999; 99US-00244253.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
 XX  
 DR WPI; 1999-540816/45.

DR P-PSDB; AAY39451.  
XX New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX  
XX  
XX Disclosure; Page 57-58; 245pp; English.  
XX  
XX This sequence encodes the heavy chain of the antibody ABX-CXL. The  
CC invention relates to a monoclonal antibody (MAB) with an isotype that  
CC fixes complement and a variable region that binds to the epitope on CD147  
CC bound by the IgM MAB ABX-CBL, providing that the antibody is not CBL1.  
CC The MAB can selectively kill activated T-cells, activated B-cells or  
CC resting or activated monocytes. The products and methods can be used for  
CC treating diseases involving activated T-cells or B-cells or monocytes,  
CC e.g. graft versus host disease (GVHD), organ transplant rejection  
CC diseases (e.g. renal transplant, ocular transplant), cancers (e.g.  
CC cancers of the blood (e.g. leukaemia's and lymphomas) and pancreatic),  
CC autoimmune diseases (e.g. lupus), and inflammatory diseases (e.g.  
CC arthritis)  
XX  
SQ Sequence 1774 BP; 460 A; 488 C; 420 G; 406 T; 0 U; 0 Other;

Query Match 72.6%; Score 301.4; DB 2; Length 1774;  
Best Local Similarity 90.7%; Pred. No. 3.8e-80;  
Matches 333; Conservative 0; Mismatches 31; Indels 3; Gaps 1;  
QY 52 TTTTCTTTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGCTTGAGGAGCTCTGGAG 111  
DB 23 TATTCATAGTTTTTCTTTAAATGGTGTCCAGAGTGAAGCTTGAGGAGCTCTGGAG 82  
QY 112 GAGGCTTGTGCAACCTGGAGGATCCATGAAGTCTCTCTAGCTCTGGATTACTT 171  
DB 83 GAGGCTTGTGCAACCTGGAGGATCCATGAAGTCTCTCTAGCTCTGGATTACTT 142  
QY 172 TCAGTGCTACTGGATGCTTTGGTCCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 231  
DB 143 TCAGTAACACTGATGAAGTGGTCCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 202  
QY 232 CTGAATAGATGAATCTGATAATATGCAACACATATGCGGAGTCTGTGAAGGGA 291  
DB 203 CTGAATAGATGAATCTGATAATATGCAACACATATGCGGAGTCTGTGAAGGGA 262  
QY 292 AGTTCACCTCAAGAGATGATCCAAAGTCTCTCTACCTGCAATGAACAGCTTAA 351  
DB 263 GGTTCACTCTCAAGAGATGATCCAAAGTCTCTCTACCTGCAATGAACAGCTTAA 322  
QY 352 GAGCTGAAGACAGTGGAGTTATTACTGTACAGATTTTCATAG---ACTGGGGCCAAAGGGA 408  
DB 323 GAGCTGAAGACAGTGGCAATTTATTCTGTACGATTACGATGCTTACTGGGGCCAAAGGGA 382  
QY 409 CACTAGT 415  
DB 383 CTCTGGT 389

RESULT 5  
AAV71155  
ID AAV71155 standard; DNA; 496 BP.  
XX  
XX AAV71155;  
XX  
XX 20-MAR-2003 (revised)  
DT 16-APR-1999 (first entry)  
XX  
XX Coding strand for mouse Br-3 heavy chain variable region.  
XX Heavy chain variable region; murine antibody Br-3; antibody ING-1;  
KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;  
KW treatment; human cancer; 58.  
XX  
XX Mus sp.  
OS  
XX  
XX Key Location/Qualifiers  
FH

CDS  
FT 69. .494  
FT /\*tag= a  
XX /note= "Partial CDS, no termination codon"  
PN US5843685-A.  
XX  
XX 01-DEC-1998.  
XX  
XX 06-JUN-1995; 95US-00466034.  
XX  
XX 06-SEP-1988; 88US-00240624.  
XX 08-SEP-1988; 88US-00241744.  
XX 13-SEP-1988; 88US-00243739.  
XX 04-OCT-1988; 88US-00253002.  
XX 19-JUN-1989; 89US-00367641.  
XX 21-JUL-1989; 89US-00382768.  
XX 06-SEP-1989; 89WO-US003852.  
XX 06-MAY-1991; 91US-00659401.  
XX 27-DEC-1994; 94US-00364001.  
XX (XOMA ) XOMA CORP.  
XX  
XX Horwitz AH, Lei S, Chang CP, Better MD, Robinson RR;  
XX WPI; 1999-044574/04.  
XX P-PSDB; AAW85059.  
XX Chimeric antibody specific for human tumour antigen - useful as  
PT immunoassay, imaging or antitumour agent.  
XX  
XX Example 3; Fig 15; 92pp; English.  
XX  
XX The present sequence encodes the heavy chain variable region of murine  
CC antibody Br-3. The sequence was used to create chimeric mouse-human  
CC immunoglobulins which recognise the human tumour antigen bound by  
CC antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The  
CC chimeric antibodies also have an antigen-binding site that competitively  
CC inhibits the binding of antibody ING-1, and mediate complement cytotoxicity to  
CC cytolysis of target cells or antibody-dependent cellular cytotoxicity to  
CC target cells. The chimeric antibodies can be used for therapeutic  
CC purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to  
CC correct PR field.)  
XX  
SQ Sequence 496 BP; 141 A; 106 C; 118 G; 131 T; 0 U; 0 Other;  
Query Match 70.7%; Score 293.6; DB 2; Length 496;  
Best Local Similarity 92.8%; Pred. No. 5.3e-78;  
Matches 308; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 52 TTTTCTTTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGCTTGAGGAGCTCTGGAG 111  
DB 91 TATTCATAGTTTTTCTTTAAAGGGTCCAGAGTGAAGCTTGAGGAGCTCTGGAG 150  
QY 112 GAGGCTTGTGCAACCTGGAGGATCCATGAAGTCTCTCTAGCTCTGGATTACTT 171  
DB 151 GAGGCTTGTGCAACCTGGAGGATCCATGAAGTCTCTCTAGCTCTGGATTACTT 210  
QY 172 TCAGTGCTACTGGATGCTTTGGTCCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 231  
DB 211 TCAGTAACTATTGGATGAAGTGGTCCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 270  
QY 232 CTGAATAGATGAATCTGATAATATGCAACACATATTCGGAGTCTGTGAAGGGA 291  
DB 271 CTGAATAGATGAATCTGATAATATGCAACACATATTCGGAGTCTGTGAAGGGA 330  
QY 292 AGTTCACCTCAAGAGATGATCCAAAGTCTCTCTACCTGCAATGAACAGCTTAA 351  
DB 331 GGTTCACTCTCAAGAGATGATCCAAAGTCTCTCTACCTGCAATGAACAGCTTAA 390  
QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 383  
DB 391 GAGCTGAAGACAGTGGCAATTTTATTACTGTACA 422





```
CC correct PF field.)
XX Sequence 497 BP; 141 A; 106 C; 118 G; 132 T; 0 U; 0 Other;
SQ Query Match 70.7%; Score 293.6; DB 2; Length 497;
Best Local Similarity 92.8%; Pred. No. 5.3e-78;
Matches 308; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 52 TTTTATTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGCTTGAGGAGTCTGGAG 111
DB 92 TATTCATAGTTTCTTTCTTTAAAGGTGTCAGAGTGAAGCTTGAGGAGTCTGGAG 151
QY 112 GAGGCTTGGTGCAACTGAGGATCCATGAACTCTCCTGTGTAGCTCTGGATTACTT 171
DB 152 GAGGCTTGGTGCAACTGAGGATCCATGAACTCTCCTGTGTAGCTCTGGATTACTT 211
QY 172 TCAGTGGCTACTGGATGTCTTGGGTCGGCCAGTCTCCAGAGAGGGGCTTGAGTGGTTG 231
DB 212 TCAGTAACTATTGGATGAAGTGGGTCGGCCAGTCTCCAGAGAGGGGCTTGAGTGGTTG 271
QY 232 CTGAAATTAGATTGAATCTGATAATTATGCAACACATATTGCGGAGTCTGTGAAGGGA 291
DB 272 CTGAAATTAGATTGAATCTGATAATTATGCAACACATATTGCGGAGTCTGTGAAGGGA 331
QY 292 AGTTCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACCTGCAAAATGAACAGCTTAA 351
DB 332 GGTTCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACCTGCAAAATGAACAGCTTAA 391
QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 383
DB 392 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 423

RESULT 8
ABX79231
ID ABX79231 standard; DNA; 497 BP.
XX AC ABX79231;
XX DE 16-APR-2003 (first entry)
XX DE DNA encoding mouse antibody heavy chain variable region #2.
XX KW Mouse; human tumour antigen; anti-human tumour antigen-antibody;
XX KW ING-1 antibody; cell line HB9812; immunoassay; imaging; tumour diagnosis;
XX KW tumour therapy; cytostatic; gene; ds; heavy chain variable region.
XX OS Mus sp.
XX PN US6461824-B1.
XX PD 08-OCT-2002.
XX PF 06-JUN-1995; 95US-00467142.
XX PR 06-SEP-1988; 88US-00240624.
XX PR 08-SEP-1988; 88US-00241744.
XX PR 13-SEP-1988; 88US-00243739.
XX PR 04-OCT-1988; 88US-00253002.
XX PR 19-JUN-1989; 89US-00367641.
XX PR 21-JUL-1989; 89US-00382768.
XX PR 06-SEP-1989; 89WO-US003852.
XX PR 06-MAY-1991; 91US-00659401.
XX PR 27-DEC-1994; 94US-00364001.
XX PA (XOMA ) XOMA TECHNOLOGY LTD.
XX PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX WI; 2003-196707/19.
XX DR P-PSDB; ABUS8893.
XX XX Antibody for detecting antigen in animal or killing cells carrying
```

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PT antigen comprises human constant region and variable region having
XX specificity for human tumor antigen bound by ING-1 antibody.
PS Example 3; Fig 15; 101pp; English.
XX The invention describes an antibody comprising a human constant region
CC and a variable region having specificity for the human tumour antigen
CC bound by the ING-1 antibody, where the ING-1 is produced by cell line
CC HB9812 as deposited with ATCC, and the antibody has the same affinity as
CC the ING-1 for the human tumour antigen. The antibody is useful in an
CC immunoassay method for detecting an antigen in a sample by contacting a
CC label-detectable antigen in the sample with the antibody, detecting the
CC label and relating the detected label to the presence of the antigen; for
CC use in an imaging method for revealing the presence of a label-detectable
CC antigen in an animal by contacting the antibody with a part of the animal
CC suspected of containing the antigen, detecting the label and relating the
CC detected label to the presence of the antigen; and for killing cells
CC carrying an antigen by contacting the cells with the antibody and
CC allowing the killing to occur. The antibodies are useful in tumour
CC diagnosis and therapy. The chimeric antibodies bind to the surface of
CC human tumour cells but do not bind detectably to normal cells, e.g.,
CC fibroblasts, endothelial cells or epithelial cells in the major organs.
CC The high biological activity of the chimeric antibodies against human
CC tumour cell lines combined with minimal reactivity with normal tissues
CC imply that these antibodies may mediate selective destruction of
CC malignant tissue. The presence of human rather than murine antigenic
CC determinants on the chimeric antibodies increases their resistance to
CC rapid clearance from the body relative to the original murine mAbs. This
CC resistance to clearance enhances the potential utility of these chimeric
CC antibodies, as well as their derivatives, in tumour diagnosis and
CC therapy. This sequence encodes a mouse antibody heavy chain variable
CC region used in the creation of an anti-human tumour antigen-antibody
XX
SQ Sequence 497 BP; 141 A; 106 C; 118 G; 132 T; 0 U; 0 Other;

Query Match 70.7%; Score 293.6; DB 8; Length 497;
Best Local Similarity 92.8%; Pred. No. 5.3e-78;
Matches 308; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 52 TTTTATTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGCTTGAGGAGTCTGGAG 111
DB 92 TATTCATAGTTTCTTTCTTTAAAGGTGTCAGAGTGAAGCTTGAGGAGTCTGGAG 151
QY 112 GAGGCTTGGTGCAACTGAGGATCCATGAACTCTCCTGTGTAGCTCTGGATTACTT 171
DB 152 GAGGCTTGGTGCAACTGAGGATCCATGAACTCTCCTGTGTAGCTCTGGATTACTT 211
QY 172 TCAGTGGCTACTGGATGTCTTGGGTCGGCCAGTCTCCAGAGAGGGGCTTGAGTGGTTG 231
DB 212 TCAGTAACTATTGGATGAAGTGGGTCGGCCAGTCTCCAGAGAGGGGCTTGAGTGGTTG 271
QY 232 CTGAAATTAGATTGAATCTGATAATTATGCAACACATATTGCGGAGTCTGTGAAGGGA 291
DB 272 CTGAAATTAGATTGAATCTGATAATTATGCAACACATATTGCGGAGTCTGTGAAGGGA 331
QY 292 AGTTCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACCTGCAAAATGAACAGCTTAA 351
DB 332 GGTTCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACCTGCAAAATGAACAGCTTAA 391
QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 383
DB 392 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 423

RESULT 9
AAQ85388
ID AAQ85388 standard; cDNA; 480 BP.
XX AC AAQ85388;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 31-AUG-1995 (first entry)
XX XX
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Db      269 CTGAATTAGAACGAAAGCTAATAATCATGCAACATCTATCTGAGTCTGTGAAAGGGA 328
QY      292 AGTTACCATCTCAAGAGATGATTCACAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAA 351
Db      329 GGTTCACCATCTCAAGAGATGATTCACAAAGTAGTGTCTACCTGCAATGAACAGCTTAA 388
QY      352 GAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTTCATAG---ACTGGGGCCCAAGGGA 408
Db      389 GAGCTGAAGACAGTGGCAATTATTACTGTACCGACTGGTGTCTACTGGGGCCCAAGGGA 448
QY      409 CACTAGT 415
Db      449 CTCTGGT 455

RESULT 11
AAQ12016 standard; DNA; 469 BP.
ID      AAQ12016
XX
AC      AAQ12016;
XX
XX      25-MAR-2003 (revised)
DT      19-AUG-1991 (first entry)
XX
XX      Sequence encoding mouse MAb 1C11 H chain V region.
DE
XX      HIV-1; chimera; ds.
XX
XX      Mus sp.
XX
XX      Key      Location/Qualifiers
FH      CDS      67..469
FT      /*tag= a
XX
XX      WO9107494-A.
XX
XX      30-MAY-1991.
XX
XX      13-NOV-1989; 89US-00433703.
XX
XX      13-NOV-1989; 89US-00433703.
XX
XX      (XOMA ) XOMA CORP.
XX
XX      (GREG ) GREEN CROSS CORP.
XX
XX      (ZOMA-) ZOMA CORP.
XX
XX      Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
XX
XX      WPI; 1991-178106/24.
XX
XX      P-PSDB; AAR12236.
XX
XX      New chimeric mouse human antibodies - used in treatment, diagnosis and
XX      prophylaxis of HIV infections.
XX
XX      Disclosure; Fig 12; 108pp; English.
XX
XX      The mouse VH gene product may be used to produce chimeric mouse- human
XX      Abs against HIV-1 comprising human Ig constant regions and murine
XX      variable regions. These novel sequence are useful in treatment, diagnosis
XX      and prophylaxis of HIV infections, and may be produced by a bacterial,
XX      yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
XX      PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX      Sequence 469 BP; 127 A; 96 C; 120 G; 126 T; 0 U; 0 Other;
XX
XX      Query Match      68.0%; Score 282.2; DB 2; Length 469;
XX      Best Local Similarity 87.5%; Pred. No. 1.4e-74;
XX      Matches 321; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

QY      52 TTTTATTTATTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGCTCTGGAG 111
Db      89 TATTATAGTTTTTCTTCTTAATGTTGTCCAGAGTGAAGTGAAGCTTGAGGAGCTCTGGAG 148

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QY      112 GAGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGTAGCCTCTGGATTTACTT 171
Db      149 GAGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGTAGCCTCTGGATTTACTT 208
QY      172 TCAGTGGCTACTCGATGTCTTTGGGTCCGCCAGTCTCCAGAGAAGGGCTTTGAGTGGGTTG 231
Db      209 TTAGTGAGCCTCGATGGAGCTGGGTCCGCCAGTCTCCAGAGAAGGGCTTTGAGTGGGTTG 268
QY      232 CTGAAATTAGAATCGAATCTGATTAATTATGCAACACATTTATGCGGAGTCTGTGAAAGGGA 291
Db      269 CTGAAATTAGAAGCAAAAGCTAATAATCATGCAACATCTATGCTGAGTCTGTGAAAGGGA 328
QY      292 AGTTACCATCTCAAGAGATGATTCACAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAA 351
Db      329 GGTTCACCATCTCAAGAGATGATTCACAAAGTAGTGTCTACCTGCAAAATGAACAGCTTAA 388
QY      352 GAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTTCATAG---ACTGGGGCCCAAGGGA 408
Db      389 GAGCTGAAGACAGTGGCAATTATTACTGTACCGACTGGTGTCTACTGGGGCCCAAGGGA 448
QY      409 CACTAGT 415
Db      449 CTCTGGT 455

RESULT 12
AAV22331 standard; cDNA to mRNA; 357 BP.
ID      AAV22331
XX
XX      AAV22331;
XX
XX      06-JUL-1998 (first entry)
DT
XX
XX      Nucleic acid encoding synthetic branched mucin type glycolipid.
DE
XX      Branched mucin type glycolipid; V region; heavy chain; antibody;
XX      cancer treatment; diagnosis; ss.
XX
XX      Synthetic.
XX
XX      JP10084963-A.
XX
XX      07-APR-1998.
XX
XX      12-SEP-1996; 96JP-00241725.
XX
XX      12-SEP-1996; 96JP-00241725.
XX
XX      (TOYU ) TOSOH CORP.
XX
XX      WPI; 1998-264850/24.
XX
XX      P-PSDB; AAW46958.
XX
XX      Recognising branched mucin type synthetic glycolipid - using gene
XX      fragment of an antibody, useful in cancer treatment and diagnosis.
XX
XX      Claim 1; Page 4-5; 6pp; Japanese.
XX
XX      The present sequence encodes a branched mucin type synthetic glycolipid.
XX      A gene fragment encoding the V region of the heavy chain of an antibody
XX      recognising the protein encoded by the present sequence is claimed. The
XX      antibody gene fragment is useful for the development of cancer treatments
XX      and diagnosing agents
XX
XX      Sequence 357 BP; 99 A; 75 C; 93 G; 90 T; 0 U; 0 Other;
XX
XX      Query Match      65.5%; Score 272; DB 2; Length 357;
XX      Best Local Similarity 94.9%; Pred. No. 1.5e-71;
XX      Matches 281; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      87 GAAGTCAAGCTTGAGGAGTCTGGAGGAGCTTGGTGCAACCTGGAGGATCCCTGAACCTC 146

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Db 1 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAATC 60  
 QY 147 TCCTGTGTAGCCTCTGGATTACCTTTTCAGTGGCTACTGGATGCTTGGGTCCGCGCAGTCT 206  
 Db 61 TCCTGTGTGCTCTGGATTACCTTTTCAGTGGCTACTGGATGCTTGGGTCCGCGCAGTCT 120  
 QY 207 CCAGAGAAGGGGCTTGAGTGGTGGTGGTGAATAGATTGAATCTGATAATTAATGCAACA 266  
 Db 121 CCAGAGAAGGGGCTTGAGTGGTGGTGGTGAATAGATTGAATCTGATAATTAATGCAACA 180  
 QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 326  
 Db 181 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 240  
 QY 327 CTCCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382  
 Db 241 GTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 296

## RESULT 13

AAC90472  
 ID AAC90472 standard; DNA; 856 BP.

XX AAC90472;

XX 13-MAR-2001 (first entry)

XX Antibody 33F12 catalytic fragment nucleotide sequence.

XX Antibody 33F12; ketone compound; antitumour; cytotoxic;  
 XX targeted drug delivery; ds.

XX Unidentified.

XX WO200071556-A1.

XX 30-NOV-2000.

XX 24-MAY-2000; 2000WO-US014366.

XX 25-MAY-1999; 99US-00318661.

XX (SCRI ) SCRIPPS RES INST.

XX Barbas CF, Shabat D, Rader C, List B, Lerner RA;

XX WPI; 2001-061339/07.

XX P-FSDB; AAB50426.

XX New ketone compounds containing active agents useful as carriers for e.g.  
 XX antitumor agents, antibiotics or fluorescent molecules.

XX Disclosure; Fig 10; 45pp; English.

XX The present sequence may be used in the activation of new ketone prodru  
 CC compounds containing active agents. The ketone derivatives are useful as  
 CC carriers for antitumour agents such as cytotoxic agents, where the  
 CC antitumour agent is a microtubule stabilising agent such as paclitaxel,  
 CC epothilone or its therapeutically active analogue or an anthracycline  
 CC antibiotic such as doxorubicin or its therapeutically active analogue.  
 CC The ketone derivatives are useful for targeted drug delivery. The  
 CC inactive molecules in the ketone compounds are converted to active  
 CC molecules by retro-Michael reaction. The antibody has bifunctional  
 CC activity and specifically immunoreacts with cell surface antigen of a  
 CC target cell. The active ingredients can be mixed effectively with  
 CC excipients as per desired amount along with the buffering agent to  
 CC enhance the effectiveness and activity of the compound

XX SQ Sequence 856 BP; 195 A; 208 C; 228 G; 225 T; 0 U; 0 Other;

XX Query Match 65.4%; Score 271.6; DB 5; Length 856;

XX Best Local Similarity 92.3%; Pred. No. 2.7e-71;

XX Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAATC 146  
 Db 460 GAGGTGATGCTGTGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAATC 519  
 QY 147 TCCTGTGTAGCCTCTGGATTACCTTTTCAGTGGCTACTGGATGCTTGGGTCCGCGCAGTCT 206  
 Db 520 TCCTGTGTGTGCTCTGGATTAAACCTTCAGTAGATTCTGGATGCTTGGGTCCGCGCAGTCT 579  
 QY 207 CCAGAGAAGGGGCTTGAGTGGTGGTGGTGAATAGATTGAATCTGATAATTAATGCAACA 266  
 Db 580 CCAGAGAAGGGGCTTGAGTGGTGGTGGTGAATAGATTGAATCTGATAATTAATGCAACA 639  
 QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 326  
 Db 640 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 699  
 QY 327 CTCCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386  
 Db 700 CTCCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 759  
 QY 387 TTCATAGACT 396  
 Db 760 TATTTTACT 769

## RESULT 14

ADR59058

ID ADR59058 standard; DNA; 408 BP.

XX ADR59058;

XX 18-NOV-2004 (first entry)

XX Anti-K88 antibody VH codon optimised DNA, SEQ ID 9.

XX Gastrointestinal; antibody; heavy chain; light chain; variable region;  
 KW enterotoxigenic Escherichia coli; ETEC; K88 antigen; K99 antigen;  
 KW animal food; enteric disease; ds.

XX Synthetic.

XX WO2004074491-A2.

XX 02-SEP-2004.

XX 16-FEB-2004; 2004WO-EP001427.

XX 18-FEB-2003; 2003US-0448429P.

XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Brown D, Campos M, Dalmia B, Demarest S, Hansen G, Heifetz PB;

XX WPI; 2004-635583/61.

XX Novel immunoglobulin heavy chain comprising bovine CH3 or CH2 domain,  
 PT murine CH2CH3 domain or human CH2CH3 domain, useful in treatment or  
 PT prevention of enteric disease in animal.

XX Claim 9; SEQ ID NO 9; 165pp; English.

XX The present invention relates to coding sequences for mammalian antibody  
 CC heavy and light chains directed against enterotoxigenic Escherichia coli  
 CC (ETEC), in particular, ETEC of a strain possessing the K88 or K99  
 CC antigen. The heavy and light chain sequences are useful for producing  
 CC transgenic plants, which express the K88 or K99 antibody. The transgenic  
 CC plants are useful for producing animal feed, food product, animal feed  
 CC additive, feed pre-mix or nutritional supplement and are also useful for  
 CC treating or preventing enteric disease in an animal. The present sequence  
 CC is the coding sequence for an anti-K88 antibody heavy chain variable  
 CC region which has been codon optimised for expression in plants.

SQ Sequence 408 BP; 105 A; 92 C; 105 G; 106 T; 0 U; 0 Other;  
Query Match 65.1%; Score 270.2; DB 13; Length 408;  
Best Local Similarity 94.0%; Pred. No. 5.5e-71;  
Matches 281; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 84 AGTGAAGTGAAGCTTGAGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAA 143  
DB 4 AGTGAAGTGAAGCTTGAGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAA 63  
QY 144 CTCCTCTGTAGCTCTCGATTTACTTTTCAGTGGCTACTGATGCTTGGGTCCGCCAG 203  
DB 64 CTCCTCTGTAGCTCTCGATTTACTTTTCAGTGGCTACTGATGCTTGGGTCCGCCAG 123  
QY 204 TCTCCAGAGAAGGGGCTTGAGTGGTGTCTGAAATTTAGATTTGAAATTTGATGCA 263  
DB 124 TCTCCAGAGAAGGGGCTTGAGTGGTGTCTGAAATTTAGATTTGAAATTTGATGCA 183  
QY 264 ACACATTTGCGGAGTCTGTGAAGGGAAGTTTCAACATCTCAAGAGATGATTTCCAAAGT 323  
DB 184 ACACATTTGCGGAGTCTGTGAAGGGAAGTTTCAACATCTCAAGAGATGATTTCCAAAGT 243  
QY 324 CGTCTCTACTCGCAATGAACAGCTTAAGAGCTGGAAGACAGTGGAGTTTATTACTGTAC 382  
DB 244 AGTGTCTACTCGCAATGAACAGCTTAAGAGCTGGAAGACAGTGGAGTTTATTACTGTAC 302

RESULT 15

AAQ85386  
ID AAQ85386 standard; DNA; 1979 BP.  
XX AAQ85386;  
AC  
XX  
DT 25-MAR-2003 (revised)  
DT 31-AUG-1995 (first entry)  
XX  
DE Anti-cataract immunotoxin in pHE19.  
XX  
KW Immunotoxin; heavy chain; light chain; variable region; antibody;  
KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;  
KW pHE19; 4197X; monoclonal antibody; MAB; ds.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 115..1779  
FT FT /\*tag= a  
FT sig\_peptide 115..195  
FT FT /\*tag= b  
FT FT /note= "phoA signal sequence"  
FT mat\_peptide 196..1776  
FT FT /\*tag= c  
XX  
XX WO9503828-A1.  
XX  
XX  
PD 09-FEB-1995.  
XX  
XX 15-JUL-1994; 94WO-US007919.  
XX  
XX 02-AUG-1993; 93US-00101329.  
XX  
XX (HOUS-) HOUSTON BIOTECHNOLOGY INC.  
XX  
XX Wood MS, Gould RM, Kelleher PJ, Wallace TL;  
XX  
XX WPI; 1995-082036/11.  
XX P-PSDB; AAR70827.  
XX  
XX New single chain immuno:toxin - binds specifically to epithelial cells,  
FT for inhibiting development of sec. cataracts after extra:capsular  
FT cataract extraction.  
XX  
XX Disclosure; Fig 4; 68pp; English.  
PS

XX The immunotoxin given in AAR70827 comprises the heavy and light chain  
CC variable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A  
CC and a hexa-histidine tag. The DNA construct encoding the immunotoxin was  
CC expressed from pHE19 in E. coli. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 1979 BP; 558 A; 426 C; 459 G; 536 T; 0 U; 0 Other;  
Query Match 65.0%; Score 269.8; DB 2; Length 1979;  
Best Local Similarity 94.3%; Pred. No. 1.3e-70;  
Matches 280; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
QY 86 TGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAAACT 145  
DB 198 TGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAAACT 257  
QY 146 CTCCTGTAGCTCTCGATTTACTTTTCAGTGGCTACTGATGCTTGGGTCCGCCAGTC 205  
DB 258 CTCCTGTAGCTCTCGATTTACTTTTCAGTAACTTTCTGGATGAACCTGGGTCCGCCAGTC 317  
QY 206 TCCAGAGAAGGGGCTTGAGTGGTGTCTGAAATTTAGATTTGAAATTTGATGCAAC 265  
DB 318 TCCAGAGAAGGGGCTTGAGTGGTGTCTGAAATTTAGATTTGAAATTTGATGCAAC 377  
QY 266 ACATTTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTTCCAAAGTCG 325  
DB 378 ACATTTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTTCCAAAGTCG 437  
QY 326 TCTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382  
DB 438 TGTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGCATTATTACTGTAC 494

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Job time : 235.448 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 14:42:49 ; Search time 1129.75 Seconds  
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2228.534 Million cell updates/sec

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Perfect score: 415

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Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	310.4	74.8	453	9	US-09-855-153-14
3	310.4	74.8	453	9	US-09-854-811-14
4	310.4	74.8	453	9	US-09-934-773-14
5	310.4	74.8	453	9	US-09-963-620-14
6	310.4	74.8	453	10	US-09-855-632-14
7	310.4	74.8	453	15	US-10-225-784-14
8	310.4	74.8	453	15	US-10-224-720-14
9	310.4	74.8	453	16	US-10-225-779-14
10	310.4	74.8	453	17	US-10-374-381-14
11	310.4	74.8	453	17	US-10-446-542-14
					Sequence 14, Appl
					Sequence 14, Appl
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					Sequence 14, Appl
					Sequence 14, Appl

12	310.4	74.8	453	18	US-10-769-308-26	Sequence 26, Appl
13	310.4	74.8	453	19	US-10-769-074-26	Sequence 26, Appl
14	271.6	65.4	856	9	US-09-883-758-3	Sequence 3, Appl
15	271.6	65.4	856	9	US-09-883-758-6	Sequence 6, Appl
16	270.4	65.2	366	19	US-10-879-994-65	Sequence 65, Appl
17	269.4	64.9	403	10	US-09-947-839-12	Sequence 12, Appl
18	265.4	63.0	765	17	US-10-239-656-68	Sequence 68, Appl
19	263.6	63.5	899	9	US-09-883-758-1	Sequence 1, Appl
20	263.6	63.5	899	9	US-09-883-758-5	Sequence 5, Appl
21	263	63.4	403	10	US-09-947-839-65	Sequence 65, Appl
22	262.4	63.2	768	17	US-10-239-656-60	Sequence 60, Appl
23	262.4	63.2	1509	17	US-10-239-656-76	Sequence 76, Appl
24	260.2	62.7	789	16	US-10-277-471A-1	Sequence 1, Appl
25	259.2	62.5	348	16	US-10-160-506-125	Sequence 125, App
26	259.2	62.5	348	16	US-10-160-506-126	Sequence 126, App
27	259.2	62.5	348	18	US-10-449-379-125	Sequence 125, App
28	259.2	62.5	348	18	US-10-449-379-126	Sequence 126, App
29	259.2	62.5	348	18	US-10-688-015-125	Sequence 125, App
30	259.2	62.5	348	18	US-10-688-015-126	Sequence 126, App
31	259.2	62.5	348	18	US-10-160-505-125	Sequence 125, App
32	259.2	62.5	348	18	US-10-160-505-126	Sequence 126, App
33	258.2	62.2	351	16	US-10-277-471A-3	Sequence 3, Appl
34	256.6	61.8	810	16	US-10-160-508-53	Sequence 53, Appl
35	256.6	61.8	810	16	US-10-160-508-55	Sequence 55, Appl
36	256.6	61.8	810	18	US-10-449-379-53	Sequence 53, Appl
37	256.6	61.8	810	18	US-10-449-379-55	Sequence 55, Appl
38	256.6	61.8	810	18	US-10-688-015-53	Sequence 53, Appl
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40	256.6	61.8	810	18	US-10-160-508-53	Sequence 53, Appl
41	256.6	61.8	810	18	US-10-160-508-55	Sequence 55, Appl
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43	256	61.7	357	9	US-09-756-301A-4	Sequence 4, Appl
44	256	61.7	357	9	US-09-766-535A-4	Sequence 4, Appl
45	256	61.7	357	9	US-09-766-535A-4	Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-09-564-329A-14  
; Sequence 14, Application US/09564329A  
; Patent No. US20010055751A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.54US14  
; CURRENT APPLICATION NUMBER: US/09/564,329A  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 60/124,658  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 09/203,939  
; PRIOR FILING DATE: 1998-12-02  
; PRIOR APPLICATION NUMBER: 09/251,835  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 09/308,503  
; PRIOR FILING DATE: 1999-05-25

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-09-564-329A-14

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Query Match	74.8%	Score 310.4	DB 9	Length 453
Best Local Similarity	92.6%	Pred. No. 2.3e-85		
Matches 326	Conservative 0	Mismatches 26	Indels 0	Gaps 0
QY	35	CATGGATTTGGCGCTGATTTTTTTTATGTGTTCTTTTAAAGGGGCTCCAGAGTGAAGTGAA	94	
DB	6	CTTCGGGTGAGCTGGGTGTTTTATATGTGTTCTTTTAAAGGGGCTCCGAGTGAAGTGAG	65	
QY	95	GCTTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGT	154	
DB	66	GCITGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGT	125	
QY	155	AGCCTCTGGATTTACTTTTCAGTGCTACTGAGATGCTTTGGTGCGCAGTCTCCAGAGAA	214	
DB	126	AGCCTCTGGATTTACTTTTCAGTAAATTTACTGATGACTTTGGTGCGCCAGTCTCCAGAGAA	185	
QY	215	GGGGCTTGAGTGGGTGCTGAAATTAGATTTGAAATCTGATAAATTTATGCAACACATATGC	274	
DB	186	GGGGCTTTGAGTGGGTGCTGAAATTCGATTTGAGATCTGAAATTTATGCAACACATATGC	245	
QY	275	GGAGTCTGTGAAAGGGAGGTTTCACCATCTCAAGAGATGATTCCAAAAGTCCGTCTCTACCT	334	
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DB	306	GCAAAATGAACAACTTTAAGACCTGAAGACAGTGGAAATTTATTACTGTACAGAT	357	

RESULT 2  
US-09-855-153-14  
; Sequence 14, Application US/09855153  
; Patent No. US20020102666A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saifran, Douglas C.  
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.54US14  
; CURRENT APPLICATION NUMBER: US/09/855,153  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 09/564,329  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 60/124,658  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 09/203,939  
; PRIOR FILING DATE: 1998-12-02  
; PRIOR APPLICATION NUMBER: 09/251,835  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 09/308,503  
; PRIOR FILING DATE: 1999-05-25

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-09-855-153-14

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Query Match	74.88;	Score 310.4;	DB 9;	Length 453;
Best Local Similarity	92.6%;	Pred. No. 2.3e-85;		
Matches 326;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0
Qy	35	CATGGATTTTGGGCTGATTTTTTTTTTATGTGTTCTTTTAAAGGGGCTCCAGAGTGAAGTCAA	94	
Db	6	CTTCGGGTTGAGCTGGGTTTTTATATGTGTTCTTTTAAAGGGGCTCCGAGTGAAGTCAG	65	
Qy	95	GCTTGGAGAGTCTGGAGGAGGCTTGGTGCAACTGGAGGATCCATGAAACCTCTCTCTGTGT	154	
Db	66	GCTTGGAGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAAACCTCTCTCTGTGT	125	
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; Patent No. US20020119157A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; TITLE OF INVENTION: PSICA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.54US14  
; CURRENT APPLICATION NUMBER: US/09/854,811  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 09/564,329  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 453  
; TYPE: DNA  
; ORGANISM: SCID Mice  
US-09-854-811-14

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QY	35	CATGGATTTTGGCGTGATTTTTTTTTTATTGTCTTTTAAAGGGGTCACAGTGAAGTGAA	94		
Db	6	CTTCGGGTGAGCTGGGTTTTTATTATTGTCTTTTAAAGGGGTCGAGTGAAGTGAG	65		
QY	95	GCTTTGAGGAGTCTGGAGAGAGCTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGT	154		
Db	66	GCTTTGAGGAGTCTGGAGAGAGCTGGGTGCACCTGGAGGATCCATGAACCTCTCTGTGT	125		





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Db		
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275	GGAGTCGTGTGAAGGGGAAGTTCACCATCTCTCAAGAGATGATTCCAAAGTGGTCTCTACCT	334
QY		
246	GGAGTCGTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACCT	305
Db		
335	GCAATGAACACGCTTAAGAGCTGGAAGACAGTCGGAGTTTATTACTGTACAGAT	386
QY		
306	GCAATGAACACCTTAAGACCTTGAAGACAGTCGGAATTTATTACTGTACAGAT	357
Db		

## RESULT 6

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US091955-632-14
: Sequence 14, Application US/09855632
: Publication No. US2003011381A1
: GENERAL INFORMATION:
: APPLICANT: Reiter, Robert E.
: APPLICANT: Witte, Owen N.
: APPLICANT: Saffran, Douglas C.
: TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

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	Query Match	74.8%	Score 310.4;	DB 10;	Length 453;
	Best Local Similarity	92.6%;	Pred. No. 2.3e-85;		
	Matches 326;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;
Qy	35	CATGATTTTCGGCTGATTTTTTTTATTGTTCTTTTAAAAAGGGGTCAGAGTGAAGTGAA	94		
Db	6	CTTCGGGTGAGCTGGGTTTTTATTATTGTTCTTTTAAAAAGGGGTCGAGTGAAGTCAG	65		
Qy	95	GCTTGAAGAGTCTGGAGAGAGGCTTGGTGCAACTCGGAGGATCCATGAAACTCTCCTGTGT	154		
Db	66	GCTTGAGAGGTCGAGAGAGGCTGGGTGCAACTCGGAGGATCCATGAAACTCTCCTGTGT	125		

Qy	155	AGCCTCTGGATTACTTTCAGTGGCTACTCGATGCTTTGGGTCCGCCAGTCTCCAGAGAA	214
Db	126	AGCCTCTGGATTACTTTCAGTAAATCTCGATGACTTGGGTCCGCCAGTCTCCAGAGAA	185
Qy	215	GGGCTTTGAGTGGGTGCTGAAATTTAGATTGAAATCTGATAATATGCAACACATTATGC	274
Db	186	GGGCTTTGAGTGGGTGCTGAAATTCGNATTGAGATCTGAAAATTTATGCAACACATTATGC	245
Qy	275	GGAGTCTGTGAAGAGGGAAGTTCCACATCTCAAGAGATGATTTCCAAAGTCGTCTTCACT	334
Db	246	GGAGTCTGTGAAGAGGGAATTCACCATCTCAAGAGATGATTTCCAGAAAGTCGTCTTCACT	305
Qy	335	GCAATGAACAGCTTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT	386
Db	306	GCAATGAACAACTTAAAGCTGAAGACAGTGGAAATTTATTACTGTACAGAT	357

## RESULT 7

US-10-225-784-14  
 ; Sequence 14, Application US/10225784  
 ; Publication No. US20030113820A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reiter, Robert E.  
 ; APPLICANT: witte, Owen N.  
 ; APPLICANT: Saffran, Douglas C.  
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

Query Match 74.8%; Score 310.4; DB 15; Length 453;  
Best Local Similarity 92.6%; Pred. No. 2.3e-85;  
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0

Qy	35	CATGGATTTTGGCTGATTTTTTTTAAATGTTCTTTTTAAAGGGGTCCAGAGTGAAGTAA	94
Db	6	CTTCGGGTTGAGCTGGGTTTTTTATTTGTTCTTTTAAAGGGGTCCGAGTGAAGTGAG	65
Qy	95	GCTTTGAGAGTCTGGAGAGCGCTTGGTGCAACCTGGAGGATCCATGAACCTCTCCTGTGT	154
Db	66	GCTTTGAGAGTCTGGAGAGCGCTGGGTGCAACCTGGAGGATCCATGAACCTCTCCTGTGT	125
Qy	155	AGCCTCTGGATTACTTTTTCAGTGCTACTGGATGCTTTGGGTCCGCCAGTCTCCAGAGAA	214
Db	126	AGCCTCTGGATTACTTTTTCAGTAAATTAATCGATGACTTGGGTCCGCCAGTCTCCAGAGAA	185

Qy	215	GGGGCTTGAGTGGGTGCTGAAATTAGAAATCTGATAATTATGCAACACATTATGC	274
Db	186	GGGGCTTGAGTGGGTGCTGAAATTCGAATCGAGATCTGAAAAATTATGCAACACATTATGC	245
Qy	275	GGAGTCTGTGAAAGGGAAGTTCCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACCT	334
Db	246	GGAGTCTGTGAAAGGGAATTCACCATCTCAAGAGATGATTCGAAGTGGTCTCTACCT	305
Qy	335	GCAATGAAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT	386
Db	306	GCAATGAAACACTTAAGACCTGAAGACAGTGGAAATTTATTACTGTACAGAT	357

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 US-10-224-720-14  
 ; Sequence 14, Application US/10224720  
 ; Publication No. US20030147806A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reiter, Robert E.  
 ; APPLICANT: Witte, Owen N.  
 ; APPLICANT: Safran, Douglas C.  
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
 ; FILE REFERENCE: 30435-54US14  
 ; CURRENT APPLICATION NUMBER: US/10/224,720  
 ; CURRENT FILING DATE: 2002-08-20  
 ; PRIOR APPLICATION NUMBER: US/09/359,326  
 ; PRIOR FILING DATE: 1999-07-20  
 ; PRIOR APPLICATION NUMBER: 08/814,279  
 ; PRIOR FILING DATE: 1997-03-10  
 ; PRIOR APPLICATION NUMBER: 60/071,141  
 ; PRIOR FILING DATE: 1998-01-12  
 ; PRIOR APPLICATION NUMBER: 60/074,675  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: 60/113,230  
 ; PRIOR FILING DATE: 1998-12-21  
 ; PRIOR APPLICATION NUMBER: 60/120,536  
 ; PRIOR FILING DATE: 1999-02-17  
 ; PRIOR APPLICATION NUMBER: 60/124,658  
 ; PRIOR FILING DATE: 1999-03-16  
 ; PRIOR APPLICATION NUMBER: 09/038,261  
 ; PRIOR FILING DATE: 1998-03-10  
 ; PRIOR APPLICATION NUMBER: 09/203,939  
 ; PRIOR FILING DATE: 1998-12-02  
 ; PRIOR APPLICATION NUMBER: 09/251,835  
 ; PRIOR FILING DATE: 1999-02-17  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 14  
 ; LENGTH: 453  
 ; TYPE: DNA  
 ; ORGANISM: SCID Mice  
 US-10-224-720-14

	Query Match	74.8%	Score 310.4;	DB 15;	Length 453;
	Best Local Similarity	92.6%;	Pred. No. 2.3e-85;		
	Matches 326;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;
QY	35	CATGGATTTTGGGCTGATTTTTTTTTTATTGTTCTTTTAAAGGGGTCCAGAGTGAAGTAA	94		
DB	6	CTTCGGGTTGAGCTGGGTTTTTATTATTGTTCTTTTAAAGGGGTCCGAGTGAAGTGA	65		
QY	95	GCTTGGAGGATCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCTGTGT	154		
DB	66	GCTTGGAGGATCTGGAGGAGGCTGGGTGCACACTTGGAGGATCCATGAAACTCTCTGTGT	125		
QY	155	AGCCTCTGGATTTACTTTTCAGTGCGTACTTGGATGTCTTGGGTCCGCCAGTCTCCAGAA	214		
DB	126	AGCCTCTGGATTTACTTTTCAGTAAATCTGGATGACTTGGGTCCGCCAGTCTCCAGAA	185		
QY	215	GGGCGCTTGAGTGGGTGCTGAAATTAGATTCGAAATCTGATAAATTATGCAACACATTAATGC	274		

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Db      186  GGGCGTGTGAGTGGGTGCTGAAATTCGATTCAGATCTGAAAAATTATCGAACACACATTA
Qy      275  GGAGTCTGTGAAAGGGAAGTTCCACCATCTCAAGAGATGATTCAAAAAGTCGTCTCTCAAC
Db      246  GGAGTCTGTGTAAGAGGGAATTCACCATCTCAAGAGATGATTCAGAAAGTCGTCTCTCAAC
Qy      335  GCAAATGAACACGCTTAAGAGCTGAAGACAGTGGAGTGTATTTACTGTGTACAGAT 386
Db      306  GCAAATGAACAACTTTAAGACCTGAAGACAGTGGAAATTTATTACTGTGTACAGAT 357

RESULT 9
US-10-225-779-14
; Sequence 14, Application US/10225779
; Publication No. US20030153016A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,779
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-10-225-779-14

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Query Match	74.8%	Score 310.4	DB 16	Length 453
Best Local Similarity	92.6%	Pred. No. 2.3e-85		
Matches 326	Conservative 0	Mismatches 26	Indels 0	Gaps 0
Qy	35	CATGGATTTCGGCTGATTTTTTTTATTTGTTCTTTTAAAGGGGTCCAGAGCTGAAGTCAA	94	
Db	6	CTTCGGGTTGAGCTGGGTTTTTATTATTTGTTCTTTTAAAGGGGTCCGAGTGAAGTGAG	65	
Qy	95	GCTTTGAGGATCTGGAGGAGCGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCTCTGTGT	154	
Db	66	GCTTTGAGGATCTGGAGGAGCGCTGGGTGCAACCTGGAGGATCCATGAAACTCTCTCTGTGT	125	
Qy	155	AGCCTCTGGATTTTACTTTTCAGTGGCTACTGGATGCTTTGGGTCCGCCAGTCTCCAGAGAA	214	
Db	126	AGCCTCTGGATTTTACTTTTCAGTAATTTACTGGAAGTCTGGGTCCGCCAGTCTCCAGAGAA	185	
Qy	215	GGGGCTTGAGTGGGTTCCTGAAATTAGATTGAAATCTGATAAATTATGCAACACATTATGC	274	
Db	186	GGGGCTTTGAGTGGGTTCCTGAAATTCGAAATTCGATTGAGATCTGAAAAATTTATGCAACACATTATGC	245	
Qy	275	GGAGTCTGTGAAAGGGGAAGTTTACCATCTCCAGAGAGATGATTCCAAAAGTCCGCTCTCACTC	334	

Db 246 GGAGTCTGTGAAGGGAATTCACCATCTCAAGAGATGATTCAGAGTCGTCTTACCT 305  
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Db 306 GCAATGAACACTTAAGACCTGAAGACAGTGGATTTATTACTGTACAGAT 357

RESULT 10  
US-10-374-381-14  
; Sequence 14, Application US/10374381  
; Publication No. US2003028318A1  
; GENERAL INFORMATION:  
; APPLICANT: Witte, Robert E.  
; APPLICANT: Reiter, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; TITLE OF INVENTION: PSCT: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.54US14  
; CURRENT APPLICATION NUMBER: US/10/374,381  
; PRIOR FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: US/09/564,329A  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: 60/113,230  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 60/124,658  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 09/203,939  
; PRIOR FILING DATE: 1998-12-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 453  
; TYPE: DNA  
; ORGANISM: SCID Mice  
US-10-374-381-14

Query Match 74.8%; Score 310.4; DB 17; Length 453;  
Best Local Similarity 92.6%; Pred. No. 2.3e-85;  
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
Qy 35 CATGGATTTGGGCTGATTTTTTTTATTGTTCTTTTAAAGGGGTCAGAGTGAAGTGA 94  
Db 6 CTTCGGGTGAGCTGGGTTTATTGTTCTTTTAAAGGGGTCGGAGTGAAGTGA 65  
Qy 95 GCTTGAGAGTCTGGAGAGGCTTGGTGCAACCTGGAGGATCCATGAACTCTCTGTGT 154  
Db 66 GCTTGAGAGTCTGGAGAGGCTGGTGCAACCTGGAGGATCCATGAACTCTCTGTGT 125  
Qy 155 AGCCTCTGGATTTACTTTTCAGTGCTACTGATGCTTTGGTCCGCCAGTCTCCAGAA 214  
Db 126 AGCCTCTGGATTTACTTTTCAGTAATTTCTGATGACTTTGGTCCGCCAGTCTCCAGAA 185  
Qy 215 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTTGAAATCTGATAATTTATGCAACATATGC 274  
Db 186 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTTGAAATTTATGCAACATATGC 245  
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Db 186 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTTGAAATTTATGCAACATATGC 245  
Qy 275 GGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCGAAAGTCTCTTACCT 334  
Db 246 GGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCGAAAGTCTCTTACCT 305

Qy 335 GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386  
Db 306 GCAATGAACACTTAAGACCTGAAGACAGTGGATTTATTACTGTACAGAT 357  
RESULT 11  
US-10-446-542-14  
; Sequence 14, Application US/10446542  
; Publication No. US20040018571A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; TITLE OF INVENTION: PSCT: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.54US14  
; CURRENT APPLICATION NUMBER: US/10/446,542  
; PRIOR FILING DATE: 2003-05-27  
; PRIOR APPLICATION NUMBER: US/09/855,153  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 09/564,329  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 60/124,658  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/038,261  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 453  
; TYPE: DNA  
; ORGANISM: SCID Mice  
US-10-446-542-14

Query Match 74.8%; Score 310.4; DB 17; Length 453;  
Best Local Similarity 92.6%; Pred. No. 2.3e-85;  
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
Qy 35 CATGGATTTGGGCTGATTTTTTTTATTGTTCTTTTAAAGGGGTCAGAGTGAAGTGA 94  
Db 6 CTTCGGGTGAGCTGGGTTTATTGTTCTTTTAAAGGGGTCGGAGTGAAGTGA 65  
Qy 95 GCTTGAGAGTCTGGAGAGGCTTGGTGCAACCTGGAGGATCCATGAACTCTCTGTGT 154  
Db 66 GCTTGAGAGTCTGGAGAGGCTGGTGCAACCTGGAGGATCCATGAACTCTCTGTGT 125  
Qy 155 AGCCTCTGGATTTACTTTTCAGTGCTACTGATGCTTTGGTCCGCCAGTCTCCAGAA 214  
Db 126 AGCCTCTGGATTTACTTTTCAGTAATTTCTGATGACTTTGGTCCGCCAGTCTCCAGAA 185  
Qy 215 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTTGAAATCTGATAATTTATGCAACATATGC 274  
Db 186 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTTGAAATTTATGCAACATATGC 245  
Qy 275 GGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCGAAAGTCTCTTACCT 334  
Db 246 GGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCGAAAGTCTCTTACCT 305  
Qy 335 GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386  
Db 306 GCAATGAACACTTAAGACCTGAAGACAGTGGATTTATTACTGTACAGAT 357



Db 126 AGCCTCTGATTACTTTTCAGTAATTAATGAGTCTGGTCCGCGAGTCTCCAGAGAA 185  
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Db 186 GGGGCTTGAGTGGTTCGAAATTAAGATGAAATCTGATAATTAATGCAACATATATGC 245  
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Db 246 GGAGTCTGGAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAGTCTCTACCT 305  
QY 335 GCAATGAACAGCTTAAGAGCTGAAGACAGATGAGTGTATTAATGATGACAGAT 386  
Db 306 GCAATGAACAGCTTAAGAGCTGAAGACAGATGAGTGTATTAATGATGACAGAT 357

RESULT 14  
US-09-883-758-3  
; Sequence 3, Application US/09883758  
; Patent No. US20020058804A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbas III, Carlos F.  
; APPLICANT: Shabat, Doron  
; APPLICANT: Rader, Christoph  
; APPLICANT: List, Benjamin  
; APPLICANT: Lerner, Richard A.  
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
; FILE REFERENCE: PLF00115  
; CURRENT APPLICATION NUMBER: US/09/883,758  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US/09/318,661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 856  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
; OTHER INFORMATION: residue sequence of catalytic fragment.  
; NAME/KEY: CDS  
; LOCATION: (1)..(855)  
US-09-883-758-3

Query Match 65.4%; Score 271.6; DB 9; Length 856;  
Best Local Similarity 92.3%; Pred. No. 3e-73;  
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 87 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTGCACCTGGAGGATCCATGAACATC 146  
Db 460 GAGGTGATCTGGTGGAGTCTGGAGGAGCTTGGTGCACCTGGAGGATCCATGAACATC 519  
QY 147 TCCTGTGTAGCCTCTCGAATTAATTAATGAGTCTGGTTCGCGCAGTCT 206  
Db 520 TCCTGTGTGTCTCGAATTAATTAATGAGTCTGGTTCGCGCAGTCT 579  
QY 207 CCAGAGAAGGGCTTGAGTGGTTCGTAATTAATTAATGAGTCTGGTTCGCGCAGTCT 266  
Db 580 CCAGAGAAGGGCTTGAGTGGTTCGTAATTAATTAATGAGTCTGGTTCGCGCAGTCT 639  
QY 267 CATTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAGTCTGT 326  
Db 640 CATTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAGTCTGT 699  
QY 327 CTCTACCTGCAATGAACAGCTTTAAGAGCTGAAGACAGATGGAGTCTTATCTGTACAGAT 386  
Db 700 CTCTACCTGCAATGAACAGCTTTAAGAGCTGAAGACAGATGGAGTCTTATCTGTACAGAT 759  
QY 387 TTCATAGACT 396  
Db 760 TATTTTACT 769

RESULT 15  
US-09-883-758-6/C  
; Sequence 6, Application US/09883758  
; Patent No. US20020058804A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbas III, Carlos F.  
; APPLICANT: Shabat, Doron  
; APPLICANT: Rader, Christoph  
; APPLICANT: List, Benjamin  
; APPLICANT: Lerner, Richard A.  
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
; FILE REFERENCE: PLF00115  
; CURRENT APPLICATION NUMBER: US/09/883,758  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US/09/318,661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 856  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
; OTHER INFORMATION: residue sequence of catalytic fragment.  
US-09-883-758-6  
Query Match 65.4%; Score 271.6; DB 9; Length 856;  
Best Local Similarity 92.3%; Pred. No. 3e-73;  
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 87 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTGCACCTGGAGGATCCATGAACATC 146  
Db 397 GAGGTGATCTGGTGGAGTCTGGAGGAGCTTGGTGCACCTGGAGGATCCATGAACATC 338  
QY 147 TCCTGTGTAGCCTCTCGAATTAATTAATGAGTCTGGTTCGCGCAGTCT 206  
Db 337 TCCTGTGTGTCTCGAATTAATTAATGAGTCTGGTTCGCGCAGTCT 278  
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Db 277 CCAGAGAAGGGCTTGAGTGGTTCGTAATTAATTAATGAGTCTGGTTCGCGCAGTCT 218  
QY 267 CATTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAGTCTGT 326  
Db 217 CATTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAGTCTGT 158  
QY 327 CTCTACCTGCAATGAACAGCTTTAAGAGCTGAAGACAGATGGAGTCTTATCTGTACAGAT 386  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0  
Searched: 45554873 seqs, 20411521753 residues  
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Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	415	100.0	415	30	US-09-674-716B-1
2	415	100.0	415	30	US-09-674-716B-46
3	310.4	74.8	453	21	US-09-359-326A-14
4	310.4	74.8	453	36	US-09-854-811-14
5	310.4	74.8	453	36	US-09-855-153-14
6	310.4	74.8	453	50	US-10-224-720-14
7	310.4	74.8	453	50	US-10-225-779-14
8	310.4	74.8	453	50	US-10-225-784-14
9	310.4	74.8	453	53	US-10-374-381-14
10	310.4	74.8	453	54	US-10-446-542-14
11	310.4	74.8	453	62	US-10-769-074-26
12	310.4	74.8	453	62	US-10-769-308-26
13	310.4	74.8	453	67	US-10-997-735-14
14	310.4	74.8	453	68	US-11-021-950-14
15	294.2	70.9	412	33	US-09-724-671-4993
16	294.2	70.9	924	48	US-10-144-771-46557
17	294.2	70.9	924	106	US-60-360-207-46557
18	293.4	70.7	435	33	US-09-724-671-4676
19	291.2	70.2	400	33	US-09-724-671-5111
20	291	70.1	481	7	US-08-101-329-1
21	289.8	69.8	839	48	US-10-144-771-14209
22	289.8	69.8	839	106	US-60-360-207-14209
23	282.2	68.0	431	33	US-09-724-671-4759
24	279.6	67.4	463	33	US-09-724-671-4435
25	272	65.5	389	33	US-09-724-671-5070
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28	269.4	64.9	403	5	US-07-977-706A-12
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34	269.2	64.9	445	56	US-10-507-941-1
35	267.8	64.5	360	11	US-08-541-373-27
36	267.8	64.5	360	11	US-08-541-373A-27
37	267.2	64.4	366	10	US-08-477-512A-1
38	267.2	64.4	366	10	US-08-486-817A-1
39	266.2	64.1	1515	1	PCT-US02-25766-11314
40	265.4	64.0	765	50	US-10-239-656-68
41	265.2	63.9	809	5	US-07-900-407D-1
42	263	63.4	403	41	US-09-947-839-65
43	263	63.4	403	41	US-09-947-839B-65
44	262.4	63.2	768	50	US-10-239-656-60
45	262.4	63.2	1509	50	US-10-239-656-76

ALIGNMENTS

RESULT 1

US-09-674-716B-1  
; Sequence 1, Application US/09674716B  
; GENERAL INFORMATION:  
; APPLICANT: BONNEFOY, Jean-Yves M.P.  
; APPLICANT: CROWE, James S.  
; APPLICANT: ELLIS, Jonathan H.  
; APPLICANT: RAPSON, Nicholas T.  
; APPLICANT: SHEARIN, Jean  
; TITLE OF INVENTION: Antibodies to CD23, derivatives thereof, and their therapeutic use  
; FILE REFERENCE: 1430-256 / PG3433USW0  
; CURRENT APPLICATION NUMBER: US/09/674,716B  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: CA 2,328,606  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: PCT/GB99/01434  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: GB 9809839.5  
; PRIOR FILING DATE: 1998-05-09  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: MS Word  
; SEQ ID NO 1  
; LENGTH: 415  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)..(413)  
US-09-674-716B-1

Query Match 100.0%; Score 415; DB 30; Length 415;  
Best Local Similarity 100.0%; Pred. No. 2.3e-108;  
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 TTGTTCTTTTAAAGGGTCCAGAGTGAAGTCTGAGAGTCTGAGAGGAGGCTTGG 120  
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QY 181 ACTGATGTCTTGGTCCGCCAGTCTCCAGAGAGGGGCTTCAGTGGGTTGCTGAAATTA 240  
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QY 241 GATTGAAATCTGATTAATTATGCAACACATTTATGCGAGTCTGTAAAGGGAAGTTCA 300  
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QY 301 TCTCAAGAGATGATTCCAAAGTCTCTCTACTCTGCAAAATGAACAGCTTAAGAGCTGA 360  
Db 301 TCTCAAGAGATGATTCCAAAGTCTCTCTACTCTGCAAAATGAACAGCTTAAGAGCTGA 360  
QY 361 ACAGTGGAGTTTATTACTCTAGATTTTATAGATTTTATAGATTTTATAGATTTTATAG 415  
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US-09-674-716B-46/c  
; Sequence 46, Application US/09674716B  
; GENERAL INFORMATION:  
; APPLICANT: BONNEFOY, Jean-Yves M.P.  
; APPLICANT: CROWE, James S.  
; APPLICANT: ELLIS, Jonathan H.  
; APPLICANT: RAPSON, Nicholas T.  
; APPLICANT: SHEARIN, Jean  
; TITLE OF INVENTION: Antibodies to CD23, derivatives thereof, and their therapeutic use



FILE REFERENCE: 1430-256 / PG3433USW0  
CURRENT APPLICATION NUMBER: US/09/674,716B  
CURRENT FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: CA 2,328,606  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: PCT/GB99/01434  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: GB 9809839.5  
PRIOR FILING DATE: 1998-05-09  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: MS Word  
SEQ ID NO 46  
LENGTH: 415  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-674-716B-46

Query Match 100.0%; Score 415; DB 30; Length 415;  
Best Local Similarity 100.0%; Pred. No. 2.3e-108;  
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 3  
US-09-359-326A-14  
Sequence 14, Application US/09359326A  
GENERAL INFORMATION:  
APPLICANT: Reiter, Robert E.  
APPLICANT: Witte, Owen N.  
APPLICANT: Saffran, Douglas C.  
TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
FILE REFERENCE: 30435.54US14  
CURRENT FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 08/814,279  
PRIOR FILING DATE: 1997-03-10  
PRIOR APPLICATION NUMBER: 60/071,141  
PRIOR FILING DATE: 1998-01-12  
PRIOR APPLICATION NUMBER: 60/074,675  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: 60/113,230  
PRIOR FILING DATE: 1998-12-21  
PRIOR APPLICATION NUMBER: 60/120,536  
PRIOR FILING DATE: 1999-02-17  
PRIOR APPLICATION NUMBER: 60/124,658  
PRIOR FILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/038,261  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 09/203,939  
PRIOR FILING DATE: 1998-12-02  
PRIOR APPLICATION NUMBER: 09/251,835  
PRIOR FILING DATE: 1999-02-17  
PRIOR APPLICATION NUMBER: 09/308,503  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 453  
TYPE: DNA  
ORGANISM: SCID Mice  
US-09-359-326A-14  
Query Match 74.8%; Score 310.4; DB 21; Length 453;  
Best Local Similarity 92.6%; Pred. No. 3.2e-78;  
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QY 95 GCTTGAGGATCTGAGGAGGCTTGGTGCACCTGGAGGATCCATGAAACTCTCTCTGT 154  
DB 66 GCTTGAGGATCTGAGGAGGCTTGGTGCACCTGGAGGATCCATGAAACTCTCTCTGT 125  
QY 155 AGCTCTGATTTTACATTTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 214  
DB 126 AGCTCTGATTTTACATTTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 185  
QY 215 GGGGCTTGAGTGGTTCGAAATTTAGTTGAATCTGATAATTTATGCAACACATTTAT 274  
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DB 246 GGAGTCTGTAAGGGAAGTTACCATCTCAAGAGATGATTTCCAAAGTCTCTCTACCT 305  
QY 335 GCNAAATGAACAGCTTAAGAGCTTGAACAGAGTGAAGTGAAGTGAAGTGAAGTGA 386  
DB 306 GCNAAATGAACAGCTTAAGAGCTTGAACAGAGTGAAGTGAAGTGAAGTGAAGTGA 357  
RESULT 4  
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Sequence 14, Application US/09854811  
GENERAL INFORMATION:  
APPLICANT: Reiter, Robert E.  
APPLICANT: Witte, Owen N.  
APPLICANT: Saffran, Douglas C.  
TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
FILE REFERENCE: 30435.54US14  
CURRENT FILING DATE: 2001-05-14  
PRIOR APPLICATION NUMBER: 09/564,329  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 09/359,326  
PRIOR FILING DATE: 1999-07-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 453  
TYPE: DNA  
ORGANISM: SCID Mice  
US-09-854-811-14  
Query Match 74.8%; Score 310.4; DB 36; Length 453;  
Best Local Similarity 92.6%; Pred. No. 3.2e-78;  
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
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Db 246 GGAGTCTGTAAGGGAATTCACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 305  
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386  
Db 306 GCAAAATGAACACTTAAGACCTGAAGACAGTGGAGTTTATTACTGTACAGAT 357

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; Sequence 14, Application US/10374381  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.5AUS14  
; CURRENT APPLICATION NUMBER: US/10/374,381  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: US/09/564,329A  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 60/124,658  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 09/203,939  
; PRIOR FILING DATE: 1998-12-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 453  
; TYPE: DNA  
; ORGANISM: SCID Mice  
US-10-374-381-14

Query Match 74.8%; Score 310.4; DB 53; Length 453;  
Best Local Similarity 92.6%; Pred. No. 3.2e-78;  
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 35 CATGGATTTGGGCTGATTTTTTATTGTTCTTTTAAAGGGGTCCAGAGTGAAGTAA 94  
Db 6 CTTCGGGTTCAGCTGGGTTTTTATTGTTCTTTTAAAGGGGTCCGAGTGAAGTGA 65  
QY 95 GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTCGAGAGTCCATGAAACTCTCTGTGT 154  
Db 66 GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTCGAGAGTCCATGAAACTCTCTGTGT 125  
QY 155 AGCTCTCGATTTACTTTTCAGTGGCTTCTGGATGCTTGGGTCCGCGAGTCTCCAGAA 214  
Db 126 AGCTCTCGATTTACTTTTCAGTGAATTAATTCAGTGAATTCAGTGAATTCAGTGA 185  
QY 215 GGGCTTGGTGGTCTGAAATTAAGATTGAAATCTGAAATTAATTCGAAACATTATGC 274  
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QY 215 GGGCTTGGTGGTCTGAAATTAAGATTGAAATCTGAAATTAATTCGAAACATTATGC 274  
Db 186 GGGCTTGGTGGTCTGAAATTCGATTGAGATCTGAAATTAATTCGAAACATTATGC 245  
QY 275 GGAGTCTGTAAGGGAAGTTACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 334  
Db 246 GGAGTCTGTAAGGGAATTCACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 305  
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386

Db 246 GGAGTCTGTAAGGGAATTCACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 305  
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386  
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; Sequence 14, Application US/10446542  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.5AUS14  
; CURRENT APPLICATION NUMBER: US/10/446,542  
; CURRENT FILING DATE: 2003-05-27  
; PRIOR APPLICATION NUMBER: US/09/855,153  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 09/564,329  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 60/124,658  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 453  
; TYPE: DNA  
; ORGANISM: SCID Mice  
US-10-446-542-14

Query Match 74.8%; Score 310.4; DB 54; Length 453;  
Best Local Similarity 92.6%; Pred. No. 3.2e-78;  
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 35 CATGGATTTGGGCTGATTTTTTATTGTTCTTTTAAAGGGGTCCAGAGTGAAGTAA 94  
Db 6 CTTCGGGTTCAGCTGGGTTTTTATTGTTCTTTTAAAGGGGTCCGAGTGAAGTGA 65  
QY 95 GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTCGAGAGTCCATGAAACTCTCTGTGT 154  
Db 66 GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTCGAGAGTCCATGAAACTCTCTGTGT 125  
QY 155 AGCTCTCGATTTACTTTTCAGTGGCTTCTGGATGCTTGGGTCCGCGAGTCTCCAGAA 214  
Db 126 AGCTCTCGATTTACTTTTCAGTGAATTAATTCAGTGAATTCAGTGAATTCAGTGA 185  
QY 215 GGGCTTGGTGGTCTGAAATTAAGATTGAAATCTGAAATTAATTCGAAACATTATGC 274  
Db 186 GGGCTTGGTGGTCTGAAATTCGATTGAGATCTGAAATTAATTCGAAACATTATGC 245  
QY 275 GGAGTCTGTAAGGGAAGTTACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 334  
Db 246 GGAGTCTGTAAGGGAATTCACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 305  
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386

Db 306 GCAATGAAACAACCTTAAGACCTGAAGACAGCTGGAATTTATTACTGTACAGAT 357  
US-10-769-074-26  
; Sequence 26, Application US/10769074  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: The Regents of the University of California  
; APPLICANT: Agensys, Inc.  
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof  
; FILE REFERENCE: 02307K-141589US  
; CURRENT APPLICATION NUMBER: US/10/769,074  
; CURRENT FILING DATE: 2004-01-29  
; PRIOR APPLICATION NUMBER: US/10/769,308  
; PRIOR FILING DATE: 2004-01-29  
; PRIOR APPLICATION NUMBER: US 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: US 60/228,816  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: US 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: US 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: US 09/203,939  
; PRIOR FILING DATE: 1998-12-02  
; PRIOR APPLICATION NUMBER: US 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: US 09/251,835  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: US 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 453  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:heavy chain  
; OTHER INFORMATION: variable domain region of PSCA monoclonal antibody  
; OTHER INFORMATION: 2H9  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(453)  
US-10-769-074-26  
Query Match 74.8%; Score 310.4; DB 62; Length 453;  
Best Local Similarity 92.6%; Pred. No. 3.2e-78;  
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
Qy 35 CATGGATTTGGCGCTGATTTTTTTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGTGA 94  
Db 6 CTTCCGGGTGAGCTGGGTTTTTATTTATTTGTTCTTTTAAAGGGGTCGGAGTGAAGTGA 65  
Qy 95 GCTTGAGGAGCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGT 154  
Db 66 GCTTGAGGAGCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGT 125  
Qy 155 AGCCTCTGGATTTACTTTTCACTGGCTACTCGATGTCTTGGGTCGGCCAGTCTCCAGAGAA 214  
Db 126 AGCCTCTGGATTTACTTTTCACTGGCTACTCGATGTCTTGGGTCGGCCAGTCTCCAGAGAA 185  
Qy 215 GGGGCTTGAGTGGGTGCTGCAATTGATTTGAAATCTGATAATATGCAACACATTATGC 274  
Db 186 GGGGCTTGAGTGGGTGCTGCAATTGATTTGAAATCTGATAATATGCAACACATTATGC 245

Qy 275 GGAGTCTGTGAAAGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTGTCTCTACCT 334  
Db 246 GGAGTCTGTGAAAGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTGTCTCTACCT 305  
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; Sequence 26, Application US/10769308  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: The Regents of the University of California  
; APPLICANT: Agensys, Inc.  
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof  
; FILE REFERENCE: 02307K-141589US  
; CURRENT APPLICATION NUMBER: US/10/769,308  
; CURRENT FILING DATE: 2004-01-29  
; PRIOR APPLICATION NUMBER: US 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: US 60/228,816  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: US 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: US 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: US 09/203,939  
; PRIOR FILING DATE: 1998-12-02  
; PRIOR APPLICATION NUMBER: US 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: US 09/251,835  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: US 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 453  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:heavy chain  
; OTHER INFORMATION: variable domain region of PSCA monoclonal antibody  
; OTHER INFORMATION: 2H9  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(453)  
US-10-769-308-26  
Query Match 74.8%; Score 310.4; DB 62; Length 453;  
Best Local Similarity 92.6%; Pred. No. 3.2e-78;  
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
Qy 35 CATGGATTTGGCGCTGATTTTTTTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGTGA 94  
Db 6 CTTCCGGGTGAGCTGGGTTTTTATTTATTTGTTCTTTTAAAGGGGTCGGAGTGAAGTGA 65  
Qy 95 GCTTGAGGAGCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGT 154  
Db 66 GCTTGAGGAGCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGT 125  
Qy 155 AGCCTCTGGATTTACTTTTCACTGGCTACTCGATGTCTTGGGTCGGCCAGTCTCCAGAGAA 214

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Qy	215	GGGCTCTGAGTGGTGTCTGAAATTAGAATTCGAATTCGATAAATATGCAACACATTATGC		274
Db	186	GGGCTTGTGAGTGGTGTCTGAAATTCGATTCGATCTGAAATTTATGCAACACATTATGC		245
Qy	275	GGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAAGTCGTCTCTACCT		334
Db	246	GGAGTCTGTGAAAGGGAATTCACCATCTCAAGAGATGATTCCAAAAGTCGTCTCTACCT		305
Qy	335	GCAATATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTA	CTGTGTACAGAT	386
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RESULT 13  
US-10-997-735-14  
Sequence 14, Application US/10997735  
GENERAL INFORMATION:  
APPLICANT: Reiter, Robert E.  
APPLICANT: Witte, Owen N.  
APPLICANT: Safran, Douglas C.  
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
FILE REFERENCE: 30435.54US14  
CURRENT APPLICATION NUMBER: US/10/997,735  
CURRENT FILING DATE: 2004-11-23  
PRIOR APPLICATION NUMBER: US/10/225,779  
PRIOR FILING DATE: 2002-08-21  
PRIOR APPLICATION NUMBER: US/09/564,329  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 09/359,326  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 08/814,279  
PRIOR FILING DATE: 1997-03-10  
PRIOR APPLICATION NUMBER: 60/071,141  
PRIOR FILING DATE: 1998-01-12  
PRIOR APPLICATION NUMBER: 60/074,675  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: 60/113,230  
PRIOR FILING DATE: 1998-12-21  
PRIOR APPLICATION NUMBER: 60/120,536  
PRIOR FILING DATE: 1999-02-17  
PRIOR APPLICATION NUMBER: 60/124,658  
PRIOR FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 09/038,261  
PRIOR FILING DATE: 1998-03-10  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0

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/ LENGTH: 453
/ TYPE: DNA
/ ORGANISM: SCID Mice
US-10-997-735-14

Query Match      74.8%;   Score 310.4;   DB 67;   Length 453;
Best Local Similarity 92.6%;   Pred. No. 3.2e-78;
Matches 326;   Conservative 0;   Mismatches 26;   Indels 0;   Gaps 0;

35 CATGGATTTCGGGCTGATTTTTTTTATTGTTCTTTTAAAGGGGTCACAGCTGAAGTGAA 94
Db      6 CTTGGGTTGAGCTGGGTTTATATGTTCTTTTAAAGGGGTCGGAGTGAAGTGAG 65

95 GCTTGAGAGAGTCTGGAGAGGCTGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGT 154
Db      66 GCTTGAGAGTCTGGAGAGGCTGGGTCAACCTGGAGATCCATGAAACTCTCCTGTGT 125

155 AGCCTCTGGATTACTTTTCAGTGGCTACTCGATGTCTTTGGGTCGCGCAGTCTCCAGAGAA 214
Db      126 AGCCTCTGGATTACTTTTCAGTGAATTTCTGGATGACTTGGGTCGCGCAGTCTCCAGAGAA 185

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Qy	275	GGAGTCTGTGAAAGGGAGTTCCACATCTCAAGAGATGATTTCCAAAGTCGTCCTTACCT	334
Db	246	GGAGTCTGTGAAAGGGGAAATTCACCATCTCAAGAGATGATTTCCAGAGTCGGTCTCTTACCT	305
Qy	335	GCAATGAACACAGCTTAAGAGCTGAAGACAGTGGAGTCTTTTACTCTGTACAGAT	386
Db	306	GCAATGAACCACTTTAAGACCTGAAGACAGTGGAAATTTATTACTCTGTACAGAT	357

RESULT 14  
US-11-021-950-14  
; Sequence 14, Application US/11021950  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.54US14  
; CURRENT APPLICATION NUMBER: US/11/021,950  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US/10/225,784  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US/09/564,329  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: 60/124,658  
; PRIOR FILING DATE: 1999-03-16  
; PRIOR APPLICATION NUMBER: 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; Remaining prior application data removed - See File Wrapper or PALM.

Query Match	74.8%	Score 310.4	DB 68	Length 453
Best Local Similarity	92.6%	Pred. No. 3.2e-78		
Matches 326	Conservative 0	Mismatches 26	Indels 0	Gaps 0
Qy	35	CATCGATTTCGGGCTGATTTTTTTTATTTGTTCTTTTAAAGGGGTCCAGAGTGAAGTGAA	94	
Db	6	CTTCGGGTTGAGCTGGGTTTTTATTTGTTCTTTTAAAGGGGTCCGAGTGAAGTGAG	65	
Qy	95	GCTTGCAGGAGTCTGGAGGAGGCTTTGGTGCAACCTGGAGGATCCATGAAAACTCTCTCTGT	154	
Db	66	GCTTGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAAAACTCTCTCTGT	125	
Qy	155	AGCCTCTGAGTTTACTTTTCAGTGGCTACTGATGCTTGGGTCGGCAGTCTCCAGAGAA	214	
Db	126	AGCCTCTGATTTTACTTTTCAGTAATTACTGTGATGACTTGGGTCGGCAGTCTCCAGAGAA	185	
Qy	215	GGGGCTTGAGTGGGTTGCTGAAATTTAGATTTCAAAATCTCATATATATGCAACACATATTGC	274	
Db	186	GGGGCTTGAGTGGGTTGCTGAAATTCGATTTGAGATCTGAAATTTATGCAACACATATTGC	245	
Qy	275	GGAGTCTGTGAAAGGGAGTTTCAACATCTCAAGAGATGATTTCCAAAGTCGTCTCTACT	334	

Db 246 GGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCACAGAGTCTCTCTACCT 305  
 Qy 335 GCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386  
 Db 306 GCAAATGAACAACTTAAGACCTGAAGACAGTGGAAATTTATTACTGTACAGAT 357

RESULT 15

US-09-724-671-4993  
 ; Sequence 4993, Application US/09724671  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Watson, James D  
 ; APPLICANT: Murison, James G  
 ; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
 ; FILE REFERENCE: 1050U2  
 ; CURRENT APPLICATION NUMBER: US/09/724,671  
 ; CURRENT FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: U.S. No. 60/171,678  
 ; PRIOR FILING DATE: 1999-12-23  
 ; NUMBER OF SEQ ID NOS: 21907  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4993  
 ; LENGTH: 412  
 ; TYPE: DNA  
 ; ORGANISM: Mouse  
 ; US-09-724-671-4993

Query Match 70.9%; Score 294.2; DB 33; Length 412;  
 Best Local Similarity 93.1%; Pred. No. 1.4e-73;  
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 Qy 112 GAGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTTACTT 171  
 Db 133 GAGGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTTACTT 192  
 Qy 172 TCAGTGGCTACTGGATGCTTTGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGGTG 231  
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 Qy 292 AGTTCACCATCTCAAGAGATGATTCGAAAAGTGTCTCTACCTGCAAAATGAACAGCTTAA 351  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-09-674-716B-2

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: gb\_on:.\*  
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6: gb\_pat:.\*  
7: gb\_ph:.\*  
8: gb\_pl:.\*  
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11: gb\_sts:.\*  
12: gb\_sy:.\*  
13: gb\_un:.\*  
14: gb\_vi:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	437	100.0	437	6 AX010644	Sequence
5	373.2	85.4	431	10 MUSIGKNG	M19910 Mouse Ig re
6	371.6	85.0	458	10 MUSIGKCNF	M19909 Mouse Ig re
7	333.4	76.3	1400	10 MUSIGKAH	J00553 Mouse ig ka
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9	317.2	72.6	339	6 AR072863	AR072863 Sequence
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28	293.2	67.2	396	10 MMU277812	AJ277812 Mus muscu
29	293.2	67.1	464	6 A29573	A29573 M.musculus
30	293.2	67.1	464	6 I25724	I25724 Sequence 15
31	293.2	67.1	958	10 MMU555479	AJ555479 Mus muscu
32	292.6	67.0	451	10 MMSV5PKL	Z49934 M.musculus
33	288.8	66.1	396	10 AF045509	AF045509 Mus muscu
34	287.4	65.8	773	6 AX825304	AX825304 Sequence
35	286.8	65.6	961	6 E08433	E08433 cDNA encodi
36	286.4	65.5	978	10 MUSIGKVB	M15553 Mouse germi
37	284.4	65.1	399	10 MMU92070	U92070 Mus musculu
38	284.4	65.1	426	6 AX825286	AX825286 Sequence
39	284.4	65.1	982	10 MUSIGKVA	M15552 Mouse germi
40	284	65.0	396	10 AF045515	AF045515 Mus muscu
41	280	64.1	593	10 MMIGMM65A	X57856 M.musculus
42	280	64.1	935	10 BC031349	BC031349 Mus muscu
43	276.4	63.2	399	6 A23299	A23299 M.musculus
44	276.4	63.2	399	6 AR013733	AR013733 Sequence
45	276.4	63.2	399	6 AR275126	AR275126 Sequence

ALIGNMENTS

RESULT 1	BD232418	437 bp DNA linear	PAT 17-JUL-2003
LOCUS	BD232418	Antibodies against CD23, derivatives thereof and therapeutic	
DEFINITION	BD232418	utilization of the same.	
ACCESSION	BD232418	VERSION	GI:33042188
KEYWORDS	JP 2002514421-A/2.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1 (bases 1 to 437)		
AUTHORS	Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and Shearin,J.		
TITLE	Antibodies against CD23, derivatives thereof and therapeutic		
JOURNAL	utilization of the same		
COMMENT	Patent: JP 2002514421-A 2 21-MAY-2002; GLAXO GROUP LTD		
	OS Mus musculus (mouse)		
	PN JP 2002514421-A/2		
	PD 21-MAY-2002		
	PF 07-MAY-1999 JP 2000548470		
	PR 07-MAY-1998 GB 9809839.5		
	PI JEAN YVES MARCEL PAUL BONNEFOY, SCOTT JAMES CROWE, JONATHAN PI HENRY ELLIS,		
	PI NICHOLAS TIMOTHY RAPSON, JEAN SHEARIN		
	PC C12N15/02,A61K39/395,C07K16/28,C12N15/00		
	CC Antibodies against CD23, derivatives thereof and therapeutic		
	CC utilization		
	CC of the same		
	FT Key	Location/Qualifiers	
	FT CDS	(3)..(437).	
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Query Match	100.0%;	Score 437;	DB 6; Length 437;
Best Local Similarity	100.0%;	Pred. No. 6.1e-134;	



Query Match 100.0%; Score 437; DB 6; Length 437;  
Best Local Similarity 100.0%; Pred. No. 6.1e-134;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAAGTTCTGG 60
Qy 61 GGGTGTCTTATGTTCTCGGATCTCTGAGTCACTGAGTCACTGAGGATATTTGATTAACCCAGGATGAAC 120
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Qy 181 TCCGTGTATAGGATGGGAAGACATCTTGAATGTTTCTGAGAGCCAGGACCAATCTC 240
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Qy 241 CTACGCTCCTGATGATTTGATGTCACCCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG 300
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Qy 301 GCAGTGGGTGAGGACAGATTTACCTCGGAAATCAGTAGAGTGAAGGCTGAGGATGG 360
Db 301 GCAGTGGGTGAGGACAGATTTACCTCGGAAATCAGTAGAGTGAAGGCTGAGGATGG 360
Qy 361 GTGTGTATTACTGTCACAACTTTAGAGTATCCATTCAGTTCCGCTCGGGGACAAAGT 420
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Qy 421 TGGAAATAAAACGTACG 437
Db 421 TGGAAATAAAACGTACG 437
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RESULT 4  
AX010644/c  
LOCUS AX010644 437 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 47 from Patent WO9958679.  
ACCESSION AX010644  
VERSION AX010644.1 GI:9997453  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1  
AUTHORS Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.  
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses  
JOURNAL Patent: WO 9958679-A 47 19-NOV-1999; and their therapeutic uses  
Bonnefoy Jean Yves Marcel Paul (FR); Crowe Scott James (GB); Rapson  
Nicholas Timothy (GB); Glaxo Group Ltd (GB); Ellis Jonathan Henry  
(GB); Shearin Jean (US)

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ORIGIN  
Query Match 100.0%; Score 437; DB 6; Length 437;  
Best Local Similarity 100.0%; Pred. No. 6.1e-134;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GGGTGTCTTATGTTCTCGGATCTCTGAGTCACTGAGTCACTGAGGATATTTGATTAACCCAGGATGAAC 120
Db 377 GGGTGTCTTATGTTCTCGGATCTCTGAGTCACTGAGTCACTGAGGATATTTGATTAACCCAGGATGAAC 318
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Qy 121 TCTCCAAATCCTGTCACCTTCTGGAGAAATCAGTTTCATCTCTGTCAGGTCCTAGTAAGAGTC 180
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Qy 181 TCTGTATATAGGATGGGAAGACATATCTTGAATGTTTCTGTCAGAGACCAAGGACAAATCTC 240
Db 257 TCTGTATATAGGATGGGAAGACATATCTTGAATGTTTCTGTCAGAGACCAAGGACAAATCTC 198
Qy 241 CTACGCTCCTGATGATTTGATGTCACCCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG 300
Db 197 CTACGCTCCTGATGATTTGATGTCACCCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG 138
Qy 301 GCAGTGGGTGAGGACAGATTTACCTCGGAAATCAGTAGAGTGAAGGCTGAGGATGG 360
Db 137 GCAGTGGGTGAGGACAGATTTACCTCGGAAATCAGTAGAGTGAAGGCTGAGGATGG 78
Qy 361 GTGTGTATTACTGTCACAACTTTAGAGTATCCATTCAGTTCCGCTCGGGGACAAAGT 420
Db 77 GTGTGTATTACTGTCACAACTTTAGAGTATCCATTCAGTTCCGCTCGGGGACAAAGT 18
Qy 421 TGGAAATAAAACGTACG 437
Db 17 TGGAAATAAAACGTACG 1
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RESULT 5  
MUSIGKNG  
LOCUS MUSIGKNG 431 bp mRNA linear ROD 26-MAR-1994  
DEFINITION Mouse Ig rearranged kappa-chain mRNA, clone AN06K.  
ACCESSION M19910.1  
VERSION M19910.1 GI:197027  
KEYWORDS C-region; immunoglobulin light chain; immunoglobulin-kappa;  
processed gene.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 56)  
AUTHORS Rule,G.S.  
JOURNAL Unpublished (1988)  
REFERENCE 2 (bases 1 to 431)  
AUTHORS Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.  
TITLE Sequences of 12 monoclonal anti-dinitrophenyl spin-label antibodies  
for NMR studies

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3661-3665 (1988)  
MEDLINE 88234486  
PUBMED 3375235  
COMMENT Original source text: Mouse (BALB/c) mature B cell, cDNA to mRNA,  
clone AN06K.  
Draft entry and computer-readable sequence [2] kindly submitted by  
G. Rule, 20-JUL-1988.

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32..91  
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ORIGIN  
Query Match 100.0%; Score 437; DB 6; Length 437;  
Best Local Similarity 100.0%; Pred. No. 6.1e-134;  
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAAGTTCTGG 60
Db 437 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAAGTTCTGG 378
Qy 61 GGGTGTCTTATGTTCTCGGATCTCTGAGTCACTGAGTCACTGAGGATATTTGATTAACCCAGGATGAAC 120
Db 377 GGGTGTCTTATGTTCTCGGATCTCTGAGTCACTGAGTCACTGAGGATATTTGATTAACCCAGGATGAAC 318
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JOURNAL  
MEDLINE  
PUBMED  
COMMENT

antibody variable genes  
Proc. Natl. Acad. Sci. U.S.A. 80 (11): 3439-3443 (1983)  
83221610  
6222379

Original source text: mouse cdna to myeloma m167 mrna; hybridomas  
hpcg9, hpcg10, hpcg13, hpcg22 & myelomas m511, m167 dna (see  
comment).

the v-k167 gene codes for a v region which binds phosphocholine.  
all rearrangements of the v-k167 gene reported here are productive,  
and in all cases except hybridoma hpcg13 the codon at the site of  
recombination is ccg. in hpcg13 the codon is cct. the difference  
could be due to the variability of the v-j recombination site, or  
it could be an additional somatic mutation. [3] sequenced portions  
of the j-c intron and the c-kappa gene for all of its hybridomas  
and myelomas, and found no somatic mutation in these regions. [3]  
proposes a mechanism for the generation of clustered somatic  
mutation in the v-j region.

for the germline sequences of the v-k167 v and j regions see  
<musigkhv2>, <musigkj2>. see loci beginning <musigka> for other  
rearranged kappa genes; see loci beginning <musigkv> for other  
kappa v regions and see loci beginning <musigkj> for the germline  
kappa j and c regions. in the sites table cdr=complementarity  
determining region and fr=framework region.

Complete source information:  
mouse cdna to myeloma m167 mrna [1],[2]; hybridomas hpcg9, hpcg10,  
hpcg13, hpcg22 & myelomas m511, m167 dna [3].

## FEATURES

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/notes="Ig V-K167 precursor"

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/db\_xref="GI:554091"

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SKSLLYDKGKTVLWFLRPGQSPQLLYLWSTRASGVSDRFSGSGTDFTLRIS  
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sig\_peptide

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/number=1

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409

/notes="t in germline; c in myeloma m511"

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/notes="t in germline; a in myeloma m511"

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/number=2

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variation

566

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variation

580

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variation

708

/note="a in germline; c in myeloma m167"

variation

727

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variation

764

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variation

791

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misc\_recomb

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/organism="Mus musculus"

variation

847

/note="g in hybridomas hpcg9, hpcg10, hpcg22 &amp; comment)

variation

511, m167; t in hybridoma hpcg13(see"

variation

859

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intron

885..&gt;1400

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variation

895

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variation

1082

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variation

1085

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variation

1086

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variation

1096

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variation

1159

/note="t in germline; g in hybridoma hpcg10"

variation

1229

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variation

1251

/note="c in germline; t in myeloma m167"

variation

1260

/note="t in germline; g in myeloma m167"

variation

1272

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variation

1279..1283

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variation

1289

/note="c in germline; t in hybridoma hpcg10"

variation

unreported, chromosome 6.

ORIGIN

Query Match 76.3%; Score 333.4; DB 10; Length 1400;

Best Local Similarity 95.5%; Pred. No. 2.2e-99;

Matches 343; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 79 TCTCTGGAGTCAGTGGGATATTGTGATAACCCAGAGTGAACCTCCCAATCTCTGTCACATT 138

Db 531 TTTCAGAGTCAGTGGGATATTGTGATAACCCAGAGTGAACCTCCCAATCTCTGTCACATT 590

QY 139 CTGGAGAATCAGTTTCCATCTCTCCAGGTCTAGTAAGAGTCTCTGTATAAGGATGGGA 198

Db 591 CTGGAGAATCAGTTTCCATCTCTCCAGGTCTAGTAAGAGTCTCTGTATAAGGATGGGA 650

QY 199 AGACATCTTGAATTTGGTTTCTGCAGACACAGGACATCTCTCAGCTCCCTGATGTATT 258

Db 651 AGACATCTTGAATTTGGTTTCTGCAGACACAGGACATCTCTCAGCTCCCTGATGTATT 710

QY 259 TCATGTCCACCCGTCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAG 318

Db 711 TGATGTCCACCCGTCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAG 770

QY 319 ATTTTCCCTCGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAAC 378

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Db      771 ATTTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTCGGTGTGTATTACTGTCAAC 830
Qy      379 AACTTTAGAGTATCATTCACGTTCCGGCTCGGGGACAAAGTTGGAAATPAAACGTAAG 437
Db      831 AACTTTAGAGTATCCGCTCACGTTCCGGTCTGGGACCAAGCTGGAGCTGAAACGTAAG 889

RESULT 8
MMU29425      339 bp mRNA linear ROD 03-FEB-1998
LOCUS      Mus musculus anti-PC rearranged Ig kappa chain V-J region mRNA,
DEFINITION      hybridoma 31-34-2, partial cds.
ACCESSION      U29425
VERSION      U29425.1 GI:2745913
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE      1 (bases 1 to 339)
AUTHORS      Guo,W.X., Burger,A.M., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
              Kenny,J.J.
TITLE      Sequence changes at the V-D junction of the VH1 heavy chain of
              anti-phosphocholine antibodies alter binding to and protection
              against Streptococcus pneumoniae
JOURNAL      Int. Immunol. 9 (5), 665-677 (1997)
MEDLINE      97328374
PUBMED      9184912
REFERENCE      2 (bases 1 to 339)
AUTHORS      Guo,W.X., Burger,A., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
              Kenny,J.J.
TITLE      Direct Submission
JOURNAL      Submitted (19-JUN-1995) FCRDC, NCI, P.O. Box B, Frederick, MD
              21702-1201, USA
REFERENCE      3 (bases 1 to 339)
AUTHORS      Guo,W.X., Burger,A., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
              Kenny,J.J.
TITLE      Direct Submission
JOURNAL      Submitted (05-JAN-1998) FCRDC, NCI, P.O. Box B, Frederick, MD
              21702-1201, USA
REMARK      Nucleotide and protein sequence update by submitter
COMMENT      On Jan 5, 1998 this sequence version replaced gi:903959.
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Best Local Similarity 97.9%; Pred. No. 3.2e-97;
Matches 33; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      96 GATATTGTGATAACCCAGGATGAACCTCCAATCTGCTCACTTCTGGAGAAATCAGTTTCC 155
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156 ATCTCTGCAGGCTTAGTAAGTCTCTCTATTAAGGATGGAGACATACACTTGAATTGG 215
61 ATCTCTGCAGGCTTAGTAAGTCTCTCTATTAAGGATGGAGACATACACTTGAATTGG 120

216 TTTCTGCAGAGACACAGGACAAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCGTGCA 275
121 TTTCTGCAGAGACACAGGACAAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCGTGCA 180

276 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTACCCCTGGAAATC 335
181 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTACCCCTGGAAATC 240

336 AGTAGAGTGAAGCTGAGGATGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 395
241 AGTAGAGTGAAGCTGAGGATGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 300

396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATPAAACG 433
301 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATPAAACG 338

RESULT 10
AR166313      339 bp DNA linear PAT 17-OCT-2001
LOCUS      Sequence 99 from patent US 6280987.
DEFINITION
ACCESSION      AR166313
VERSION      AR166313.1 GI:16241580
KEYWORDS

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Qy      216 TTTCTGCAGAGACACAGGACAAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCGTGCA 275
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181 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTACCCCTGGAAATC 240

336 AGTAGAGTGAAGCTGAGGATGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 395
241 AGTAGAGTGAAGCTGAGGATGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 300

396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATPAAACG 433
301 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATPAAACG 338

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LOCUS      Sequence 88 from patent US 5948658.
DEFINITION
ACCESSION      AR072863
VERSION      AR072863.1 GI:9999626
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 339)
AUTHORS      Landry,D.W.
TITLE      Anti-cocaine catalytic antibody
JOURNAL      Patent: US 5948658-A 88 07-SEP-1999;
              Location/Qualifiers
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source      1..339
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ORIGIN
Query Match      72.6%; Score 317.2; DB 6; Length 339;
Best Local Similarity 96.2%; Pred. No. 5e-94;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy      96 GATATTGTGATAACCCAGGATGAACCTCCAATCTGCTCACTTCTGGAGAAATCAGTTTCC 155
Db      1 GATATTGTGATGACCCAGGATGAACCTCCAATCTGCTCACTTCTGGAGAAATCAGTTTCC 60

156 ATCTCTGCAGGCTTAGTAAGTCTCTCTATTAAGGATGGAGACATACACTTGAATTGG 215
61 ATCTCTGCAGGCTTAGTAAGTCTCTCTATTAAGGATGGAGACATACACTTGAATTGG 120

216 TTTCTGCAGAGACACAGGACAAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCGTGCA 275
121 TTTCTGCAGAGACACAGGACAAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCGTGCA 180

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181 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTACCCCTGGAAATC 240

336 AGTAGAGTGAAGCTGAGGATGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 395
241 AGTAGAGTGAAGCTGAGGATGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 300

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301 TTCACGTTCCGGCTCGGGGACAAAGTTGGAGATAAAACG 338

RESULT 10
AR166313      339 bp DNA linear PAT 17-OCT-2001
LOCUS      Sequence 99 from patent US 6280987.
DEFINITION
ACCESSION      AR166313
VERSION      AR166313.1 GI:16241580
KEYWORDS

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Qy	216	TTTCTGCAGAGACGAGACAATCTCTCAGCTCCTGATGTATTTGATGTCCACCCCGTCCA	275
Db	121	TTTCTGCAGAGACGAGACAATCTCTCAGCTCCTGATGTATTTGATGTCCACCCCGTCCA	180
Qy	276	TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC	335
Db	181	TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC	240
Qy	336	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA	395
Db	241	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAATTTGTAGAGTATCCA	300
Qy	396	TTACAGTTCGGCTCGGGGACAAAGTTTGGAAATAAAAGC	433
Db	301	TTACAGTTCGGCTCGGGGACAAAGTTTGGAAATAAGACG	338
RESULT 12			
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LOCUS	AR166317	368 bp	DNA
DEFINITION	Sequence 107 from patent US 6280987.		
ACCESSION	AR166317		
VERSION	AR166317.1		
KEYWORDS	GI:16241584		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 368)		
AUTHORS	Landry,D.W.		
TITLE	Anti-cockaine catalytic antibody		
JOURNAL	Patent: US 6280987-A 107 28-AUG-2001;		
FEATURES	Location/Qualifiers		
source	1..368		
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Query Match	72.6%;	Score 317.2;	DB 6; Length 368;
Best Local Similarity	96.2%;	Pred. No. 5.1e-94;	
Matches	325; Conservative	0; Mismatches 13;	Indels 0; Gaps 0;
Qy	96	GATATTTGTGTATACCCAGGATGAATCTCCAATCCTGTCTCACTTCTCGAGAAATCAGTTTCC	155
Db	1	GATATGGTGTATGACGAAGCAGTCTCCATCTCTGATCTCTCGAGAAATCAGTTTCC	60
Qy	156	ATCTCTGCAGGTCTAGTAAAGTCTCTGTATATAGGATGGGAAGACATATTTGAAATGG	215
Db	61	ATCTCTGCAGGTCTAGTAAAGTCTCTATATAGGATGGGAAGACATATTTGAAATGG	120
Qy	216	TTTCTGCAGAGACGAGACAATCTCTCAGCTCCTGATGTATTTGATGTCCACCCCGTCCA	275
Db	121	TTTCTGCAGAGACGAGACAATCTCTCAGCTCCTGATGTATTTGATGTCCACCCCGTCCA	180
Qy	276	TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC	335
Db	181	TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC	240
Qy	336	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA	395
Db	241	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAATTTGTAGAGTATCCA	300
Qy	396	TTACAGTTCGGCTCGGGGACAAAGTTTGGAAATAAAAGC	433
Db	301	TTACAGTTCGGCTCGGGGACAAAGTTTGGAAATAAGACG	338
RESULT 13			
AR166319			
LOCUS	AR166319	420 bp	DNA
DEFINITION	Sequence 111 from patent US 6280987.		
ACCESSION	AR166319		
VERSION	AR166319.1		
	GI:16241586		
Qy	111	TTTCTGCAGAGACGAGACAATCTCTCAGCTCCTGATGTATTTGATGTCCACCCCGTCCA	180
Db	1	TTTCTGCAGAGACGAGACAATCTCTCAGCTCCTGATGTATTTGATGTCCACCCCGTCCA	180
Qy	180	TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC	240
Db	1	TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC	240
Qy	240	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA	300
Db	1	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAATTTGTAGAGTATCCA	300
Qy	300	TTACAGTTCGGCTCGGGGACAAAGTTTGGAAATAAAAGC	433
Db	1	TTACAGTTCGGCTCGGGGACAAAGTTTGGAAATAAGACG	338
RESULT 14			
AR166319			
LOCUS	AR166319	420 bp	DNA
DEFINITION	Sequence 111 from patent US 6280987.		
ACCESSION	AR166319		
VERSION	AR166319.1		
	GI:16241586		
Qy	111	TTTCTGCAGAGACGAGACAATCTCTCAGCTCCTGATGTATTTGATGTCCACCCCGTCCA	180
Db	1	TTTCTGCAGAGACGAGACAATCTCTCAGCTCCTGATGTATTTGATGTCCACCCCGTCCA	180
Qy	180	TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC	240
Db	1	TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC	240
Qy	240	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA	300
Db	1	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAATTTGTAGAGTATCCA	300
Qy	300	TTACAGTTCGGCTCGGGGACAAAGTTTGGAAATAAAAGC	433
Db	1	TTACAGTTCGGCTCGGGGACAAAGTTTGGAAATAAGACG	338
RESULT 15			



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KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 420)
AUTHORS        Landry, D.W.
TITLE          Anti-cocaine catalytic antibody
JOURNAL        Patent: US 6280987-A 111 28-AUG-2001;
FEATURES       Location/Qualifiers
               source
               1..420
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Query Match      72.3%; Score 316; DB 6; Length 420;
Best Local Similarity 95.8%; Pred. No. 1.3e-93;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 94 GGGATATTGTGATAAACCAGGATGAACCTCCCAATCCTGTCACTTCTGGAGAAATCAGTTT 153
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QY 154 CCATCTCTCGCAGGTCTAGTAAGAGTCTCTGTATTAAGAGTGGGAAGACATCTTGAATT 213
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Db 111 CCATCTCTCGCAGGTCTAGTAGGAGTCTCTATATAGGGATGGGAAGACATCTTGAATT 170
    |||||
QY 214 GGTTCCTGCAGACAGGACGATCTCCTCAGCTCTGTATTTGATGTCACCCGCTG 273
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Db 171 GGTTCCTGCAGACAGGACGATCTCCTCAGCTCTGTATTTGATGTCACCCGCTG 230
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QY 274 CATCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGCAGATTTTCCACCTCGAAA 333
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Db 231 CATCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGCAGATTTTCCACCTCGAAA 290
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QY 334 TCAGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTCAACACTTTGTAGATATC 393
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Db 291 TCAGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTCAACACTTTGTAGATATC 350
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QY 394 CATTCAGTTCGGCTCGGGACAAAGTTGGAATAAAGC 433
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Db 351 CATTCAGTTCGGCTCGGGACAAAGTTGGAATAAAGC 390
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RESULT 14
AX935403
LOCUS          AX935403              744 bp      DNA      linear      PAT 05-JAN-2004
DEFINITION    Sequence 7 from Patent WO03089475.
ACCESSION     AX935403
VERSION       AX935403.1 GI:40642176
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS        Peschen, D., Fischer, R., Schillberg, S., Liao, Y.C. and Dorfmueller, S.
TITLE          Antibodies, recombinant antibodies, recombinant antibody fragments
              and fusions mediated plant disease resistance against fungi
JOURNAL        Patent: WO 03089475-A 7 30-OCT-2003;
              Fraunhofer-Gesellschaft zur Foerderung der angewandten Forschung
              e.V. (DE)

FEATURES       Location/Qualifiers
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               Mus musculus."

ORIGIN
Query Match      71.7%; Score 313.2; DB 6; Length 744;
Best Local Similarity 93.4%; Pred. No. 1.1e-92;
Matches 327; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 84 GGAGTCAGTGGGGATATTGTGATAAACCAGGATGAACCTCCCAATCCTGTCACTTCTGGA 143
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Db 598 GCGCGGGTCTTGATTTGTGATGATGACCCCAATAGAGTCTCTATCTCTGTCACTTCTGGA 657
    |||||
QY 144 GAATCAGTTTCCATCTCTGCGAGGCTCTAGTAAGAGTCTCTCTATATAAGGATGGGAAGACA 203
    |||||
Db 658 GAATCAGTTTCCATCTCTGCGAGGCTCTAGTAAGAGTCTCTATATAAGGATGGGAAGACA 717
    |||||
QY 204 TACTTGAATTGGTTTCTGCAGAGACCGAGCAATCTCCTCAGCTCTGTATTTGATG 263
    |||||
Db 718 TACTTGAATTGGTTTCTGCAGAGACCGAGCAATCTCCTCAGCTCTGTATTTGATG 777
    |||||
QY 264 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGCAGATTTTC 323
    |||||
Db 778 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGCAGATTTTC 837
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QY 324 ACCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTCAACAACATT 383
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QY 84 GGAGTCAGTGGGGATATTGTGATAAACCAGGATGAACCTCCCAATCCTGTCACTTCTGGA 143
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QY 144 GAATCAGTTTCCATCTCTGCGAGGCTCTAGTAAGAGTCTCTCTGTATAAGGATGGGAAGACA 203
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Db 451 GAATCAGTTTCCATCTCTGCGAGGCTCTAGTAAGAGTCTCTCTATATAAGGATGGGAAGACA 510
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QY 204 TACTTGAATTGGTTTCTGCAGAGACCGAGCAATCTCCTCAGCTCTGTATTTGATG 263
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QY 264 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGCAGATTTTC 323
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Db 571 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGCAGATTTTC 630
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QY 324 ACCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTCAACAACATT 383
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Db 631 ACCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTCAACAACATT 690
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QY 384 GTAGAGTATCCATTACGTTCCGCTCGGGACAAAGTTGGAATAAAGC 433
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RESULT 15
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LOCUS          AX935454              951 bp      DNA      linear      PAT 05-JAN-2004
DEFINITION    Sequence 58 from Patent WO03089475.
ACCESSION     AX935454
VERSION       AX935454.1 GI:40642202
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS        Peschen, D., Fischer, R., Schillberg, S., Liao, Y.C. and Dorfmueller, S.
TITLE          Antibodies, recombinant antibodies, recombinant antibody fragments
              and fusions mediated plant disease resistance against fungi
JOURNAL        Patent: WO 03089475-A 58 30-OCT-2003;
              Fraunhofer-Gesellschaft zur Foerderung der angewandten Forschung
              e.V. (DE)

FEATURES       Location/Qualifiers
               1..951
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Description of Artificial Sequence: precursor
               fusion protein comprising AG - linker - scFv VDM1."

ORIGIN
Query Match      71.7%; Score 313.2; DB 6; Length 951;
Best Local Similarity 93.4%; Pred. No. 1.2e-92;
Matches 327; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 84 GGAGTCAGTGGGGATATTGTGATAAACCAGGATGAACCTCCCAATCCTGTCACTTCTGGA 143
    |||||
Db 598 GCGCGGGTCTTGATTTGTGATGATGACCCCAATAGAGTCTCTATCTCTGTCACTTCTGGA 657
    |||||
QY 144 GAATCAGTTTCCATCTCTGCGAGGCTCTAGTAAGAGTCTCTCTATATAAGGATGGGAAGACA 203
    |||||
Db 658 GAATCAGTTTCCATCTCTGCGAGGCTCTAGTAAGAGTCTCTATATAAGGATGGGAAGACA 717
    |||||
QY 204 TACTTGAATTGGTTTCTGCAGAGACCGAGCAATCTCCTCAGCTCTGTATTTGATG 263
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Db 718 TACTTGAATTGGTTTCTGCAGAGACCGAGCAATCTCCTCAGCTCTGTATTTGATG 777
    |||||
QY 264 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGCAGATTTTC 323
    |||||
Db 778 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGCAGATTTTC 837
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QY 324 ACCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTCAACAACATT 383
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Job time : 1944.07 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 437

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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2: gb\_est2.\*

3: gb\_hic.\*

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5: gb\_est4.\*

6: gb\_est5.\*

7: gb\_est6.\*

8: gb\_ges1.\*

9: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	292.6	67.0	342	5	BY215764 BY215764
5	290	66.4	906	2	BF785914 602112548
6	281.2	64.3	400	2	AW912881 uf46b05.y
7	266.8	61.1	313	5	BY220511 BY220511
8	259.8	59.5	524	6	CD700306 CD700306
9	258.2	59.1	597	6	CD689298 EST5820.h
10	258.2	59.1	771	6	CB956254 AGENCOURT
11	256.6	58.7	475	6	CD699289 EST15812
12	256.6	58.7	498	6	CD699812 EST16336
13	256.6	58.7	743	6	CB987308 AGENCOURT
14	256.6	58.7	757	6	CB985283 AGENCOURT
15	256.6	58.7	817	6	CB957285 AGENCOURT
16	256	58.6	725	4	EG963055 602828068
17	255	58.4	583	6	CD684087 EST607.hu
18	255	58.4	600	6	CD700169 EST16693
19	255	58.4	739	6	CB986287 AGENCOURT
20	253.4	58.0	634	4	BM783161 K-EST0061
21	253.4	58.0	791	6	CB955891 AGENCOURT
22	252.4	57.8	554	6	CD696178 EST12701
23	251.8	57.6	522	4	BM511309 i146b08.y
24	251.8	57.6	623	6	CD694404 EST10927

#### ALIGNMENTS

##### RESULT 1

##### BF023001

##### LOCUS

##### DEFINITION

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### COMMENT

##### FEATURES

##### source

25 251.8 57.6 734 6 CB957433 CB957433 AGENCOURT  
26 251.8 57.6 743 6 CB957183 CB957183 AGENCOURT  
27 250.2 57.3 550 6 CD699641 EST16037  
28 250.2 57.3 561 6 CD699709 EST16233  
29 250.2 57.3 558 6 CB958484 AGENCOURT  
30 250.2 57.3 700 6 CB987545 AGENCOURT  
31 250.2 57.3 719 6 CB958133 AGENCOURT  
32 250.2 57.3 743 6 CB956921 AGENCOURT  
33 250.2 57.3 751 4 BG542438 602569513  
34 250.2 57.3 773 6 CB959401 AGENCOURT  
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36 250.2 57.3 874 6 BG536224 602565445  
37 250.2 57.3 830 6 CB985612 AGENCOURT  
38 250.2 57.3 839 6 CB986712 AGENCOURT  
39 250.2 57.3 995 5 BQ712430 AGENCOURT  
40 249.2 57.0 491 2 BF174573 BF174573 MYE3409a  
41 248.6 56.9 425 1 AF1734035 AF1734035 2U566D02.y  
42 248.6 56.9 442 1 AA405415 AA405415 2U566D02.y  
43 248.6 56.9 512 6 CD709518 CD709518 EST26045  
44 248.6 56.9 562 6 CD706813 CD706813 EST23340  
45 248.6 56.9 565 6 CD691296 CD691296 EST7819.h

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ux02c02.y1 Soares\_thymus\_2NDMT Mus musculus cDNA clone  
IMAGE:3470306 5' similar to SW:KV2B MOUSE P01627 IG KAPPA CHAIN  
V-II REGION VKAPPA167 PRECURSOR. ; mRNA sequence.

BF023001 GI:10754334

EST.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

This clone is available royalty-free through LML ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGi:1389666

Trace considered overall poor quality

Seq primer: -40RP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..343

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/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:3470306"

/sex="male"

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/dev\_stage="4 weeks"

/lab\_host="DH10B"

/clone\_lib="Soares\_thymus\_2NDMT"

/note="Vector: pr7T3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5,

TGTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTTTTTT

3]); double-stranded cDNA was ligated to Eco RI adaptors

and Eco RI sites of the modified pr7T3 vector. RNA

provided by Dr. Bertrand Jordan. Library went through two

rounds of normalization, and was constructed by Bento

Soares and M.Fatima Bonaldo."

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ORIGIN
Query Match          73.0%; Score 318.8; DB 2; Length 343;
Best Local Similarity 97.9%; Pred. No. 8.9e-87;
Matches 323; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 65 GCTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAAACCAGATGAATCTTC 124
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Db 13 GCTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAAACCAGATGAATCTTC 72
    |||

QY 125 CAATCTGTGTCACCTCTGGAGATCACTTCCATCTCTCTCGAGTCTAGTAAGAGTCTCT 184
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Db 73 CAATCTGTGTCACCTCTGGAGATCACTTCCATCTCTCTCGAGTCTAGTAAGAGTCTCT 132
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QY 185 GTATAAGATGGGAAGACATACCTTGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 244
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Db 133 ATATAGGATGGGAGACATACCTTGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 192
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QY 245 GTCCTGATGTTATGATGTCACCCGTCAGTCAGATCAGAGTCTCAGACGGTGGTGGTGGT 304
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QY 305 TGGGTACGACACAGATTTTCACTCTGGAATCAGTAGTGAAGCTGAGGATGTTGGTGT 364
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Db 253 TGGGTACGACACAGATTTTCACTCTGGAATCAGTAGTGAAGCTGAGGATGTTGGTGT 312
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QY 365 GTATTACTGTCAACAACTTGTAGAGTATCC 394
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RESULT 2  
BB870732 351 bp mRNA linear EST 27-NOV-2001  
LOCUS BB870732 RIKEN full-length enriched, adult male jejunal and colic lymph node Mus musculus cDNA clone G630024M15 5', mRNA sequence.

ACCESSION BB870732  
VERSION BB870732.1 GI:17116942

KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

#### ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 351)  
Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hirao, K., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyota, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

#### JOURNAL

COMMENT Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.

and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-Format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

#### e mouse tissues.

FEATURES  
source Location/Qualifiers  
1..351  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="G630024M15"  
/sex="male"  
/tissue\_type="jejunal and colic lymph node"  
/dev\_stage="adult"  
/clone\_lib="RIKEN full-length enriched, adult male jejunal and colic lymph node"

#### ORIGIN

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Query Match          71.3%; Score 311.4; DB 2; Length 351;
Best Local Similarity 96.7%; Pred. No. 1.7e-84;
Matches 318; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 24 CAGGACCTCACCATGAGGTCTCTGTTCAGTTCCTGGGGTGCTTATGTTCTGATCTCT 83
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Db 23 CAGTTCCTCAGATGAGGTGCTCTCTTCAGTTCCTGGGGTGCTTATGTTCTGATCTCT 82
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QY 84 GAGTCAGTGGGATATTGTGATACCCAGATGAATCTCAATCTCTCACTCTCTGGA 143
    |||
Db 83 GGAGTCAGTGGGATATTGTGATACCCAGATGAATCTCAATCTCTCACTCTCTGGA 142
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QY 144 GAATCAGTTTCCATCTCTCGAGGTCTAGTAAGAGTCTCTGTATAAGATGGGAAGACA 203
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Db 143 GAATCAGTTTCCATCTCTCGAGGTCTAGTAAGAGTCTCTGTATAAGATGGGAAGACA 202
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QY 204 TACTTGAATTTGTTCTCGAGAGCACGAGCAATCTCTCAGCTCTCTGATGTTGATG 263
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Db 203 TACTTGAATTTGTTCTCGAGAGCACGAGCAATCTCTCAGCTCTCTGATGTTGATG 262
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QY 264 TCCACCCGTGATCAGGAGTCTCAGACCGTTTGTAGTGCAGTGGGTGAGGACAGATTTC 323
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QY 324 ACCCTGGAAATCAGTAGAGTGAAGGCTGA 352
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Db 323 ACCCTGGAAATCAGTAGAGTGAAGGCTGA 351
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#### RESULT 3

BY220367

LOCUS BY220367

DEFINITION BY220367 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830211P11 5', mRNA sequence.

ACCESSION BY220367

VERSION BY220367.1 GI:26401459

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 353)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusick, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E., and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Nature 420, 563-573 (2002)  
22354683  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numata, K., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES  
SOURCE

Location/Qualifiers  
1. 353  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="NOD"  
/db\_xref="taxon:10090"  
/clone="F830211P11"  
/tissue\_type="activated spleen"  
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ORIGIN

Query Match 69.8%; Score 305.2; DB 5; Length 353;  
Best Local Similarity 94.6%; Pred. No. 1.4e-92;  
Matches 316; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 24 CAGGACTCACCAGTGGGTTCTCTGTTTCAGTTCTTCTGGGGTGTATGTTCTGATCTCT 83  
Db 20 CAAGTTCTCAGATGAGGTGCTCTCTTCAGTTCTTCTGGGATGCTTATGTTCTGATCTCT 79

QY 84 GGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTTCCAAATCTGTCACTTCTGGA 143  
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QY 144 GAATCAGTTTCCATCTCTGCAGGTCTAGTAAGAGTCTCTCTGTATAGGATGGGAAGACA 203  
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QY 204 TACTTGAATTTGGTTCTGCAGAGACAGGACAAATCTCTCAGTCTCTGTATTTGATG 263  
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RESULT 4

BY215764

LOCUS

DEFINITION

BY215764

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY215764 342 bp mRNA linear EST 10-DEC-2002  
CDNA clone F830038M23 5', mRNA sequence.

BY215764  
EST.  
BY215764.1 GI:26396501

Mus musculus (house mouse)  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 342)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schombach, C., Gojbori, T., Baldarelli, R., Hill, B.P., Bult, C.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusick, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

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Nature 420, 563-573 (2002)

TITLE

JOURNAL

MEDLINE  
PUBMED  
COMMENT

22354683  
12466851  
Contact: Yoshitake Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
Hirozane, T., Inotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
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Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in Riken.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
Trust/MRC building Addenbrookes Hospital Cambridge) whose  
assistance we gratefully acknowledge.  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
FEATURES  
source  
1. .342  
/organism="Mus musculus"  
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/strain="NOD"  
/db\_xref="taxon:10090"  
/clone="F830038M23"  
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Best Local Similarity 94.1%; Pred. No. 1e-78;  
Matches 304; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 24 CAGGACCTCACATGAGTCTCTGTTTCAGTTTCGGGGTGCTTATGTTCTGGATCTCT 83  
DB 20 CAAGTTCTCAGATGAGTGCTCTCTTCAGTTTCGGGGTGCTTATGTTCTGGATCTCT 79

QY 84 GGAGTCAGTGGGATATGATTAACCCAGAGTAACCTCCATCTCTGTTATAGGATGGGAGACA 143  
DB 80 GGAGTCAGTGGGATATGATTAACCCAGAGTAACCTCCATCTCTGTTATAGGATGGGAGACA 139

QY 144 GAATCAGTTTCATCTCTGTCAGGTCTAGTAAGAGTCTCTCTGTATAGGATGGGAGACA 203  
DB 140 GAATCAGTTTCATCTCTGTCAGGTCTAGTAAGAGTCTCTCTGTATAGGATGGGAGACA 199

QY 204 TACTTGAATGGTTTTCGACAGACACAGGACAATCTCTCTGTCAGTCTCTGTTATGATG 263  
DB 200 TACTTGAATGGTTTTCGACAGACACAGGACAATCTCTCTGTCAGTCTCTGTTATGATG 259

QY 264 TCCACCCGTGATCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTTCAGGACAGATTTTC 323  
DB 260 TCCACCCGTGATCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTTCAGGACAGATTTTC 319

QY 324 ACCCTGGAATCAGTAGAGTGAA 346  
DB 320 ACACCTGGAATCAGTAGAGTGAA 342

RESULT 5  
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LOCUS 602112548F1 NCI\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:4240762  
DEFINITION 5', mRNA sequence.  
ACCESSION BF785914  
VERSION BF785914.1 GI:12090950  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 906)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LAM9855 row: p column: 11  
High quality sequence stop: 718.

FEATURES  
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/clone\_lib="NCI CGAP Kid14"  
/note="Organ: kidney; Vector: pCMV-Sport6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library. |"

ORIGIN  
Query Match 66.4%; Score 290; DB 2; Length 906;  
Best Local Similarity 81.7%; Pred. No. 8.5e-78;  
Matches 335; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 24 CAGGACCTCACATGAGTCTCTGTTTCAGTTTCGGGGTGCTTATGTTCTGGATCTCT 83  
DB 3 CAAGTTCTCAGATGAGTGCTCTCTGAGTTTCCTGGGGTGCTTATGTTCTGGATCTCT 62

QY 84 GGAGTCAGTGGGATATGATTAACCCAGAGTAACCTCCATCTCTGTTATAGGATGGGAGACA 143  
DB 63 GGAGTCAGTGGGATATGATTAACCCAGAGTAACCTCTGTACCTCTGTACCTCTCTGGA 122

QY 144 GAATCAGTTTCATCTCTGTCAGGTCTAGTAAGAGTCTCTCTGTATAGGATGGGAGACA 203  
DB 123 GAGTCAGTATTCATCTCTCTGTCAGGTCTAGTAAGAGTCTCTCTGTCAGTCTCTGATG 182

QY 204 TACTTGAATGGTTTTCGACAGACACAGGACAATCTCTCTGTCAGTCTCTGTTATGATG 263  
DB 183 GACTTGTATGGTTCTCTACAGAGGCCAGCCAGTCTCTCTGATATATATCGGATG 242

QY 264 TCCACCCGTGATCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTTCAGGACAGATTTTC 323  
DB 243 TCCACCTTGGCTCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTTCAGGAACTGCTTTC 302

QY 324 ACCCTGGAATCAGTAGAGTGAA 346

Db	303	ACACTGAGATCAGTAGAGTGGAGGCTGAGGATGTGGTGTATTACTTCTTTCACATC 362
Qy	384	GTGAGATATCATTCAGCTTCGGCTCGGACAAAGTTGGAATAAAACG 433
Db	363	CTAGAATATCGTACACGTTTCGGAGGGGGGACCAAGCTGGAATAAAACG 412
RESULT 6		
AW912881		400 bp mRNA linear EST 25-MAY-2000
LOCUS		uf46b05.y1 Soares mammary gland NMLMG Mus musculus cDNA clone
DEFINITION		IMAGE:1514385 5' similar to gb:J00560 mouse ig kappa mRNA from
		mopc21 & other myeloma mrna 3' (MOUSE);, mRNA sequence.
ACCESSION		AW912881
VERSION		AW912881.1 GI:8078508
KEYWORDS		EST.
SOURCE		Mus musculus (house mouse)
ORGANISM		Mus musculus
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE		1 (bases 1 to 400)
JOURNAL		NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
		Tumor Gene Index
		Unpublished (1997)
		Contact: Robert Strausberg, Ph.D.
		Email: cgaps-r@mail.nih.gov
		This clone is available royalty-free through LLNL; contact the
		IMAGE Consortium (info@image.llnl.gov) for further information.
		MGI:941237
FEATURES		Seq primer: -40RP from Gibco.
source		Location/Qualifiers
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		gland tissue from a lactating female, and was then primed
		with a Not I - oligo(dT) primer. Double-stranded cDNA was
		ligated to Eco RI adaptors (Pharmacia), digested with Not
		I and cloned into the Not I and Eco RI sites of the
		modified p773 vector. Library is normalized. Library
		was constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN		
Query Match	64.3%	Score 281.2; DB 2; Length 400;
Best Local	Similarity	81.7%; Pred.No. 3.5e-75;
Matches	325; Conservative	0; Mismatches 73; Indels 0; Gaps 0;
Qy	36	ATGAGGTTCTCTGTTCAGTTCTCGGGGCTCTATGTTCTGAGTCTCTGAGTCAGTGGG 95
Db	2	ATTCGGTACGAGGCTGTTTCTGGGGCTCTGCTCTGGATCCCTGGAGCCATTGGG 61
Qy	96	GATATTGTGTATACCCAGGATGAATCTTCAATCTCTGTCATCTTCTGGAGAAATCAGTTTCC 155
Db	62	GATATTGTGTATGACTCAGGCTGCACCCCTCTGTACCTCTGCTCTCTGAGAGTCAGTATCC 121
Qy	156	ATCTCTCGAGGCTCTAGTAGTCTCTCTATAGAGTGGGAAGCATCTTGAATTGG 215
Db	122	ATCTCTCGAGGCTCTAGTAAAGTCTCTGATATGATGAGCAACCTTATTATTATGG 181
Qy	216	TTTCTGACAGACACGAGCAATCTCTCAGCTCTCTGATGTATTGTATGTCACCCCGTGA 275
Db	182	TTCTGACAGAGCCAGGCAAGTCTCTCAGCTCTCTGATATGATGATGATGATGATGATG 241
Qy	276	TCAGGAGTCTCAGACCGGTTTATGGCAGTGGGTCTAGGACAGATTTCACCCCTGGAATC 335

Db	242	TCAGGAGTCCGACAGAGTTTCACTGCGAGTGGGTCAAGAACTCTTTCACATCAGAGATC 301
Qy	336	AGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCA 395
Db	302	AGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTATGCAACATCTAGAGTATCCG 361
Qy	396	TTACAGTTCGGTTCGGGGACAAAGTTGGAAATAAAACG 433
Db	362	TACACGTTGGAGGGGGGACCAAGCTGGAATAAAACG 399
RESULT 7		
BY220511		313 bp mRNA linear EST 10-DEC-2002
LOCUS		BY220511 RIKEN full-length enriched, activated spleen Mus musculus
DEFINITION		cDNA clone F830212P03 5', mRNA sequence.
ACCESSION		BY220511
VERSION		BY220511.1 GI:26401613
KEYWORDS		EST.
SOURCE		Mus musculus (house mouse)
ORGANISM		Mus musculus
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
		1 (bases 1 to 313)
		Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
		Nikaido,I., Oato,N., Saito,R., Suzuki,H., Yamanaka,I.,
		Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
		Schonbach,C., Gojohori,T., Baldarelli,R., Hill,D.P., Bult,C.,
		Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
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		Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
		Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
		Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
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		Nemata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
		Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
		Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
		Sandelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K.,
		Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
		Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
		Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
		Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
		Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
		Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
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		Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
		Rogers,J., Birney,E. and Hayashizaki,Y.
		Analysis of the mouse transcriptome based on functional annotation
		of 60,770 full-length cDNAs
		Nature 420, 563-573 (2002)
JOURNAL		12466851
MEDLINE		22354683
PUBMED		
COMMENT		Contact: Yoshihide Hayashizaki
		Laboratory for Genome Exploration Research Group, RIKEN Genomic
		Sciences Center (GSC), Yokohama Institute
		The Institute of Physical and Chemical Research (RIKEN)
		1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
		Tel: 81-45-503-9222
		Fax: 81-45-503-9216
		Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
		Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
		Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
		Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
		Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
		Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
		Hayashizaki,Y. Direct Submission
		Computational Analysis of Full-Length Mouse cDNAs Compared with
		Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
		Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

Location/Qualifiers

1. 313  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="NOD"  
 /db\_xref="taxon:10090"  
 /clone="F830212P03"  
 /tissue\_type="activated spleen"  
 /clone\_lib="RIKEN full-length enriched, activated spleen"

## ORIGIN

Query Match 61.1%; Score 266.8; DB 5; Length 313;  
 Best Local Similarity 94.2%; Pred. No. 9e-71; Indels 0; Gaps 0;  
 Matches 277; Conservative 0; Mismatches 17;

QY 24 CAGGACCTCACCATGAGTTCTCTGTCTAGTTTCTGGGGTGCTTATGTTCTGGATCTCT 83  
 DB 20 CAAATTCTCAGATGAGGTGCTCTCTTCACTTCTGGGGATGCTTATGTTCTGGATCTCT 79  
 QY 84 GGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTCCATCTCTGATCTCTGGA 143  
 DB 80 GGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTCCATCTCTGATCTCTGGA 139  
 QY 144 GAATCAGTTTCCATCTCTCTGAGTCTAGTAGAGTCTCTGTATAGGATGGAGACA 203  
 DB 140 GAATCAGTTTCCATCTCTCTGAGTCTAGTAGAGTCTCTGTATAGGATGGAGACA 199  
 QY 204 TACTTGAATGGTTTCTCAGAGACCAGGACAAATCTCTCAGCTCTCTGATGATTGATG 263  
 DB 200 TACTTGAATGGTTTCTCAGAGGCCAGGACAGTCTCTCAGCTCTCTGATGATTGATG 259  
 QY 264 TCCACCCGTGCATCAGAGTCTCAGACCGTTTGTAGTGGAGTGGTCCAGGCACA 317  
 DB 260 TCCACCCGTGCATCAGAGTCTCAGACCGTTTGTAGTGGAGTGGTCCAGGCACA 313

## RESULT 8

CD700306  
 LOCUS EST16830 human nasopharynx Homo sapiens cDNA, mRNA linear EST 25-JUN-2003  
 DEFINITION  
 ACCESSION CD700306  
 VERSION CD700306.1 GI:32230410  
 KEYWORDS EST.

## SOURCE

Homo sapiens (human)  
 ORGANISM

REFERENCE 1 (bases 1 to 524)  
 AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.  
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Yixin Zeng  
 Cancer Center

Sun Yat-sen University  
 651 DongFeng Road East, GuangZhou 510060, China  
 Tel: 86-1380-9770-743  
 Fax: 86-20-8775-4506  
 Email: yxzeng@gzsums.edu.cn

## FEATURES

source

1. 524  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="normal nasopharynx"  
 /clone\_lib="human nasopharynx"  
 /note="PSTs generated from a normal nasopharynx cDNA library from southern Chinese"

## ORIGIN

Query Match 59.5%; Score 259.8; DB 6; Length 524;  
 Best Local Similarity 77.4%; Pred. No. 1.5e-68;  
 Matches 315; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 30 CTCACATGAGGTTCCTCTGTTTCAGTTTCTGGGGTGCTTATGTTCTGGATCTCTGGATC 89  
 DB 50 CTCACATGAGGTTCCTCTGTTTCAGTTTCTGGGGTGCTTATGTTCTGGATCCTCTGGATC 109  
 QY 90 AGTGGGGATATTGTGATAACCCAGGATGAATCTCTCAATCTCTGTCACCTCTCTGGAGATCA 149  
 DB 110 AGTGGGGATATTGTGATAACCCAGGATGAATCTCTCAATCTCTGTCACCTCTCTGGAGATCA 169  
 QY 150 GTTTCATCTCTCTGAGGTCTAGTAGAGTCTCTGTATAGGATGGAGATGGAGATGATCTTG 209  
 DB 170 GCTCCATCTCTCTGAGGTCTAGTAGAGTCTCTGTATAGGATGGAGATGATCTTG 229  
 QY 210 AATTGGTTTTCAGAGACCAGGACAAATCTCTCAGCTCTCTGATGATTGATGTCACC 269  
 DB 230 GATTGGTACCTTCAGAGGCCAGGACAGTCTCCACAGTCTCTGATCTATTTGACGTCTAAT 289  
 QY 270 CTTGATCAGAGTCTCAGACCGTTTGTAGTGGAGTGGTTCAGTGGATGATGATGATGATG 329  
 DB 290 CCGGCTCTCGGGTCCCTGACAGTTCAGTGGAGTGGATGATGATGATGATGATGATGATG 349  
 QY 330 GAAATCAGTAGAGTGAAGGCTGAGGATGTTGTTTGTATGTTGTTGTTGTTGTTGTTGTTG 389  
 DB 350 ACAATCAGCAGAGTGGAGGCTGAAGATGTTGGGATTATTTACTGATGATGATGATGATGATG 409  
 QY 390 TATCCATTCAGTTCGGCTCGGGACAAAGTTGGAAATTAACGTTAC 436  
 DB 410 ACTCCCTCACTTTCGGGGAGGGACCAAGGTGGAAATCAACGAAC 456

## RESULT 9

CD689298  
 LOCUS EST5820 human nasopharynx Homo sapiens cDNA, mRNA linear EST 25-JUN-2003  
 DEFINITION  
 ACCESSION CD689298  
 VERSION CD689298.1 GI:32208911  
 KEYWORDS EST.

## SOURCE

Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 597)  
 AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.

## TITLE

Transcriptional Gene Expression Profile of Human Nasopharynx  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Yixin Zeng  
 Cancer Center

Sun Yat-sen University  
 651 DongFeng Road East, GuangZhou 510060, China  
 Tel: 86-1380-9770-743  
 Fax: 86-20-8775-4506  
 Email: yxzeng@gzsums.edu.cn

## FEATURES

Location/Qualifiers



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source 1. .597
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 59.1%; Score 258.2; DB 6; Length 597;
Best Local Similarity 77.1%; Pred. No. 4.7e-68;
Matches 314; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 30 CTCACATGAGTTCTCTGTTTCAGTTCTTGGGGTGTCTATGTTCTGGATCTCTGGAGTC 89
Db 44 CTCACATGAGTTCTCTGTTTCAGTTCTTGGGGTGTCTATGTTCTGGATCTCTGGATCT 103

Qy 90 AGTGGGATATTGTGATTAACCCAGGATGAATCTTCAATCTCTGATCTCTGGAGATCA 149
Db 104 AGTGGGATATTGTGATTAACCCAGGATGAATCTTCAATCTCTGATCTCTGGAGATCA 163

Qy 150 GTTTCATCTCTCCAGGTTCTAGTAAGAGTCTCTGTATTAAGGATGGAGACATCTTG 209
Db 164 GCCTCCATCTCTCCAGGTTCTAGTAAGAGTCTCTGTATTAAGGATGGAGACATCTTG 223

Qy 210 AATTGGTTTCTGCAGAGACAGGACAAATCTCTCAGCTCTCTGATGATTTGATGTCAC 269
Db 224 GATTGGTACCTGCAGAGACAGGACAAATCTCTCAGCTCTCTGATGATTTGATGTCAC 283

Qy 270 CGTGATCAGAGTCTCAGACCGGTTTGTGGAGTGGGTCAGGACAGATTTTCAACCTG 329
Db 284 CGGCGCTTCCGGGTCCTGACAGGTTTCAAGTGGAGTGGGTCAGGACAGATTTTCAACCTG 343

Qy 330 GAAATCAGTATGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 389
Db 344 AAAATCAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 403

Qy 390 TATCCATTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAGCTAC 436
Db 404 ACTCTTACAGTTCCGGGACAAAGTGGAAATAAAGCTAC 450

RESULT 10
CB956254
AGENCOURT 13666919 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30353574 5', mRNA sequence.

CB956254
CB956254.1 GI:30212371
EST.
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 771)
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM154 row: i column: 07
High quality sequence stop: 543.
Location/Qualifiers
1. .771
/organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30353574"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattatggcc); Site_2: SfiI (ggccctcgcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-ATCTAGAGCCGAGCCGACATG-3' and 3' adaptor sequence:
5'-ATCTAGAGCCGAGCCGACATG-3' (30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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ORIGIN

Query Match 59.1%; Score 258.2; DB 6; Length 771;  
Best Local Similarity 77.1%; Pred. No. 5.1e-68;  
Matches 314; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 30 CTCACATGAGTTCTCTGTTTCAGTTCTTGGGGTGTCTATGTTCTGGATCTCTGGAGTC 89  
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Qy 90 AGTGGGATATTGTGATTAACCCAGGATGAATCTTCAATCTCTGATCTCTGGAGATCA 149  
Db 90 AGTGGGATATTGTGATTAACCCAGGATGAATCTTCAATCTCTGATCTCTGGAGATCA 149

Qy 150 GTTTCATCTCTCCAGGTTCTAGTAAGAGTCTCTGTATTAAGGATGGAGACATCTTG 209  
Db 150 GCCTCCATCTCTCCAGGTTCTAGTAAGAGTCTCTGTATTAAGGATGGAGACATCTTG 209

Qy 210 AATTGGTTTCTGCAGAGACAGGACAAATCTCTCAGCTCTCTGATGATTTGATGTCAC 269  
Db 210 GATTGGTACCTGCAGAGACAGGACAAATCTCTCAGCTCTCTGATGATTTGATGTCAC 269

Qy 270 CGTGATCAGAGTCTCAGACCGGTTTGTGGAGTGGGTCAGGACAGATTTTCAACCTG 329  
Db 270 CGGCGCTTCCGGGTCCTGACAGGTTTCAAGTGGAGTGGGTCAGGACAGATTTTCAACCTG 329

Qy 330 GAAATCAGTATGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 389  
Db 330 AAAATCAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 389

Qy 390 TATCCATTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAGCTAC 436  
Db 390 ACCCGCTCACCTTCGGCGGAGGACCAAGTGGAGATCAACGAC 436

RESULT 11  
CD699289 475 bp mRNA linear EST 25-JUN-2003  
EST15812 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
CD699289  
CD699289.1 GI:32228425  
EST.  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 475)  
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and  
Zeng, Y.-X.  
Transcriptional Gene Expression Profile of Human Nasopharynx  
Unpublished (2003)  
Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 DongFeng Road East, GuangZhou 510060, China

Tel: 86-1380-9770-743  
 Fax: 86-20-8775-4506  
 Email: yxzeng@gzsums.edu.cn.  
 Location/Qualifiers  
 1. .475

# FEATURES

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/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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## ORIGIN

Query Match 58.7%; Score 256.6; DB 6; Length 475;  
 Best Local Similarity 76.9%; Pred. No. 1.4e-67;  
 Matches 313; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 30 CTCACCATGAGGTTCTGTTCAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTC 89  
 DB 65 CTCACATGAGGCTCCCTGCTAGCTCTGGGGCTCTAATGCTCTGGTCTCTGGATCC 124

QY 90 AGTGGGGATATTGTGATACCCAGGATGAATCTCCAAATCTGTCTACTTCTGGAGATCA 149  
 DB 125 AGTGGGGATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCAACCCCTGGAGAGCG 184

QY 150 GTTTCATCTCTGAGGCTTAGTAGAGTCTCTGTATAGGATGGAGACATACCTTG 209  
 DB 185 GCCTCCATCTCTGCAAGGCTTAGTCAGAGCCTCTGTATAGTAATGGATCAACTATTG 244

QY 210 AATTGGTTTCTGCAGAGACGAGACAAATCTCTCAGCTCTCTGATGTATTGATGTCAC 269  
 DB 245 GATTGGTACTGTCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGGGTTCTAAT 304

QY 270 CGTGCAATCAGGAGTCTCAGACCGGTTAGTGGCAGTGGGTGAGGTCAGGACAGATTTCAC 329  
 DB 305 CGGGCTCCGGGCTCCCTGACAGGTTTCTGAGGTCAGTGGCAGTGGATCAGGACAGATTTCAC 364

QY 330 GAATCAGTAGAGTGTAGGCTGAGGATGGGTGCTGTTACTTACTGTCAACAATCTGTAGAG 389  
 DB 365 AATATCAGCAGAGTGTAGGCTGAGGATGGGTGCTGTTACTTACTGTCAAGTCTTACAA 424

QY 390 TATCCATTACGTTCCGGCTCGGGACAAAGTTGGAATAAAACGTAC 436  
 DB 425 CCTCTCCGACGTTCCGCCAAGGACCAAGTGGTAATCAACGAAC 471

## RESULT 12

CD699812  
 LOCUS  
 DEFINITION EST16336 human nasopharynx Homo sapiens cdna, mRNA sequence.  
 ACCESSION CD699812  
 VERSION CD699812.1 GI:32229450  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 498)  
 AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.  
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Yixin Zeng  
 Cancer Center  
 Sun Yat-sen University  
 651 Dongfeng Road East, Guangzhou 510060, China  
 Tel: 86-1380-9770-743  
 Fax: 86-20-8775-4506  
 Email: yxzeng@gzsums.edu.cn.  
 Location/Qualifiers  
 1. .498  
 /organism="Homo sapiens"

## FEATURES

source

/organism="Homo sapiens"

/mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /clone\_lib="human nasopharynx"  
 /note="ESTs generated from a normal nasopharynx cdna library from southern Chinese"

## ORIGIN

Query Match 58.7%; Score 256.6; DB 6; Length 498;  
 Best Local Similarity 76.9%; Pred. No. 1.4e-67;  
 Matches 313; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 30 CTCACCATGAGGTTCTGTTCAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTC 89  
 DB 47 CTCACATGAGGCTCCCTGCTAGCTCTGGGGCTGTAATGCTCTGGTCTCTGGATCC 106

QY 90 AGTGGGGATATTGTGATACCCAGGATGAATCTCCAAATCTCTGTCACATCTCTGGAGATCA 149  
 DB 107 AGTGGGGATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCG 166

QY 150 GTTTCATCTCTGAGGCTTAGTAGAGTCTCTGTATAGGATGGAGACATACCTTG 209  
 DB 167 GCCTCCATCTCTGCTGATGCTAGTCAGAGCCTCTCCACAGCTCTGATCTATTGGGTTCTAAT 226

QY 210 AATTGGTTTCTGCAGAGACGAGACAAATCTCTCAGCTCTCTGATGTATTGATGTCAC 269  
 DB 227 GATTGGTACTGTCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGGGTTCTAAT 286

QY 270 CGTGCAATCAGGAGTCTCAGACCGGTTAGTGGCAGTGGGTGAGGTCAGGACAGATTTCAC 329  
 DB 287 CGGGCTCCGGGCTCCCTGACAGGTTTCTGAGGTCAGTGGCAGTGGATCAGGACAGATTTCAC 346

QY 330 GAATCAGTAGAGTGTAGGCTGAGGATGGGTGCTGTTACTTACTGTCAACAATCTGTAGAG 389  
 DB 347 AATATCAGTAGAGTGTAGGCTGAGGATGGGTGCTGTTACTTACTGTCAATCTCTACAA 406

QY 390 TATCCATTACGTTCCGGCTCGGGACAAAGTTGGAATAAAACGTAC 436  
 DB 407 ATTCCGTGGACGTTCCGCCAAGGACCAAGTGGTAATCAACGAAC 453

## RESULT 13

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 DEFINITION IMAGE:30328074 5', mRNA sequence.  
 ACCESSION CB987308  
 VERSION CB987308.1 GI:30281828  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 743)  
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: NDCM138 row: b column: 19  
 High quality sequence stop: 557.

## FEATURES

source

Location/Qualifiers  
 1. .743  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"



REFERENCE 1 (bases 1 to 817)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-f@mail.nih.gov](mailto:cgapbs-f@mail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: NDCM155 row: n column: 23  
High quality sequence stop: 534.

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/clone="IMAGE:30354094"  
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/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site\_1:  
SfiI (ggcgcctggcc); Site\_2: SfiI (ggcgcctggcc); cDNA  
Library is oligo-dT primed and directionally cloned. cDNA  
was prepared from a glandular pool of tissues from thyroid,  
parathyroid, adrenal, cortex and pineal gland. 5' and 3',  
adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGCGCGGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.38  
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN		Query Match	58.7%; Score 256.6; DB 6; Length 817;
		Best Local Similarity	76.9%; Pred. No. 1.e-67;
		Matches 313; Conservative 0;	Mismatches 94; Indels 0; Gaps 0;
Qy	30	CTCACCATGAGTCTCTGTTTCTGCGGGTCTTATGTTCTGATCTCTGGAGTC	89
Db	30	CTCACAATGAGCTCCCTCTGCTGCTGCGGCTGTAATGCTCTGGGTCTTGGATCC	89
Qy	90	AGTGGGATATTGTGATAACCCAGGATGAATCTCCAACTCTGTCATCTTGGAGATCA	149
Db	90	AGTGGGATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGGAGCCG	149
Qy	150	GTTTCCATCTCTGAGGCTCTAGTAAGAGTCTCTGTATAGGATGGAGACATCTTG	209
Db	150	GCCTCCATCTCTGAGGCTCTAGTCAGAGCCTCTGTCATAGTCAAGATCAACTATTG	209
Qy	210	AATTGGTTCTGCGAGACAGGACAATCTCTCAGCTCTCTGATGATTTGATGTCACC	269
Db	210	GATTGGTACCTGCGAGACAGGAGCTCTCCAGCTCTGATCTATTGGGTCTTAAT	269
Qy	270	CGTGATCAGAGTCTCAGACCGGTTTGTAGTGGAGTGGGTGAGGACAGATTTACCCCTG	329
Db	270	CGGGCTCCGGGTCCTGACAGGTTTCACTGGCAGTGGATCAGGCACAGATTTTACGCTG	329
Qy	330	GAAATCAGTGAAGCTGAGGATGTTGGTGTGTTATTACTGTCAACACTTGTAGAG	389
Db	330	AAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGCATGCAAGCTCTACAA	389
Qy	390	TATCCATTACGTTCCGGTCCGGGACAAAGTTGGAAATAAAACGTAC	436
Db	390	ACTCCACTCATTTCGGCGGAGGACCAAGTGGAGATCAAAACGAAC	436

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 245.823 Seconds  
(without alignments)  
10523.523 Million cell updates/sec

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Perfect score: 437  
Sequence: 1 agctttacagttactcagc.....agttggaataaaacgtacg 437

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
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9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	437	100.0	437	3	Aaz34746 Mouse ant
2	366.4	83.8	429	2	Aaq12056 Sequence
3	366.4	83.8	429	2	Aaq12012 Sequence
4	317.2	72.6	340	2	Aav09791 DNA encod
5	317.2	72.6	368	2	Aav09789 DNA encod
6	316	72.3	420	2	Aav09802 DNA encod
7	313.2	71.7	744	10	ADG32298 Mouse scf
8	313.2	71.7	951	10	ADG32349 DNA encod
9	309.2	70.8	368	2	Aav09793 DNA encod
10	294	67.3	399	12	Ado43548 Nucleotid
11	293.2	67.1	464	2	Aaq33097 C242:11 M
12	293.2	67.1	464	2	Aaq36950 C242 kapp
13	289.2	66.2	399	12	Ado43552 Nucleotid
14	287.4	65.8	773	10	Acf36530 Anti-huma
15	286.8	65.6	720	12	Adm72038 ChimERIC
16	286.8	65.6	961	2	Aaq79929 Anti-toba
17	284.4	65.1	426	10	Acf36518 Anti-huma
18	284.4	64.2	825	10	Add25795 Binding d
19	280.4	64.2	1536	10	Add25796 Binding d
20	280.4	64.2	1696	10	Add25797 Binding d

21	280.4	64.2	1596	10	AdE86043 DNA encod
22	280.4	64.2	1596	12	AdK00035 cDNA enco
23	278	63.6	399	10	Add25794 Binding d
24	277.2	63.4	441	2	Aaq08602 B38.1 Lig
25	277.2	63.4	441	2	Aat43434 MAb B38-1
26	277.2	63.4	441	2	Aav71152 Coding st
27	277.2	63.4	441	8	Abx79221 DNA encod
28	276.4	63.2	399	2	Aaq38878 CTMO1 VL
29	276.4	63.2	399	2	Aat85855 Anti-HMFG
30	276.4	63.2	399	3	Aaz46913 MAb CT-M-
31	273	62.5	720	11	AdL23132 Mouse/hum
32	271.4	62.1	720	3	AbK10999 DNA encod
33	260.2	59.5	720	11	AdL23167 Mouse/hum
34	258.6	59.2	720	11	AdL23171 Mouse/hum
35	257.2	58.9	348	3	Aaz34747 Humanised
36	257	58.8	720	11	AdL23136 Mouse/hum
37	257	58.8	720	11	AdL23175 Mouse/hum
38	255.6	58.5	720	3	AaA13924 Human PTH
39	255.4	58.4	720	10	AdE28460 Human ant
40	255.4	58.4	720	11	AdL23165 Mouse/hum
41	255	58.4	772	2	Aaz24418 Human bla
42	254.6	58.3	720	3	AaA13927 Human PTH
43	253.8	58.1	720	11	AdL23169 Mouse/hum
44	253.4	58.0	1081	6	AbS51811 Human mdd
45	253	57.9	720	3	AaA13926 Human PTH

ALIGNMENTS

RESULT 1  
AAZ34746  
ID AAZ34746 standard; cDNA; 437 BP.  
XX  
AC AAZ34746;  
XX  
DT 15-FEB-2000 (first entry)  
XX  
DE Mouse anti-CD23 MAb C11 light chain variable region cDNA.  
XX  
KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
KW therapy; ds.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT CDS 3..413  
FT /\*tag= a  
XX  
PN WO958679-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-GB001434.  
XX  
PR 09-MAY-1998; 98GB-00009839.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
XX  
XX WFI; 2000-053101/04.  
DR P-PSDB; AAY32261.  
XX  
PT Cell receptor specific antibodies useful for treating e.g. arthritis,

PT diabetes, multiple sclerosis and psoriasis.

PS Claim 16; Fig 2; 81pp; English.

XX This DNA sequence encodes the light chain variable region (VL) of murine  
CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides  
CC altered antibodies, such as chimeric or humanised antibodies (see  
CC AAZ34747 and AAZ34748), which comprise sufficient of the amino acid  
CC sequences of the C11 light and heavy chain complementarity determining  
CC regions (see AA32254-59) to render them capable of binding to the CD23  
CC type II molecule expressed on haematopoietic cells. The antibodies are  
CC used to block soluble CD23 formation in human therapy, for the treatment  
CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
CC malignancies (claimed). They are also useful for studying interactions  
CC between CD23 and various ligands and determining the binding agents

XX SQ Sequence 437 BP; 108 A; 93 C; 114 G; 122 T; 0 U; 0 Other;

Query Match 100.0%; Score 437; DB 3; Length 437;

Best Local Similarity 100.0%; Pred. No. 6.3e-124;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTTACAGTTACTCAGACACAGAGACCTCACCATGAGTTCTCTGTTCAAGTTCTG 60

DB 1 AAGCTTTACAGTTACTCAGACACAGAGACCTCACCATGAGTTCTCTGTTCAAGTTCTG 60

QY 61 GGGTGTCTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGATAAACCCAGGATGAAC 120

DB 61 GGGTGTCTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGATAAACCCAGGATGAAC 120

QY 121 TCTCCAACTCTGTCACTCTGGAGATCACTGTTTCCATCTCTGAGGTCAGTAAGATC 180

DB 121 TCTCCAACTCTGTCACTCTGGAGATCACTGTTTCCATCTCTGAGGTCAGTAAGATC 180

QY 181 TCTGTATTAAGATGGAGACATCTGTAATGTTTCTGACAGACACAGCAATCTC 240

DB 181 TCTGTATTAAGATGGAGACATCTGTAATGTTTCTGACAGACACAGCAATCTC 240

QY 241 CTCAGTCTCTGATGATTTGATCTCCACCGTCATCAGAGTCTCAGACCGGTTTAGTG 300

DB 241 CTCAGTCTCTGATGATTTGATCTCCACCGTCATCAGAGTCTCAGACCGGTTTAGTG 300

QY 301 GCAGTGGGTCAGGACAGATTTCCACCTGGAAATCAGTAGAGGCTGAGGATGTGG 360

DB 301 GCAGTGGGTCAGGACAGATTTCCACCTGGAAATCAGTAGAGGCTGAGGATGTGG 360

QY 361 GTGTGTATTACTGTCAACACTTGTAGATATCCATTACGTTCCGCTCGGGACAAAGT 420

DB 361 GTGTGTATTACTGTCAACACTTGTAGATATCCATTACGTTCCGCTCGGGACAAAGT 420

QY 421 TGGAAATAAAACGTACG 437

DB 421 TGGAAATAAAACGTACG 437

RESULT 2

AAQ12056

ID AAQ12056 standard; DNA; 429 BP.

XX AAQ12056;

AC

XX 25-MAR-2003 (revised)

DT 15-AUG-1991 (first entry)

XX Sequence encoding light (kappa) chain variable region of murine 2E12

DE immunoglobulin.

XX

KW Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.

XX Mus musculus.

XX Key Location/Qualifiers

OS 34..429

FT /\*tag= a

FT /product= "mouse Mab 2E12 L(kappa)-chain variable region"

XX WO9107493-A.

XX 30-MAY-1991.

XX 13-NOV-1989; 89US-00433730.

XX 13-NOV-1989; 89US-00433730.

XX (XOMA ) XOMA CORP.

XX (GREC ) GREEN CROSS CORP.

XX Better MD, Horwitz AH, Ghoshdasti P, Robinson R;

XX WPI; 1991-178105/24.

XX P-PSDB; AAR12354.

XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV

XX -1 antigen from sample.

XX Disclosure; Fig 1; 107pp; English.

XX This sequence encodes the light (kappa)- chain variable (V) region of a  
CC mouse monoclonal antibody (Mab), 2E12, specific for an HIV-1 viral  
CC antigen. It is used in the construction of a chimeric Mab comprising  
CC heavy and light chains having murine V regions and human C regions. The  
CC chimeric Mabs are more effective than murine Mab 2E12 since they have an  
CC increased compatibility in humans. The heavy and light chain V-regions  
CC are joined by manipulating their respective joining (J) regions, to  
CC generate restriction enzyme recognition sites. The chimeric Mabs can be  
CC used as immuno- conjugates, in association with e.g. toxins for HIV  
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12057-  
CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)

XX SQ Sequence 429 BP; 103 A; 92 C; 120 G; 114 T; 0 U; 0 Other;

Query Match 83.8%; Score 366.4; DB 2; Length 429;

Best Local Similarity 93.6%; Pred. No. 3.2e-102;

Matches 382; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 24 CAGGACCTCACCATGAGTTCTCTGTTCAAGTTTCTGGGGTCTTATGTTCTGGATCTCT 83

DB 22 CAAGTTCTCAGATGAGGTCTCTCTTCAGTTTCTGGGGTCTTATGTTCTGGATCTCT 81

QY 84 GGAGTCAGTGGGGATTTGTGTATACCCAGAGTAACTCTCAATCTCTCACTTCTGA 143

DB 82 GGAGTCAGTGGGGAGATTGTGATACCCAGAGTAACTCTCAATCTCTCACTTCTGA 141

QY 144 GAATCAGTTTCCATCTCTGAGGTCAGTAGAGTCTCTCTATATAAGATGGAGACA 203

DB 142 GAATCAGTTTCTCTCTGAGGTCAGTAGAGTCTCTCTATATAAGATGGAGACA 201

QY 204 TACTTGAATTGGTTTCTGCAGAGACAGGACAACTCTCTCAGCTCTCTGATGTTTGA 263

DB 202 TACTTGAATTGGTTTCTGCAGAGACAGGACAACTCTCCGAGCTCTCTGATCTAT 261

QY 264 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTATGGCAGTGGGTGAGGCACAGATTTC 323

DB 262 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTATGGCAGTGGGTGAGGCACAGATTTC 321

QY 324 ACCCTGGAAATCAGTAGAGTGAAGCTCAGGATGTTGGTGTCTATTACTGTCAACACTT 383

DB 322 ACCCTGGAAATCAGTAGAGTGAAGCTCAGGATGTTGGTGTCTATTACTGTCAACACTT 381

QY 384 GTAGAGTATCCATTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAA 431  
 |||||  
 Db 382 GTAGAGTATCCGATACACATTCGGAGGGGGACCAAGCTGGAATAAAA 429  
 |||||

## RESULT 3

AAQ12012  
 ID AAQ12012 standard; DNA; 429 BP.

XX AC AAQ12012;  
 XX

XX 25-MAR-2003 (revised)  
 DT 19-AUG-1991 (first entry)  
 DT

XX Sequence encoding mouse MAb 2E12 L chain V region.  
 DE  
 XX HIV-1; chimera; ds.  
 KW  
 XX Mus sp.

XX Key  
 FH CDS  
 FT  
 FT  
 FT

XX Location/Qualifiers  
 34..429  
 /\*tag= a

XX WO9107494-A.  
 PN

XX 30-MAY-1991.  
 PD

XX 13-NOV-1989; 89US-00433703.  
 PF

XX 13-NOV-1989; 89US-00433703.  
 PR

XX (XOMA ) XOMA CORP.  
 PA (GREG ) GREEN CROSS CORP.  
 PA (ZOMA-) ZOMA CORP.

XX Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;  
 PI

XX WPI; 1991-178106/24.  
 DR P-PSDB; AAR12232.

XX New chimeric mouse human antibodies - used in treatment, diagnosis and  
 PT prophylaxis of HIV infections.

XX Disclosure; Fig 1; 108pp; English.  
 PS

XX The mouse VL gene product may be used to produce chimeric mouse- human  
 CC Abs against HIV-1 comprising human Ig constant regions and murine  
 CC variable regions. These novel sequence are useful in treatment, diagnosis  
 CC and prophylaxis of HIV infections, and may be produced by a bacterial,  
 CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct  
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
 CC

XX Sequence 429 BP; 103 A; 92 C; 120 G; 114 T; 0 U; 0 Other;  
 SQ

Query Match 83.8%; Score 366.4; DB 2; Length 429;  
 Best Local Similarity 93.6%; Pred. No. 3.2e-102;  
 Matches 382; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 24 CAGGACCTCACATGAGGTTCTCTGTTTCAGTTCTGGGGTGCTTATGTTCTGGATCTCT 83  
 |||||  
 Db 22 CAAGTTCTCAGAATGAGTGCTCTCTTCACTTCTGGGGTGCTTATGTTCTGGATCTCT 81  
 |||||

QY 84 GGAGTCAGTGGGATATTTGGATAACCCAGGATGAACTCTCCAACTCTGTCACCTCTGGA 143  
 |||||  
 Db 82 GGAGTCAGTGGGAGATTTGGATAACCCAGGATGAACTCTCCAACTCTGTCACCTCTGGA 141  
 |||||

QY 144 GAATCAGTTTCCATCTCTCTCAGGTCCTAGTAAGAGTCTCTCTGTAAGGATGGGAAGACA 203  
 |||||  
 Db 142 GAATCAGTTTCTCTCTCTCAGGTCCTAGTAAGAGTCTCTCTGTAAGGATGGGAAGACA 201  
 |||||

QY 204 TACTTGAATGGTTTCTGACAGACCAAGGACAAATCTCCTCAGTCTCTGATGTTTGTG 263  
 |||||

Db 202 TACTTGAGTTGGTTTCTGACAGACCAAGGACAAATCTCCGAGCTCCTGATCTATCTGATG 261  
 |||||  
 QY 264 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTCAGGCACAGATTTC 323  
 |||||  
 Db 262 TCCACCCGTTGATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTCAGGAACAGATTTC 321  
 |||||  
 QY 324 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTCTCAACAATT 383  
 |||||  
 Db 322 ACCCTGGAATCAGTAGGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTCTCAACAATT 381  
 |||||  
 QY 384 GTAGAGTATCCATTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAA 431  
 |||||  
 Db 382 GTAGAGTATCCGATACACATTCGGAGGGGGACCAAGCTGGAATAAAA 429  
 |||||

## RESULT 4

AAV09791  
 ID AAV09791 standard; cDNA; 340 BP.

XX AC AAV09791;  
 XX

XX 16-JUN-1998 (first entry)  
 DT

XX DNA encoding the light chain of the catalytic antibody 3B9.  
 DE

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction; ss.  
 XX

XX Mus sp.  
 XX

XX Key  
 FH CDS  
 FT  
 FT  
 FT

XX Location/Qualifiers  
 1..340  
 /\*tag= a  
 /notes= "no stop codon given"

XX WO9749800-A1.  
 PN

XX 31-DEC-1997.  
 PD

XX 25-JUN-1997; 97WO-US010965.  
 PF

XX 25-JUN-1996; 96US-00672345.  
 PR

XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA

XX Landry DW;  
 PI

XX WPI; 1998-077166/07.  
 DR P-PSDB; AAW39801.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 PT

XX Disclosure; Fig 17; 147pp; English.  
 PS

XX The present sequence encodes the light chain of a catalytic antibody  
 CC which is capable of degrading cocaine. A series of cocaine transition  
 CC state analogues (TSAs) were prepared and used to immunise mice for  
 CC production of hybridomas. Catalytic antibodies were identified by their  
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
 CC antibodies reduce the concentration of cocaine in a subject, and are used  
 CC particularly for the treatment of an overdose. They are also used for  
 CC treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX Sequence 340 BP; 86 A; 72 C; 88 G; 93 T; 0 U; 1 Other;  
 SQ

Query Match 72.6%; Score 317.2; DB 2; Length 340;  
 Best Local Similarity 96.2%; Pred. No. 4e-87;  
 Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTCATACCCAGGATGAATCTCTCAATCTCTGTCACCTTCTGGAGAAATCAGTTTCC 155  
 DB 1 GATATTGTCATACCCAGGATGAATCTCTCAATCTCTGTCACCTTCTGGAGAAATCAGTTTCC 60  
 QY 156 ATCTCTGTCAGGTCCTAGTAAAGTCTCTCTGTCATTAAGGATGGGAGACATCTTGAATTGG 215  
 DB 61 ATCTCTGTCAGGTCCTAGTAAAGTCTCTCTGTCATTAAGGATGGGAGACATCTTGAATTGG 120  
 QY 216 TTCTCTGAGAGACCCAGGACAAATCTCTCAGCTCTCTGATGATATTTGATGTCACCCGTCGA 275  
 DB 121 TTCTCTGAGAGACCCAGGACAAATCTCTCAGCTCTCTGATGATATTTGATGTCACCCGTCGA 180  
 QY 276 TCAGGAGTCTCAGACCCGTTTCTAGTGGCAGTGGGTCTAGGCACAGATTTTCACTTGAATTC 335  
 DB 181 TCAGGAGTCTCAGACCCGTTTCTAGTGGCAGTGGGTCTAGGCACAGATTTTCACTTGAATTC 240  
 QY 336 AGTAGAGTGAAGCTCAGGATGTCAGTGGTCTAGTCTCACTCTGATGATATTTGATGTCACCCGTCGA 395  
 DB 241 AGTAGAGTGAAGCTCAGGATGTCAGTGGTCTAGTCTCACTCTGATGATATTTGATGTCACCCGTCGA 300  
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTTGGAAATAAAACG 433  
 DB 301 TTCACGTTCCGCTCGGGGACAAAGTTTGGAGATAAAACG 338

## RESULT 5

AAV09789  
 ID AAV09789 standard; cDNA; 368 BP.

AC AAV09789;

XX 16-JUN-1998 (first entry)

XX DNA encoding the light chain of the catalytic antibody 2A10.

KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction; ss.

XX Mus sp.

XX Key Location/Qualifiers  
 XX CDS 1..339

XX /\*tag= a

XX /note= "no stop codon given"

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX P-PSDB; AAW39882.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX Disclosure; Fig 21; 147pp; English.

XX The present sequence encodes the light chain of a catalytic antibody  
 CC which is capable of degrading cocaine. A series of cocaine transition  
 CC state analogues (TSAs) were prepared and used to immunise mice for  
 CC production of hybridomas. Catalytic antibodies were identified by their

CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
 CC antibodies reduce the concentration of cocaine in a subject, and are used  
 CC particularly for the treatment of an overdose. They are also used for  
 CC treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX SQ Sequence 368 BP; 95 A; 81 C; 94 G; 98 T; 0 U; 0 Other;

Query Match 72.6%; Score 317.2; DB 2; Length 368;  
 Best Local Similarity 96.2%; Pred. No. 4.1e-87;  
 Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTCATACCCAGGATGAATCTCTCAATCTCTGTCACCTTCTGGAGAAATCAGTTTCC 155  
 DB 1 GATATTGTCATACCCAGGATGAATCTCTCAATCTCTGTCACCTTCTGGAGAAATCAGTTTCC 60  
 QY 156 ATCTCTGTCAGGTCCTAGTAAAGTCTCTCTGTCATTAAGGATGGGAGACATCTTGAATTGG 215  
 DB 61 ATCTCTGTCAGGTCCTAGTAAAGTCTCTCTGTCATTAAGGATGGGAGACATCTTGAATTGG 120  
 QY 216 TTCTCTGAGAGACCCAGGACAAATCTCTCAGCTCTCTGATGATATTTGATGTCACCCGTCGA 275  
 DB 121 TTCTCTGAGAGACCCAGGACAAATCTCTCAGCTCTCTGATGATATTTGATGTCACCCGTCGA 180  
 QY 276 TCAGGAGTCTCAGACCCGTTTCTAGTGGCAGTGGGTCTAGGCACAGATTTTCACTTGAATTC 335  
 DB 181 TCAGGAGTCTCAGACCCGTTTCTAGTGGCAGTGGGTCTAGGCACAGATTTTCACTTGAATTC 240  
 QY 336 AGTAGAGTGAAGCTCAGGATGTCAGTGGTCTAGTCTCACTCTGATGATATTTGATGTCACCCGTCGA 395  
 DB 241 AGTAGAGTGAAGCTCAGGATGTCAGTGGTCTAGTCTCACTCTGATGATATTTGATGTCACCCGTCGA 300  
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTTGGAAATAAAACG 433  
 DB 301 TTCACGTTCCGCTCGGGGACAAAGTTTGGAGATAAAACG 338

## RESULT 6

AAV09802  
 ID AAV09802 standard; cDNA; 420 BP.

XX AAV09802;

XX 16-JUN-1998 (first entry)

XX DNA encoding the light chain of the catalytic antibody 12H1.

KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction; ss.

XX Mus sp.

XX Key Location/Qualifiers  
 XX CDS 53..391

XX /\*tag= a  
 XX /note= "no stop codon given"

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX P-PSDB; AAW39803.



XX New catalytic antibodies able to decompose cocaine, single-chain  
PT analogues - used to treat cocaine overdose and addiction, required in far  
PT smaller doses than antibodies that antagonise cocaine by simply binding.  
XX  
XX Disclosure; Fig 23; 147pp; English.

CC The present sequence encodes the light chain of a catalytic antibody  
CC which is capable of degrading cocaine. A series of cocaine transition  
CC state analogues (TSAs) were prepared and used to immunise mice for  
CC production of hybridomas. Catalytic antibodies were identified by their  
CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
CC antibodies reduce the concentration of cocaine in a subject, and are used  
CC particularly for the treatment of an overdose. They are also used for  
CC treating addiction (by reducing the in vivo concentration that can be  
CC achieved)

XX Sequence 420 BP; 98 A; 95 C; 115 G; 108 T; 0 U; 4 Other;

Query Match 72.3%; Score 316; DB 2; Length 420;  
Best Local Similarity 95.6%; Pred. No. 1e-86;  
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 94 GGGATATTGTGATAACCCAGGATGAACCTCTCCAACTCTGTCACTTCTGGAGAATCAGTTT 153  
DB 51 GCGATATGGTGTATGACGCGAGGATGAACCTCTCCAACTCTGTCACTTCTGGAGAATCAGTTT 110  
QY 154 CCATCTCTCCAGGCTCTAGTAACAGTCTCCTGTATAGGATGGGAACATACCTCAATT 213  
DB 111 CCATCTCTCCAGGCTCTAGTAACAGTCTCCTGTATAGGATGGGAACATACCTCAATT 170  
QY 214 GGTTCCTGCAGACACAGGACCAATCTCTCAGCTCTCTGTATTTGATGTCACCCGCTG 273  
DB 171 GGTTCCTGCAGACACAGGACCAATCTCTCAGCTCTCTGTATTTGATGTCACCCGCTG 230  
QY 274 CATCAGAGTCTCAGACCCGTTTGTAGTGGCAGTGGGTGAGGCAAGATTTTCACTTGAAAA 333  
DB 231 CATCAGAGTCTCAGACCCGTTTGTAGTGGCAGTGGGTGAGGCAAGATTTTCACTTGAAAA 290  
QY 334 TCAGTAGAGTAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATC 393  
DB 291 TCAGTAGAGTAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATC 350  
QY 394 CATTCAGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG 433  
DB 351 CATTCAGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG 390

RESULT 7  
ADG32298

ID ADG32298 standard; cDNA; 744 BP.

XX AC

XX ADG32298;

XX 26-FEB-2004 (first entry)

XX Mouse scFV VDM1 antibody cDNA targeted against V\_dahliae SeqID 7.

XX mouse; murine; scFV; gene; ss; anti-fungal peptide; AFP; scFV;  
KW disease resistant; transgenic; plant; fungal infection; antibody;  
KW pathogen-specific antibody; fungicidal; agriculture.

XX Mus sp.

XX W02003089475-A2.

XX 30-OCT-2003.

XX 14-APR-2003; 2003WO-EP003852.

XX 22-APR-2002; 2002EP-00008929.

XX 28-MAY-2002; 2002EP-00011807.

XX

PA

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DR

DR

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PT

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PS

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(FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

Peschchen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;

WPI: 2003-854088/79.

P-PSDB; ADG32323.

New fusion protein comprising an anti-fungal protein or peptide and an

antibody fragment, useful in agriculture and horticulture for producing

Ascomyceta-resistant transgenic plants, plant cells or plant tissues.

Claim 25; SEQ ID NO 7; 47pp; English.

This invention relates to a novel fusion protein comprising an anti-

fungal protein or peptide (AFP) and an antibody fragment (scFV).

Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta

and a cellular targeting sequence, which can be used to generate disease

resistant transgenic plants that are protected against fungal infection.

Accordingly, a method is described for antibody based resistance in

plants such that the undesirable and expensive chemical controls often

used in agriculture are not required. The present invention provides

antibodies, recombinant antibodies and fragments thereof, as well as

fusion proteins that can be used as pathogen-specific antibodies targeted

to different plant cell compartments. As such, these fungicidal agents

confer a broad spectrum of disease resistance in both economically

important crops and ornamental plants. This polynucleotide is a cDNA

sequence encoding an antibody of the invention.

Sequence 744 BP; 181 A; 165 C; 218 G; 180 T; 0 U; 0 Other;

Query Match 71.7%; Score 313.2; DB 10; Length 744;

Best Local Similarity 93.4%; Pred. No. 9.2e-86;

Matches 327; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 84 GGAGTCAGTGGGGATATTGTGATTAACCCAGGATGAACCTCTCCAACTCTGTCACTTCTGGA 143

DB 391 GCGCGCGTCTGTGATATTGTGATGACCCCAAAATGAGCTCTCTATCTCTGTCACTTCTGGA 450

QY 144 GAATCAGATTTCCATCTCTCGCAGGTCTAGTAAGAGTCTCTGTATAAGATGGGAAGACA 203

DB 451 GAATCAGATTTCCATCTCTCGCAGGTCTAGTAAGAGTCTCTGTATAAGATGGGAAGACA 510

QY 204 TACTTGAATTTGGTTTTCGAGAGACAGCAATCTCTCAGCTCTCTGTATTTGATG 263

DB 511 TACTTGAATTTGGTTTTCGAGAGACAGCAATCTCTCAGCTCTCTGTATTTGATG 570

QY 264 TCCACCCGTGCATCAGGAGTCTCAGACCCGTTTAGTGGCAGTGGGTGAGGATTTTC 323

DB 571 TCCACCCGTGCATCAGGAGTCTCAGACCCGTTTAGTGGCAGTGGGTGAGGATTTTC 630

QY 324 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTT 383

DB 631 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTT 690

QY 384 GTAGAGTATCCATTCCAGTTCGGCTCGGGGACAAAGTTGGAATAAAACG 433

DB 691 GTAGAGTATCCAGTTCGGCTCGGGGACAAAGTTGGAATAAAACG 740

RESULT 8

ADG32349

ID ADG32349 standard; DNA; 951 BP.

XX AC

XX ADG32349;

XX 26-FEB-2004 (first entry)

XX DNA encoding the precursor fusion protein of AFP AG-scFV VDM1 SeqID 58.

XX scFV; ds; anti-fungal peptide; AFP; scFV; disease resistant; transgenic;

XX plant; fungal infection; antibody; pathogen-specific antibody;

XX fungicidal; agriculture; mouse; chimeric; murine; gene.

XX

XX

XX

XX

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XX

XX

XX

XX

XX

XX

XX

OS Chimeric.  
OS Synthetic.  
OS Aspergillus giganteus.  
OS Mus musculus.

XX WO2003089475-A2.

XX 30-OCT-2003.

XX 14-APR-2003; 2003WO-EP003852.

XX 22-APR-2002; 2002EP-00008929.

XX 28-MAY-2002; 2002EP-00011807.

XX (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;

XX WPI; 2003-854088/79.

XX P-PSDB; ADG32360.

XX New fusion protein comprising an anti-fungal protein or peptide and an antibody fragment, useful in agriculture and horticulture for producing Ascomyceta-resistant transgenic plants, plant cells or plant tissues.

XX Example 15; SEQ ID NO 58; 47pp; English.

XX This invention relates to a novel fusion protein comprising an anti-fungal protein or peptide (AFP) and an antibody fragment (scFv). Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta and a cellular targeting sequence, which can be used to generate disease resistant transgenic plants that are protected against fungal infection. Accordingly, a method is described for antibody based resistance in plants such that the undesirable and expensive chemical controls often used in agriculture are not required. The present invention provides antibodies, recombinant antibodies and fragments thereof, as well as fusion proteins that can be used as pathogen-specific antibodies targeted to different plant cell compartments. As such, these fungicidal agents confer a broad spectrum of disease resistance in both economically important crops and ornamental plants. This polynucleotide is a DNA sequence encoding a precursor fusion protein of the order [AFP - linker - antibody fragment] of the invention.

XX Sequence 951 BP; 236 A; 221 C; 287 G; 207 T; 0 U; 0 Other;

Query Match 71.7%; Score 313.2; DB 10; Length 951;  
Best Local Similarity 93.4%; Pred. No. 1e-85;  
Matches 327; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 84 GGAGTCAGTGGGATATTGTGATACCCAGGATGAACCTCCAACTCTGTCACTTCTGGA 143

DB 598 GCGCGGGTCTGATATTGTGATGACCCAAATGAGCTCTCTATCTCTGCTCACTTCTGA 657

QY 144 GAATCAGTTTCCATCTCCGAGGTCTAGTAAGTCTCTGTATAGGATGGGAGACA 203

DB 658 GAATCAGTTTCCATCTCCGAGGTCTAGTAAGTCTCTGTATAGGATGGGAGACA 717

QY 204 TACTTCAATTTGTTTCTGCAGAGACCAGACAACTCTCCAGCTCTGTATGATGATG 263

DB 718 TACTTCAATTTGTTTCTGCAGAGACCAGACAACTCTCCAGCTCTGTATGATGATG 777

QY 264 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTC 323

DB 778 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTC 837

QY 324 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACACTT 383

DB 838 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACACTT 897

QY 384 GTAGAGTATCCATTACGTTTCGGCTCGGGGACAAAGTTTGGAAATAAAACG 433

DB 898 GTAGAGTATCCGCTACGTTTCGGCTCGGGGACAAAGTTTGGAGCTGAAACG 947

RESULT 9

AAV09793

ID AAV09793 standard; cDNA; 368 BP.

XX AC

XX AAV09793;

XX 18-JUN-1998 (first entry)

XX DNA encoding the light chain of the catalytic antibody 6A12.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
KW overdose; addiction; ss.

XX Mus sp.

XX Key

XX Location/Qualifiers

XX 1..339

XX /\*tag= a

XX /note= "no stop codon given"

XX FT

XX WO9749800-A1.

XX PD

XX 31-DEC-1997.

XX PP

XX 25-JUN-1997; 97WO-US010965.

XX PR

XX 25-JUN-1996; 96US-00672345.

XX PA

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI

XX Landry DW;

XX XX

XX WPI; 1998-077166/07.

XX DR

XX P-PSDB; AAW39886.

XX PT

XX New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS

XX Disclosure; Fig 19; 147pp; English.

XX CC

XX The present sequence encodes the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The

XX antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)

XX CC

XX Sequence 368 BP; 95 A; 80 C; 93 G; 100 T; 0 U; 0 Other;

XX SQ

Query Match 70.8%; Score 309.2; DB 2; Length 368;

Best Local Similarity 94.7%; Pred. No. 1.2e-84;

Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCTCCAACTCTGTCACTTCTGGAGAAATCAGTTTCC 155

DB 1 GATATGGTGATGACGCAAGATGAACCTCTCCAACTCTGTCACTTCTGGAGAAATCAGTTTCC 60

QY 156 ATCTCTCCAGGTCTAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 215

DB 61 ATCTCTCCAGGTCTAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 120

QY 216 TTCTTCGACAGACACAGGACAACTCTCCAGCTCTGTATAGTATTTGATCTCACCCGTCGA 275

DB 121 TTTCTGACAGACACAGGACAACTCTCCAGCTCTGTATAGTATTTGATCTCACCCGTCGA 180

QY 276 TCAGAGTCTCAGACCCGGTTTGTAGTGGCAGTGGGTGAGCAGATTTTCCCTCGAAATC 335

```

Db      181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGAACAGATTTCACCTCGGAATC 240
QY      336 AGTAGAGTGAAGCTCAGGAGTGGGTGCTATTACTGTCAACAACTTGTGAGAGTATCCA 395
Db      241 AGTAGAGTGAAGCTCAGGAGTGGGTGCTATTACTGTCAACAACTTGTGAGAGTATCCA 300
QY      396 TTCACGTTCCGCTCGGGGACAAAAGTTGGAAATAAAACG 433
Db      301 TTCACGTTCCGCTCGGGGACAAAATTTGGAGATAAAACG 338

```

## RESULT 10

```

AD043548
ID      AD043548 standard; DNA; 399 BP.
XX
AC      AD043548;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Nucleotide sequence of murine A34 variable light chain clone 209-970.
XX
KW      human; A34 protein; A33-like 3 protein; A33/JAM family; chromosome X;
KW      chromosome 1; cancer; oesophageal cancer; ovarian cancer; stomach cancer;
KW      gene; ss; antibody.
XX
OS      Mus musculus.
XX
FH      Key
FT      CDS
FT      Location/Qualifiers
FT      1..399
FT      /*tag= a
FT      /partial
FT      /product= "A34 variable light chain"
XX
PN      WO2004037999-A2.
XX
PD      06-MAY-2004.
XX
PF      23-OCT-2003; 2003WO-US033707.
XX
PR      23-OCT-2002; 2002US-0420285P.
XX
PA      (LUDW-) LUDWIG INST CANCER RES.
XX
PI      Scanlan M, Ritter G, Old L, Jungbluth A;
XX
WPI: 2004-365509/34.
P-PSDB; AD043549.
XX

```

New pure immunoglobulin molecule that binds specifically to A34 antigen, useful in preparing a composition for diagnosing or treating cancer.

Example 4; Fig 21; 99pp; English.

The present sequence encodes a murine A34 variable light chain. The specification describes A34 and A33-like 3 proteins, and immunoglobulin molecules that bind specifically to their antigens. A34 and A33-like 3 proteins are members of the A33/JAM family. The A34 gene is mapped to chromosome X, and the A33-like 3 gene is mapped to chromosome 1. Immunoglobulin molecules of the invention useful in preparing a composition for diagnosing or treating cancer, especially oesophageal, ovarian and stomach cancers.

Sequence 399 BP; 87 A; 94 C; 109 G; 109 T; 0 U; 0 Other;

Query Match 67.3%; Score 294; DB 12; Length 399;  
 Best Local Similarity 83.7%; Pred. No. 5.8e-80;  
 Matches 333; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

```

QY      36 ATGAGTTCCTCTCAGTTTCGGGGTGGTCTTATGTTCTGGATCTCTGAGTCAGTGGG 95
Db      1 ATGAGTGGCTTCTGTTCTGAGTTTCGGGGTGGTCTTATGTTCTGGATCTCTGAGTCAGTGGG 60

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```

QY      96 GATATTGTGATAACCCAGGATGAACCTCTCAATCCCTGTCACTTCTGGAGAAATCAGTTTCC 155
Db      61 GATATTGTGATGACTCAGGCTGCACCCTCTGTCCCTGTCACTCTGGAGAGTCAGTATCC 120
QY      156 ATCTCTCTGAGGCTCTAGTAAAGATCTCCCTGTATAGGATGGGAGACATCTTGAATTGG 215
Db      121 ATCTCTCTGAGGCTCTAGTAAAGATCTCCCTGTATAGGATGGGAGACATCTTGAATTGG 180
QY      216 TTTCTGCAGAGACCCAGGACAAATCTCTCAGCTCCTGATGTATTGTGATGTCCACCCGTTGCA 275
Db      181 TTTCTGCAGAGACCCAGGACAAATCTCTCAGCTCCTGATGTATTGTGATGTCCACCCGTTGCA 240
QY      276 TCAGGAGTCTCAGACCCGTTTATGTGTCAGTGGGTTCAGGCACAGATTTCACCTGGAAATC 335
Db      241 TCAGGAGTCCAGACAGGTTTCAGTGGGTTCAGGCACAGATTTCACCTGGAAATC 300
QY      336 AGTAGAGTGAAGCTCAGGAGTGGGTGCTATTACTGTCAACAACTTGTGAGAGTATCCA 395
Db      301 AGTAGAGTGGAGCTGAGGATGGGTGCTATTACTGTATGCAACATCTAGAATATCCT 360
QY      396 TTCACGTTCCGCTCGGGGACAAAAGTTGGAAATAAAACG 433
Db      361 TTCACGTTCCGAGGGGGGACCAAACTGGAAATAAAACG 398

```

## RESULT 11

```

AAQ33097
ID      AAQ33097 standard; DNA; 464 BP.
XX
AC      AAQ33097;
XX
DT      25-MAR-2003 (revised)
DT      06-MAY-1993 (first entry)
XX
DE      C242:11 MAB kappa chain variable region coding sequence.
XX
KW      Kappa; chain; heavy; MAB; monoclonal antibody; C242:11; murine; IgG;
KW      hybridoma; cell line; spleen; human; colonic; adenocarcinoma; myeloma;
KW      Sp2/0; antigen; endocytosis; ss.
XX
OS      Synthetic.
XX
FH      Key
FT      CDS
FT      Location/Qualifiers
FT      42..464
FT      /*tag= a
FT      misc_RNA 102..441
FT      /*tag= b
FT      /note= "Kappa variable region, VK"
FT      misc_RNA 442..464
FT      /*tag= c
FT      /note= "Start of kappa constant region, CK"
XX
PN      EP521842-A2.
XX
PD      07-JAN-1993.
XX
PF      03-JUL-1992; 92BP-00850166.
XX
PR      03-JUL-1991; 91SE-00002074.
XX
PA      (KABI ) KABI PHARMACIA AB.
PA      (PHAA ) PHARMACIA & UPJOHN AB.
XX
PI      Lindholm L, Holmgren J, Lind P;
XX
WPI: 1993-002345/01.
P-PSDB; AAR30454.
XX

```

Monoclonal antibody reacting with CA-242 antigen - obtd. by culturing hybridoma cell line C242:11 or mutants, useful for diagnosis and therapy of pancreatic or colorectal cancers.

Disclosure; Fig 3; 15pp; English.



RESULT 13  
 ADO43552 standard; DNA; 399 BP.  
 XX  
 AC ADO43552;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Nucleotide sequence of murine A34 variable light chain clone 209-564.  
 XX  
 KW human; A34 protein; A33-like 3 protein; A33/JAM family; chromosome X;  
 KW chromosome 1; cancer; oesophageal cancer; ovarian cancer; stomach cancer;  
 KW gene; ss; antibody.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..399  
 FT /\*tag= a  
 FT /partial  
 FT /product= "A34 variable light chain"  
 XX  
 PN WO2004037999-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 23-OCT-2003; 2003WO-US033707.  
 XX  
 PR 23-OCT-2002; 2002US-0420285P.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Scanlan M, Ritter G, Old L, Jungbluth A;  
 XX  
 DR WPI; 2004-365509/34.  
 XX  
 DR P-PSDB; ADO43553.  
 XX  
 PT New pure immunoglobulin molecule that binds specifically to A34 antigen,  
 PT useful in preparing a composition for diagnosing or treating cancer.  
 XX  
 PS Example 4; Fig 22; 99pp; English.  
 XX  
 CC The present sequence encodes a murine A34 variable light chain. The  
 CC specification describes A34 and A33-like 3 proteins, and immunoglobulin  
 CC molecules that bind specifically to their antigens. A34 and A33-like 3  
 CC proteins are members of the A33/JAM family. The A34 gene is mapped to  
 CC chromosome X, and the A33-like 3 gene is mapped to chromosome 1.  
 CC immunoglobulin molecules of the invention useful in preparing a  
 CC composition for diagnosing or treating cancer, especially oesophageal,  
 CC ovarian and stomach cancers.  
 XX  
 SQ Sequence 399 BP; 85 A; 95 C; 112 G; 107 T; 0 U; 0 Other;  
 Query Match 66.2%; Score 289.2; DB 12; Length 399;  
 Best Local Similarity 82.9%; Pred. No. 1.7e-78;  
 Matches 330; Conservative 0; Mismatches 68; Indels 0; Gaps 0;  
 QY 36 ATGAGGTTCTGTTTCAGTTTCTGGGGTCTGTTATGTTCTGGATCTCTGAGTCAGTGGG 95  
 DB 1 ATGAGGTCCTTGTCTAGCTCTCTGGGGCTGTTGTTGCTCTGGATCCTCTGGAGCCATTGGG 60  
 QY 96 GATATTGTGATAACCCAGGATGAATCTCCAATCTCTGTCACCTCTGGAGATCAGTTTCC 155  
 DB 61 GATATTGTGATGACTCAGGCTGCACCTCTGTACCTGTCTCTCTGGAGATCAGTATCC 120  
 QY 156 ATCTCTGCAGGCTAGTAAGATGTTCTCTGTATAGGATGGGAGACATATTGAATTGG 215  
 DB 121 ATCTCTGCAGGCTAGTACAGTCTCTCTGCATGTTAATGGCAACATTACTTGTATTGG 180  
 QY 216 TTCTGTCAGACGACGACATCTCTCAGCTCTCTGATGTTATTTGATGTCACCCCTGCA 275  
 DB 181 TTCTGTCAGAGGCCAGGCCAGTCTCTCAGTCTCTGATATATCGGATGTCTCAACCTTGCC 240

QY 276 TCAGGAGTCTCAGACCCGGTTTACTGGCAGTGGGTCTAGGCACAGATTTCCCTCGAAATC 335  
 DB 241 TCAGGAGTCCACACAGAGTTTCAGTGGCAGTGGGTCTAGGAACTGCTTTACACTGAGATC 300  
 QY 336 AGTAGAGTGAAGCTGAGGATGTTGGTGTGTATTTACTGTCAACAACCTTGAGAGTATCCA 395  
 DB 301 AGTAGAGTGGAGCTGAGGATGTTGGTGTATTTACTGTATGAGCATCTAGAATATCCT 360  
 QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACG 433  
 DB 361 TTCACGTTCCGAGGGGGGACCAAGCTGGAAATAAAACG 398

## RESULT 14

ACF36530  
 ID ACF36530 standard; cDNA; 773 BP.  
 XX  
 AC ACF36530;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Anti-human tenascin ST2146 MAB light chain variable region (VL) cDNA.  
 XX  
 KW ST2146; tenascin C; monoclonal antibody; EGF; epidermal growth factor;  
 KW cytostatic; antibody therapy; vaccine; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 292..718  
 FT /\*tag= a  
 FT /product= "ST2146 light chain variable region"  
 FT /partial  
 FT /notes= "the stop codon is not indicated"  
 FT sig\_peptide 292..351  
 FT /\*tag= b  
 FT mat\_peptide 352..718  
 FT /\*tag= c  
 XX  
 PN WO2003072608-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-IT000098.  
 XX  
 PR 26-FEB-2002; 2002US-0359299P.  
 XX  
 PA (SIGT) SIGMA-TAU IND FARM RIUNITE SPA.  
 XX  
 PI De Santis R, Anastasi AM;  
 XX  
 DR WPI; 2003-679945/64.  
 DR P-PSDB; ABR82929.  
 XX

New anti-human tenascin ST2146 monoclonal antibody, and its proteolytic fragments that bind to an antigenic epitope within the EGF-like repeat of human tenascin C, useful for treating tumors, e. g. gliomas, cystic brain tumors.

Example 1; Fig 10; 55pp; English.

The invention relates to an anti-human tenascin ST2146 monoclonal antibody (MAB) whose light and heavy chain variable region sequences and their proteolytic fragments that bind to an antigenic epitope within the EGF (epidermal growth factor)-like repeat of human tenascin C. The antibody, its fragment, recombinant or conjugate derivatives, immunoglobulin molecule and biotinylated derivatives are useful for a diagnostic means for detecting, or preparing a medicament for treating, diseases expressing tenascin, e.g. tumor such as gliomas, mammary, cystic brain tumors, lung carcinomas, fibrosarcomas, and squamous cell carcinomas. The diagnostic means is used in vivo imaging techniques. The medicament is in the form of a kit suitable for carrying out the three-step pre-targeting method. The antibody, in combination with a

CC second tenascin-specific antibody are useful in sandwich assay for  
 CC detecting the level of circulating tenascin. The present sequence  
 CC represents the S12146 MAB light chain variable region encoding cDNA  
 XX  
 SQ Sequence 773 BP; 186 A; 204 C; 178 G; 205 T; 0 U; 0 Other;

Query Match 65.8%; Score 287.4; DB 10; Length 773;  
 Best Local Similarity 81.4%; Pred. No. 8e-78;  
 Matches 333; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 25 AGGACCTCACCATGAGGTTCTCTGTTTCAGTTTCTGGGGTGTCTATGTTCTGGATCTGTG 84  
 DB 281 AAGTTCTCAGAAATGAGGTGCTAGCTAGTTCCTGGGGTGTCTGTTGCTCTGGATCCCTG 340

QY 85 GAGTCAGTGGGGATATGATAAACCAGGATCACTCTCCATCCTGTCACTTCTGGAG 144  
 DB 341 GAGCCATTGGGGATATGATGACTCAGGCTGCACCCCTCTGTACCTGTCACTCTGGAG 400

QY 145 AATCAGTTTCCATCTCTCTGAGGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACAT 204  
 DB 401 AGTCAGATCCATCTCTCGAGTCTAGTAAGAGTCTCTGTATAGTATGGCAACATT 460

QY 205 ACTTGAATTGGTTTCTGACAGACCCAGGACATCTCTCAGTCTCTGATGTAATTGATGT 264  
 DB 461 ACTTGTATTGGTTCTTACAGAGCCAGGCTCTCTCAGTCTCTGATATATCGGATGT 520

QY 265 CCACCCGTGCATCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCCAGGACAGATTCA 324  
 DB 521 CCAACTTGGCTCAGAGTCCAGACAGGTTTCTAGTGGCAGTGGTCCAGGACAGTCTTCA 580

QY 325 CCCTGGAATTCAGTAGAGTGAAGGCTGAGGATGGGTGTATTAATCTGTCAACACTTG 384  
 DB 581 CACTGAGATCAGTAGAGTGGAGCTGAGGATGGGTGTATTAATCTGTATGCAACATC 640

QY 385 TAGAGTATCAATTCAGTTCTGGTCTGGGGACAAAGTTGGAAATAAAACG 433  
 DB 641 TAGAATATCGCTCAGGTTCTGGTCTGGGACCAAGCTGGAGCTGAAACG 689

RESULT 15  
 ADM72038  
 ID ADM72038 standard; DNA; 720 BP.  
 XX  
 AC ADM72038;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Chimeric mouse-human antibody M18D04 light chain encoding DNA.  
 XX  
 KW GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;  
 KW cytosstatic; gene; ds; M18D04.  
 XX  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..720  
 FT /\*tag= a  
 FT /product= "M18D04 light chain"  
 XX  
 WO2004022739-A1.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 04-SEP-2003; 2003WO-JP011318.  
 XX  
 PR 04-SEP-2002; 2002WO-JP008999.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;  
 XX

DR WPI: 2004-269573/25.  
 DR P-PSDB; ADM72039.  
 XX Antibody against the N terminus of glypican 3 (GPC3) causes cell  
 PT disruption and is useful as an anticancer agent.  
 XX  
 PS Example 4; SEQ ID NO 23; 122pp; Japanese.  
 XX  
 CC The invention relates to an antibody against the N terminus of glypican 3  
 CC (GPC3). The antibody can be used for causing cell disruption and can be  
 CC uses as an anti-cancer agent. The present sequence represents a chimeric  
 CC mouse-human antibody M18D04 light chain encoding DNA.  
 XX  
 SQ Sequence 720 BP; 183 A; 186 C; 181 G; 170 T; 0 U; 0 Other;

Query Match 65.6%; Score 286.8; DB 12; Length 720;  
 Best Local Similarity 82.1%; Pred. No. 1.2e-77;  
 Matches 330; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTGTCTATGTTCTGTGATCTCTGGAGTCAGTGGG 95  
 DB 1 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTGTCTATGTTCTGTGATCTCTGGATCCCTGGATCCACTGCA 60

QY 96 GATATTGTGATAAACCAGGATGAATCTTCCAAATCTGTCACTTCTGGAGAATCAGTTTCC 155  
 DB 61 GATATTGTGATGACGCGGCTGCATTTCCAAATCCAGTCACTTCTTGGAAACATCAACTTCC 120

QY 156 ATCTCTCTGAGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 215  
 DB 121 ATCTCTCTGAGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 180

QY 216 TTTCTGCGAGACCCAGGACAAATCTCTCAGCTCTCTGATGTAATTGATGCCACCGTGCA 275  
 DB 181 TATCTGCGAGACCCAGGACAAATCTCTCAGCTCTCTGATGTAATTGATGCCACCGTGCC 240

QY 276 TCAGAGTCTCAGACCGGTTTATGTTGGCAGTGGGTTCAGGCACAGATTTCAACCTGGAAATC 335  
 DB 241 TCAGGAGTCCCAAGACAGAGTTTCAGTAGCAGTGGGTTCAGGAACTGATTTTCACACTGAGAATC 300

QY 336 AGTAGAGTCAAGGCTGAGGATGGGTGTGTTTACTGTCAACAACTTGTAGAGTATCCA 395  
 DB 301 AGCAGAGTGGAGGCTGAGGATGGGTGTGTTTACTGTGCTCAAAATCTAGAACTTCCG 360

QY 396 TTCAGGTTCTGGCTCGGGGACAAAGTTGGAAATAAAACGTAACG 437  
 DB 361 TATACGTTCCGATCGGGGACCAAGCTGGAAATAAAACGTAACG 402

Search completed: April 18, 2005, 11:34:44  
 Job time : 248.823 secs



Db 61 ATCTCTCGAGGTCTAGTAGGAGTCTCTATATAGGATGGGAAGACATACATGAATTGG 120  
QY 216 TTCTCGAGAGACAGGACAACTCTCTCAGCTCTCTGATGATGATTTGATGTCACCCGTGCA 275  
Db 121 TTCTCGAGAGACAGGACAACTCTCTCAGCTCTCTGATGATGATTTGATGTCACCCGTGCA 180  
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC 335  
Db 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC 240  
QY 336 AGTAGAGTGAAGCTCAGGATGTTGGTGTGTTATTACTGTCAACAACCTTGTAGAGTATCCA 395  
Db 241 AGTAGAGTGAAGCTCAGGATGTTGGTGTGTTATTACTGTCAACAACCTTGTAGAGTATCCA 300  
QY 396 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAAACG 433  
Db 301 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAAACG 338

## RESULT 2

US-09-940-727B-107  
; Sequence 107, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940, 727B  
; PRIORITY FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 107  
; LENGTH: 368  
; TYPE: DNA  
; ORGANISM: mouse  
US-09-940-727B-107

Query Match 72.6%; Score 317.2; DB 10; Length 368;  
Best Local Similarity 96.2%; Pred. No. 5.2e-98;  
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 96 GATATTGTGATAACCCAGGATGAACCTCTCCAAATCCTGTCTCACTTCTGGAGAATCAGTTTCC 155  
Db 1 GATATGGTGATGACGCAAGACGAACTCTCCAAATCCTGTCTCACTTCTGGAGAATCAGTTTCC 60  
QY 156 ATCTCTCGAGTCTAGTAGGAGTCTCTGTATAGGATGGGAAGACATACACTTGAATTGG 215  
Db 61 ATCTCTCGAGTCTAGTAGGAGTCTCTGTATAGGATGGGAAGACATACACTTGAATTGG 120  
QY 216 TTCTCGAGAGACAGGACAACTCTCTCAGCTCTCTGATGATTTGATGTCACCCGTGCA 275  
Db 121 TTCTCGAGAGACAGGACAACTCTCTCAGCTCTCTGATGATTTGATGTCACCCGTGCA 180  
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC 335  
Db 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAAATC 240  
QY 336 AGTAGAGTGAAGCTCAGGATGTTGGTGTGTTATTACTGTCAACAACCTTGTAGAGTATCCA 395  
Db 241 AGTAGAGTGAAGCTCAGGATGTTGGTGTGTTATTACTGTCAACAACCTTGTAGAGTATCCA 300  
QY 396 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAAACG 433  
Db 301 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAAACG 338

## RESULT 3

US-09-940-727B-111  
; Sequence 111, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940, 727B  
; PRIORITY FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 111  
; LENGTH: 420  
; TYPE: DNA  
; ORGANISM: mouse  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: any nucleotide  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (13)..(13)  
; OTHER INFORMATION: any nucleotide  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (402)..(402)  
; OTHER INFORMATION: any nucleotide  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (404)..(404)  
; OTHER INFORMATION: any nucleotide  
US-09-940-727B-111

Query Match 72.3%; Score 316; DB 10; Length 420;  
Best Local Similarity 95.6%; Pred. No. 1.4e-97;  
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 94 GGGATATTGTGATTAACCCAGGATGAACCTCTCCAAATCCTGTCTCACTTCTGGAGAATCAGTTT 153  
Db 51 GGGATATTGTGATTAACCCAGGATGAACCTCTCCAAATCCTGTCTCACTTCTGGAGAATCAGTTT 110  
QY 154 CCATCTCTCTGCAAGTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACACTTGAATT 213  
Db 111 CCATCTCTCTGCAAGTCTAGTAGGAGTCTCTGTATAAGGATGGGAAGACATACACTTGAATT 170  
QY 214 GGTTCCTCGAGACACAGGACAACTCTCTCAGCTCTCTGATGATTTGATGTCACCCGTG 273  
Db 171 GGTTCCTCGAGACACAGGACAACTCTCTCAGCTCTCTGATGATTTGATGTCACCCGTG 230  
QY 274 CATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAA 333  
Db 231 CATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCCCTTGGAA 290  
QY 334 TCAGTAGAGTGAAGGCTCAGGATGTTGGTGTGTTATTACTGTCAACAACCTTGTAGAGTATC 393  
Db 291 TCAGTAGAGTGAAGGCTCAGGATGTTGGTGTGTTATTACTGTCAACAACCTTGTAGAGTATC 350  
QY 394 CATTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAAACG 433  
Db 351 CATTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAAACG 390

## RESULT 4

US-09-940-727B-103  
; Sequence 103, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:





QY 156 ATCTCTCGAGGCTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATATCTGTAATTGG 215  
Db 121 ATCTCTCGAGGCTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATATCTGTAATTGG 180  
QY 216 TTTCTGCAGAGACAGGACAACTCTCTAGCTCCCTGATGTTATTTGATGTCACCGTGCA 275  
Db 181 TTCTCTACAGAGGCGGAGGCTCTCTAGCTCCCTGATATATCGGATGTCACACCTTGCC 240  
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTCTAGGACAGATTTTACCCCTGGAAATC 335  
Db 241 TCAGGAGTCCAGACAGGTTTCTAGTGGCAGTGGGTCTAGGACAGTCTTTCACACTGAGATC 300  
QY 336 AGTAGAGTGAAGCTCAGAGATGTTGGGTGTATTAATCTGTCAACAACTTTAGAGTATCCA 395  
Db 301 AGTAGAGTGGAGCTCAGGATGTTGGGTGTTTATTAATCTGTATCAACATCTAGATATCCG 360  
QY 396 TTCACGTTCCGTCGGGGACAAAGTTGGAATAAAACG 433  
Db 361 CTCACGTTCCGTCGGGACCAAGCTGGAGCTGAAACG 398

RESULT 7  
US-10-207-655-356  
; Sequence 356, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 356  
; LENGTH: 825  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion polynucleotide  
US-10-207-655-356

Query Match 64.2%; Score 280.4; DB 15; Length 825;  
Best Local Similarity 81.1%; Pred. No. 3.1e-85;  
Matches 326; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 32 CACCATGAGGTTCTCTGTTTCAGTTTCTGGGGGTGCTTATGTTCTGGATCTCTGGAGTCAG 91  
Db 9 CGCCATGAGGTTCTCTGCTCAGCTTCTGGGGGTGCTTGTGCTCTGGATCCCTGGATCCAC 68  
QY 92 TGGGGATATTGTGATAACCCAGAGTGAATCTTCAATCTCTGCTCACTCTGAGAAATCAGT 151  
Db 69 TGCAGATATTGTGATGACGCGAGGTGCAATTTCCAACTCAGTCACTCTTGGACATCAGC 128  
QY 152 TTCCATCTCTCCAGGCTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTGA 211  
Db 129 TTCCATCTCTCCAGGCTCTAGTAAGAGTCTCTACATAGTAATGTCATCACTTATTGTA 188  
QY 212 TTGGTTTCTGCAGAGACCCAGACATCTCTCAGTCTCTGATGTTTGTGATGTCACCCG 271  
Db 189 TTGGTATCTGCAGAGACCCAGGCTCTCTCAGTCTCTGATTTATCAGATGTCACCT 248  
QY 272 TGCATCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCACTGGA 331  
Db 249 TGCTCAGAGTCCAGACAGGTTTCACTAGCAGTGGGTGAGGACAGTATTCACACTGAG 308  
QY 332 AATCAGTAGAGTGAAGCTCAGAGTGTGGGTGTATTAATCTGTCAACAACTTTAGAGTA 391  
Db 309 AATCAGCAGAGTGGAGGCTGAGGATGTTGGGTGTTTATTACTGTCTCAAAATCTAGAACT 368  
QY 392 TCCATTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433  
Db 369 TCCGCTCAGTTCGGGTGCTGGGACCAAGCTGGAGCTGAAACG 410

RESULT 9  
US-10-207-655-358  
; Sequence 358, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 358  
; LENGTH: 1696  
; TYPE: DNA

Db 369 TCCGCTCAGGTTCCGTCGGGACCAAGCTGGAGCTGAAACG 410

RESULT 8  
US-10-207-655-357  
; Sequence 357, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 357  
; LENGTH: 1536  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion polynucleotide  
US-10-207-655-357

Query Match 64.2%; Score 280.4; DB 15; Length 1536;  
Best Local Similarity 81.1%; Pred. No. 4.1e-85;  
Matches 326; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 32 CACCATGAGGTTCTCTGTTTCAGTTTCTGGGGGTGCTTATGTTCTGGATCTCTGGAGTCAG 91  
Db 9 CGCCATGAGGTTCTCTGCTCAGCTTCTGGGGGTGCTTGTGCTCTGGATCCCTGGATCCAC 68  
QY 92 TGGGGATATTGTGATAACCCAGAGTGAATCTTCAATCTCTGCTCACTCTGAGAAATCAGT 151  
Db 69 TGCAGATATTGTGATGACGCGAGGTGCAATTTCCAACTCAGTCACTCTTGGACATCAGC 128  
QY 152 TTCCATCTCTCCAGGCTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTGA 211  
Db 129 TTCCATCTCTCCAGGCTCTAGTAAGAGTCTCTACATAGTAATGTCATCACTTATTGTA 188  
QY 212 TTGGTTTCTGCAGAGACCCAGACATCTCTCAGTCTCTGATGTTTGTGATGTCACCCG 271  
Db 189 TTGGTATCTGCAGAGACCCAGGCTCTCTCAGTCTCTGATTTATCAGATGTCACCT 248  
QY 272 TGCATCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCACTGGA 331  
Db 249 TGCTCAGAGTCCAGACAGGTTTCACTAGCAGTGGGTGAGGACAGTATTCACACTGAG 308  
QY 332 AATCAGTAGAGTGAAGCTCAGAGTGTGGGTGTATTAATCTGTCAACAACTTTAGAGTA 391  
Db 309 AATCAGCAGAGTGGAGGCTGAGGATGTTGGGTGTTTATTACTGTCTCAAAATCTAGAACT 368  
QY 392 TCCATTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433  
Db 369 TCCGCTCAGTTCGGGTGCTGGGACCAAGCTGGAGCTGAAACG 410

RESULT 9  
US-10-207-655-358  
; Sequence 358, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 358  
; LENGTH: 1696  
; TYPE: DNA

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RESULT 10
US-10-107-991B-2
; Sequence 2, Application US/10107991B
; Publication No. US20040058445A1
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: HELLSTROM, INGEGERD
; APPLICANT: HELLSTROM, KARL ERIK
; TITLE OF INVENTION: ACTIVATION OF TUMOR-REACTIVE LYMPHOCYTES VIA ANTIBODIES
; TITLE OF INVENTION: OR GENES RECOGNIZING CD3 OR 4-1BB
; FILE REFERENCE: 034474.0004
; CURRENT APPLICATION NUMBER: US/10/107,991B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/286,585
; PRIOR FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 2.1
; SEQ ID NO 2
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mouse-Human Hybrid Gene
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1680)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (13)..(71)
; OTHER INFORMATION: codes 5B9 mouse anti-human 4-1BB VL leader peptide sequence
; FEATURE:
; NAME/KEY: V region
; LOCATION: (72)..(412)
; OTHER INFORMATION: codes 5B9 mouse anti-human 4-1BB VL domain

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RESULT 11
US-10-207-655-355
; Sequence 355, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 355
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polynucleotide
US-10-207-655-355

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QY 276 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGGTCTAGGCGACAGATTTCACCCCTGGAATC 335  
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Db 241 TCAGGAGTCCAGACAGGTTTCAGTAGCAGTGGGTCTAGGAACTGATTTCACACTGAGAATC 300  
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QY 336 ASTAGAGTGAAGCTGAGGATGGGTGTCTATCTGTCACAACTGTGTAGAGTATCCA 395  
|||||  
Db 301 AGCAGAGTGGAGGCTGAGGATGGGTGTCTATCTGTCACAACTGTGTAGAGTATCCA 360  
|||||  
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAACGTAC 436  
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Db 361 CGGACGTTCCGTTGGGACCAACAGCTTGAGATGAACGAAC 401  
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RESULT 14  
US-10-404-724-40  
; Sequence 40, Application US/10404724  
; Publication No. US20030203447A1  
; GENERAL INFORMATION:  
; APPLICANT: Horwitz, Arnold H.  
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant  
; FILE REFERENCE: Polypeptides  
; CURRENT APPLICATION NUMBER: US/10/404,724  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/368,530  
; PRIOR FILING DATE: 2002-03-29  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 40  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: P2=P Human Engineered (low risk) INGI light Chain with one  
; OTHER INFORMATION: moderate risk proline change; proline at position 15 (P2)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(717)  
; FEATURE:  
; NAME/KEY: mat peptide  
; LOCATION: (61)..()  
US-10-404-724-40

Query Match 59.5%; Score 260.2; DB 17; Length 720;  
Best Local Similarity 78.1%; Pred. No. 2.5e-78;  
Matches 313; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 36 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95  
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Db 1 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGATCTCACTGCA 60  
|||||  
QY 96 GATATTGTGATACCCAGGATGAATCTCCAATCTCTGTCAGTCTCTGGAGAAATCAGTTTCC 155  
|||||  
Db 61 GACATCGTGTATGACCCAGTCTGCACCTCTCCAATCCAGTCACTCTGGAGAGTCAGTTCC 120  
|||||  
QY 156 ATCTCTCGCAGTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACATATCTTGAATGG 215  
|||||  
Db 121 ATCTCTCGCGGTCTAGTAAGAGTCTCTACATAGTAATGGCATCACTTATTTGTATTGG 180  
|||||  
QY 216 TTTCTGCAGAGACCCAGGACAAATCTCTCAGCTCCTGATGTTATGTCACCCCTGCA 275  
|||||  
Db 181 TATCTGCGGTTCTAGTAAGAGTCTCTACATAGTAATGGCATCACTTATTTGTATTGG 180  
|||||  
QY 216 TTTCTGCAGAGACCCAGGACAAATCTCTCAGCTCCTGATGTTATGTCACCCCTGCA 275  
|||||  
Db 181 TATCTGCGGTTCTAGTAAGAGTCTCTACATAGTAATGGCATCACTTATTTGTATTGG 180  
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QY 276 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGGTCTAGGCGACAGATTTCACCCCTGGAATC 335  
|||||  
Db 241 TCAGGAGTCCAGACAGGTTTCAGTAGCAGTGGATCTGGGACAGATTTCACTCTCAAGATC 300  
|||||  
QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCAACAACTGTGTAGAGTATCCA 395  
|||||  
Db 301 AGCAGAGTGGAGGCTGAAGATGGGAGTTTATTACTGTCTCAGAACCTTAGAGCTTCCG 360  
|||||  
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAACGTAC 436  
|||||  
Db 361 CGGACGTTCCGTTGGGACCAACAGCTTGAGATGAACGAAC 401  
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Search completed: April 19, 2005, 00:13:28  
Job time : 1190.64 secs

Db 361 CGGACGTTCCGTTGGGACCAACAGCTTGAGATGAACGAAC 401  
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RESULT 15  
US-10-816-276-36  
; Sequence 36, Application US/10816276  
; Publication No. US20050009097A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Horwitz, Arnold H.  
; TITLE OF INVENTION: Human Engineered to Antibodies to Ep-CAM  
; FILE REFERENCE: 14923US02  
; CURRENT APPLICATION NUMBER: US/10/816,276  
; PRIOR FILING DATE: 2004-03-31  
; PRIOR APPLICATION NUMBER: 60/459,334  
; PRIOR FILING DATE: 2003-03-31  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 36  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: P2=P Human Engineered (low risk) INGI light Chain with one  
; OTHER INFORMATION: moderate risk proline change; proline at position 15 (P2)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(717)  
; FEATURE:  
; NAME/KEY: mat peptide  
; LOCATION: (61)..()  
US-10-816-276-36

Query Match 59.5%; Score 260.2; DB 19; Length 720;  
Best Local Similarity 78.1%; Pred. No. 2.5e-78;  
Matches 313; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 36 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95  
|||||  
Db 1 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGATCTCACTGCA 60  
|||||  
QY 96 GATATTGTGATACCCAGGATGAATCTCCAATCTCTGTCAGTCTCTGGAGAAATCAGTTTCC 155  
|||||  
Db 61 GACATCGTGTATGACCCAGTCTGCACCTCTCCAATCCAGTCACTCTGGAGAGTCAGTTCC 120  
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QY 156 ATCTCTCGCAGTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACATATCTTGAATGG 215  
|||||  
Db 121 ATCTCTCGCGGTCTAGTAAGAGTCTCTACATAGTAATGGCATCACTTATTTGTATTGG 180  
|||||  
QY 216 TTTCTGCAGAGACCCAGGACAAATCTCTCAGCTCCTGATGTTATGTCACCCCTGCA 275  
|||||  
Db 181 TATCTGCGGTTCTAGTAAGAGTCTCTCAGCTCCTCATCTATCAGATGTCTAACAGAGCC 240  
|||||  
QY 276 TCAGGAGTCTCAGACCGGTTTATGTTGGCAGTGGGTCTAGGCGACAGATTTTCACCCCTGGAATC 335  
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Db 241 TCAGGAGTCCAGACAGGTTTCAGTAGCAGTGGATCTGGGACAGATTTCACTCTCAAGATC 300  
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QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCAACAACTGTGTAGAGTATCCA 395  
|||||  
Db 301 AGCAGAGTGGAGGCTGAAGATGGGAGTTTATTACTGTCTCAGAACCTTAGAGCTTCCG 360  
|||||  
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAACGTAC 436  
|||||  
Db 361 CGGACGTTCCGTTGGGACCAACAGCTTGAGATGAACGAAC 401  
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 84.297 Seconds  
(without alignments)  
8482.539 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 437

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Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

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- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	317.2	72.6	339	2	US-08-672-345C-88
2	317.2	72.6	339	3	US-09-214-095D-99
3	317.2	72.6	368	2	US-08-672-345C-86
4	317.2	72.6	368	3	US-09-214-095D-107
5	316	72.3	420	3	US-09-214-095D-111
6	309.2	70.8	368	2	US-08-672-345C-90
7	309.2	70.8	368	3	US-09-214-095D-103
8	293.2	67.1	464	1	US-08-438-123-15
9	276.4	63.2	399	1	US-08-253-877C-9
10	276.4	63.2	399	2	US-08-452-164A-9
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12	276.4	63.2	399	4	US-08-450-809-2
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14	248.4	56.8	339	3	US-09-406-532-13
15	247	56.5	968	4	US-10-000-489-7
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17	241.2	55.2	954	4	US-09-479-614-21
18	240	54.9	882	1	US-08-392-419-3
19	238.4	54.6	726	4	US-09-479-614-23
20	238.4	54.6	726	4	US-09-479-614-24
21	236	54.0	373	3	US-08-732-708C-40
22	230.8	52.8	1095	3	US-08-875-811-52
23	230.8	52.8	1098	3	US-08-875-811-54
24	226.2	51.8	405	1	US-08-259-372A-11
25	226.2	51.8	405	1	US-08-468-671-11
26	223.6	51.2	427	1	US-08-053-171-8
27	221.4	50.7	325	1	US-08-468-661-4

28	221.4	50.7	325	1	US-08-466-272A-4	Sequence 4, Appli
29	221.4	50.7	325	1	US-08-478-857-4	Sequence 4, Appli
30	221.4	50.7	325	1	US-08-471-771-4	Sequence 4, Appli
31	221.4	50.7	325	3	US-09-130-783-4	Sequence 4, Appli
32	219	50.1	434	1	US-08-053-171-4	Sequence 4, Appli
33	212.8	48.7	394	1	US-08-129-930B-93	Sequence 93, Appli
34	212.8	48.7	394	3	US-08-134-346A-48	Sequence 48, Appli
35	212.8	48.7	394	3	US-08-976-288A-93	Sequence 93, Appli
36	211.6	48.4	393	4	US-09-647-468-16	Sequence 16, Appli
37	211.6	48.4	720	3	US-08-487-550-5	Sequence 5, Appli
38	211.6	48.4	720	4	US-09-526-098-5	Sequence 5, Appli
39	211.6	48.4	720	4	US-09-383-916-5	Sequence 5, Appli
40	211.2	48.3	394	1	US-07-977-696C-64	Sequence 64, Appli
41	211.2	48.3	394	1	US-08-129-930B-64	Sequence 64, Appli
42	211.2	48.3	394	3	US-08-976-288A-64	Sequence 64, Appli
43	210	48.1	409	4	US-09-254-180C-146	Sequence 146, App
44	208.4	47.7	393	4	US-09-647-468-17	Sequence 17, Appli
45	206.6	47.3	424	3	US-08-589-939-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-08-672-345C-88  
; Sequence 88, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 339 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-672-345C-88

Query Match 72.6%; Score 317.2; DB 2; Length 339;  
Best Local Similarity 96.2%; Pred. No. 1.1e-97;  
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 96 GATATTGTGATACCCAGGATGAACCTCCAAATCTGTCTCACTTCGGAGATCAGTTTCC 155  
Db 1 GATATTGTGATACCCAGGATGAACCTCCAAATCTGTCTCACTTCGGAGATCAGTTTCC 60  
QY 156 ATCTCTCGAGGCTCTAGTAGAGTCTCTGTATAGAGTGGGAGACATACCTGAATGG 215

Db 61 ATCTCTCGAGGTCTAGTAGAGTCTCTATATAGGATGGGAAGACATACCTTGAATTGG 120  
QY 216 TTTCTCGAGAGACGAGACAATCTCTCAGCTCTGATGATTTGATGTCACCCGTTGCA 275  
Db 121 TTTCTCGAGAGACGAGACAATCTCTCAGCTCTGATGATTTGATGTCACCCGTTGCA 180  
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAAATC 335  
Db 181 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAAATC 240  
QY 336 AGTAGAGTGAAGCTCAGAGTGGGTGATTAATCTGTCACCAACCTTGTAGAGTATCCA 395  
Db 241 AGTAGAGTGAAGCTCAGAGTGGGTGATTAATCTGTCACCAACCTTGTAGAGTATCCA 300  
QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433  
Db 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

## RESULT 2

US-09-214-095D-99  
; Sequence 99, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214, 095D  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 99  
; LENGTH: 339  
; TYPE: DNA  
; ORGANISM: Murine  
US-09-214-095D-99

Query Match 72.6%; Score 317.2; DB 3; Length 339;

Best Local Similarity 96.2%; Pred. No. 1.1e-97;

Matches 335; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATACCCAGGATGAACCTCCAAATCTCTGTCACCTTCTGGAGAATCAGTTTCC 155  
Db 1 GATATTGTGATACCCAGGATGAACCTCCAAATCTCTGTCACCTTCTGGAGAATCAGTTTCC 60  
QY 156 ATCTCTCGAGGTCTAGTAGAGTCTCTGATAGGATGGGAAGACATACCTTGAATTGG 215  
Db 61 ATCTCTCGAGGTCTAGTAGAGTCTCTGATAGGATGGGAAGACATACCTTGAATTGG 120  
QY 216 TTTCTCGAGAGACGAGACAATCTCTCAGCTCTGATGATTTGATGTCACCCGTTGCA 275  
Db 121 TTTCTCGAGAGACGAGACAATCTCTCAGCTCTGATGATTTGATGTCACCCGTTGCA 180  
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAAATC 335  
Db 181 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAAATC 240  
QY 336 AGTAGAGTGAAGCTCAGAGTGGGTGATTAATCTGTCACCAACCTTGTAGAGTATCCA 395  
Db 241 AGTAGAGTGAAGCTCAGAGTGGGTGATTAATCTGTCACCAACCTTGTAGAGTATCCA 300  
QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433  
Db 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

## RESULT 3

US-08-672-345C-86  
; Sequence 86, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 368 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-672-345C-86

Query Match 72.6%; Score 317.2; DB 2; Length 368;

Best Local Similarity 96.2%; Pred. No. 1.2e-97;

Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATACCCAGGATGAACCTCCAAATCTCTGTCACCTTCTGGAGAATCAGTTTCC 155  
Db 1 GATATTGTGATACCCAGGATGAACCTCCAAATCTCTGTCACCTTCTGGAGAATCAGTTTCC 60  
QY 156 ATCTCTCGAGGTCTAGTAGAGTCTCTGATAGGATGGGAAGACATACCTTGAATTGG 215  
Db 61 ATCTCTCGAGGTCTAGTAGAGTCTCTGATAGGATGGGAAGACATACCTTGAATTGG 120  
QY 216 TTTCTCGAGAGACGAGACAATCTCTCAGCTCTGATGATTTGATGTCACCCGTTGCA 275  
Db 121 TTTCTCGAGAGACGAGACAATCTCTCAGCTCTGATGATTTGATGTCACCCGTTGCA 180  
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAAATC 335  
Db 181 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAAATC 240  
QY 336 AGTAGAGTGAAGCTCAGAGTGGGTGATTAATCTGTCACCAACCTTGTAGAGTATCCA 395  
Db 241 AGTAGAGTGAAGCTCAGAGTGGGTGATTAATCTGTCACCAACCTTGTAGAGTATCCA 300  
QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433  
Db 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

## RESULT 4

US-09-214-095D-107  
; Sequence 107, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214, 095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121



; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 107  
; LENGTH: 368  
; TYPE: DNA  
; ORGANISM: Murine  
US-09-214-095D-107

Query Match 72.6%; Score 317.2; DB 3; Length 368;  
Best Local Similarity 96.2%; Pred. No. 1.2e-97;  
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy	96	GATATTGTGATAACCCAGGATGAATCTCCCAATCCTGTCACTTCTGGAGAAATCAGTTTC	155
Db	1	GATATGGTGATGACGCAAGACGAATCTCCAATCCTGTCACTTCTGGAGAAATCAGTTTC	60
Qy	156	ATCTCCTCGAGGTCTAGTAAGAGTCTCCTGTATAGGATGGAAGACATATCTTCAATTTGG	215
Db	61	ATCTCCTCGAGGTCTAGTAAGAGTCTCCTATATAGGATGGAAGACATATCTTCAATTTGG	120
Qy	216	TTTCTGCAGAGACAGGACAAATCTCCTCAGCTCCTGTATTTGTATTTGATGTCCACCGTGCA	275
Db	121	TTTCTGCAGAGACAGGACAAATCTCCTCAGCTCCTGTATTTGTATTTGATGTCCACCGTGCA	180
Qy	276	TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTTCAACCTGGAATC	335
Db	181	TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGAAACAGATTTTCAACCTGGAATC	240
Qy	336	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTTGTAGAGTATCCA	395
Db	241	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTTGTAGAGTATCCA	300
Qy	396	TTACGTTTCGGCTCGGGGACAAAGTTTGGAAATAAAACG	433
Db	301	TTACGTTTCGGCTCGGGGACAAAGTTTGGAAATAAGACG	338

## RESULT 5

US-09-214-095D-111  
; Sequence 111, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 111  
; LENGTH: 420  
; TYPE: DNA  
; ORGANISM: Murine  
; FEATURE:  
; NAME/KEY: V\_segment  
; LOCATION: (1)..(403)  
; OTHER INFORMATION: n at any position represents any nucleotide including c.g,t,a,u  
US-09-214-095D-111

Query Match 72.3%; Score 316; DB 3; Length 420;  
Best Local Similarity 95.6%; Pred. No. 3.2e-97;  
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy	94	GGGATATTGTGATAACCCAGGATGAATCTCCCAATCCTGTCACTTCTGGAGAAATCAGTTT	153
Db	51	GGGATATTGTGATGACCGCAGAGTGAATCTCCCAATCCTGTCACTTCTGGAGAAATCAGTTT	110
Qy	154	CCATCTCCTGCAGTCTAGTAAGAGTCTCCTGTATTAAGGATGGGAAGACATATCTTGAATT	213
Db	111	CCATCTCCTGCAGTCTAGTAGGAGTCTCCTATATAGGATGGGAAGACATATCTTGAATT	170
Qy	214	GGTTTCTGCAGAGACAGGACAAATCTCCTCAGCTCCTGTATTTGTATTTGATGTCCACCGTG	273
Db	171	GGTTTCTGCAGAGACAGGACAAATCTCCTCAGCTCCTGTATTTGTATTTGATGTCCACCGTG	230

Qy	274	CATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTTCAACCTGGAAA	333
Db	231	CATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTTCAACCTGGAAA	290
Qy	334	TCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTTGTAGAGTATC	393
Db	291	TCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTTGTAGAGTATC	350
Qy	394	CATTACGTTTCGGCTCGGGGACAAAGTTTGGAAATAAAACG	433
Db	351	CATTACGTTTCGGCTCGGGGACAAAGTTTGGAAATAAAACG	390

## RESULT 6

US-08-672-345C-90  
; Sequence 90, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 90:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 368 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-672-345C-90

Query Match 70.8%; Score 309.2; DB 2; Length 368;  
Best Local Similarity 94.7%; Pred. No. 6.2e-95;  
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy	96	GATATTGTGATAACCCAGGATGAATCTCCTCAATCCTGTCACTTCTGGAGAAATCAGTTTTC	155
Db	1	GATATTGTGATGACGCAAGATGAATCTCCTCAATCCTGTCACTTCTGGAGAAATCAGTTTTC	60
Qy	156	ATCTCCTCGAGGTCTAGTAAGAGTCTCCTGTATTAAGGATGGGAAGACATATCTTGAATTGG	215
Db	61	ATCTCCTCGAGGTCTAGTAGGAGTCTCCTATATAGGATGGGAAGACATATCTTGAATTGG	120
Qy	216	TTTCTGCAGAGACAGGACAAATCTCCTCAGCTCCTGTATTTGTATTTGATGTCCACCGTGCA	275
Db	121	TTTCTGCAGAGACAGGACAAATCTCCTCAGCTCCTGTATTTGTATTTGATGTCCACCGTGCA	180
Qy	276	TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTTCAACCTGGAAATC	335
Db	181	TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTTCAACCTGGAAATC	240



NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/253,877C  
FILING DATE: 03-JUN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3246  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 399 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..399  
US-08-253-877C-9

Query Match 63.2%; Score 276.4; DB 1; Length 399;  
Best Local Similarity 80.9%; Pred. No. 9.4e-84;  
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY	36	ATGAGGTTCTCTGTTACAGTTCTGGGGGTCCTTATGTTCTGGATCTCTGGAGTCAGTGGG	95
Db	1	ATGAGGTGCTAGCTAGTTCTGGGGGTCCTTGTGCTCTGGATCTCTGGAGCCATTGGG	60
QY	96	GATATTGTGATACCCAGGATGAATCTCCAAATCTGTCTCACTCTGAGAAATCAGTTTCC	155
Db	61	GATATTGTGATGACTCAGGCTGCACCTCTGTTCTCTGCTCTGGAGATCATTTATCC	120
QY	156	ATCTCTGCAAGTCTAGTAAGAGTCTCTGTAAGAGATGGGAAGACATATCTTGAATTGG	215
Db	121	ATTTCTGTCAGGCTAGTAAGAGTCTCTTATAGTAATGGGACACTTCTTGTATTGG	180
QY	216	TTTCTGACAGACAGGACAAATCTCTCAGCTCTGATGATTTGATGTCACCCCTGCA	275
Db	181	TTCTCTGACAGGCGGCGGCTCTCTCACTCTGATATATCGGATGTCCAACTTGGC	240
QY	276	TCAGGAGTCTCAGACCGGTTTGTAGTGGGTCAGGTCAGGACAGATTTTCACTTGAATC	335
Db	241	TCCGGAGTCCAGACAGGTTTCTAGTGGGTCAGGTCAGGTCAGGTCAGGTCAGGTC	300
QY	336	AGTAGAGTGAAGGTCAGGATGTTGGTGTGTTATTTACTGTCAACAACTTTAGAGTATCCA	395
Db	301	AGTAGAGTGAAGGTCAGGATGTTGGTGTGTTATTTACTGTATGCAATCTAGATATCCT	360
QY	396	TTACGTTTGGGTCGGGACAAAGTTTGAATTTAAACG	433
Db	361	TTACGTTTGGGTCGGGACAAAGTGGAGTGAACG	398

## RESULT 10

US-08-452-164A-9  
; Sequence 9, Application US/08452164A  
; Patent No. 5877296

GENERAL INFORMATION:  
APPLICANT: Hamann, Philip R.  
APPLICANT: Hamann, Lois  
APPLICANT: Hollander, Irwin  
APPLICANT: Holcomb, Ryan  
APPLICANT: Hallett, William  
APPLICANT: Tsou, Hwei-Ru  
APPLICANT: Weiss, Martin J.  
TITLE OF INVENTION: Conjugates of Methylothio Antitumor  
Agents and Intermediates for Their Synthesis  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Home Products Corporation  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,164A  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2158  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 399 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..399  
US-08-452-164A-9

Query Match 63.2%; Score 276.4; DB 2; Length 399;  
Best Local Similarity 80.9%; Pred. No. 9.4e-84;  
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY	36	ATGAGGTTCTCTGTTACAGTTCTGGGGGTCCTTATGTTCTGGATCTCTGGAGTCAGTGGG	95
Db	1	ATGAGGTGCTAGCTAGTTCTGGGGGTCCTTGTGCTCTGGATCTCTGGAGCCATTGGG	60
QY	96	GATATTGTGATACCCAGGATGAATCTCCAAATCTGTCTCACTCTGAGAAATCAGTTTCC	155
Db	61	GATATTGTGATGACTCAGGCTGCACCTCTGTTCTCTGCTCTGGAGATCATTTATCC	120
QY	156	ATCTCTGCAAGTCTAGTAAGAGTCTCTGTAAGAGATGGGAAGACATATCTTGAATTGG	215
Db	121	ATTTCTGTCAGGCTAGTAAGAGTCTCTTATAGTAATGGGACACTTCTTGTATTGG	180
QY	216	TTTCTGACAGACAGGACAAATCTCTCAGCTCTGATGATTTGATGTCACCCCTGCA	275
Db	181	TTCTCTGACAGGCGGCGGCTCTCTCACTCTGATATATCGGATGTCCAACTTGGC	240
QY	276	TCAGGAGTCTCAGACCGGTTTGTAGTGGGTCAGGTCAGGACAGATTTTCACTTGAATC	335
Db	241	TCCGGAGTCCAGACAGGTTTCTAGTGGGTCAGGTCAGGTCAGGTCAGGTCAGGTC	300
QY	336	AGTAGAGTGAAGGTCAGGATGTTGGTGTGTTATTTACTGTCAACAACTTTAGAGTATCCA	395
Db	301	AGTAGAGTGAAGGTCAGGATGTTGGTGTGTTATTTACTGTATGCAACATCTAGATATCCT	360

QY 396 TTCACGTCGGCTCGGGGACAAAGTTGGAATAAAACG 433  
Db 361 TTCACGTCGGCTCGGGACCAAGCTGGAGCTGAAACG 398

## RESULT 11

US-08-603-024-3  
; Sequence 3, Application US/08603024  
; Patent No. 6015562  
; GENERAL INFORMATION:  
; APPLICANT: Hinman, Lois M.  
; APPLICANT: Menendez, Ana T.  
; APPLICANT: Hanann, Philip R.  
; TITLE OF INVENTION: TARGETED FORMS OF METHYLTRITHIO  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Home Products Corporation  
; STREET: One Campus Drive  
; CITY: Parsippany  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/603,024  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 31,932-03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 973-683-2158  
; TELEFAX: 973-683-4117  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 399 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..399  
US-08-603-024-3

Query Match 63.2%; Score 276.4; DB 3; Length 399;  
Best Local Similarity 80.9%; Pred. No. 9.4e-84;  
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCGGGGGTCATTATGTTCTGGATCTCTGAGTCAGTGGG 95  
Db 1 ATGAGGTGCTAGCTGAGTTCTCTGGGGGCTGTTGCTCTGGATCCCTGGAGCCATTGGG 60  
QY 96 GATATTGTGATACCCAGGATGAACCTCCAAATCTCTGTCACCTCTCGGAGATCAGTTTCC 155  
Db 61 GATATTGTGATGACTCAGGCTGACCCCTCTGTTCTCTGTCACCTCTCGGAGATCATTATCC 120  
QY 156 ATCTCTCGAGGCTTAGTAAGAGTCTCCTGATAAGGATGGGAAGACATACCTTGAATTGG 215  
Db 121 ATTTCTCGAGGCTTAGTAAGAGTCTCCTTCATAGTATGGGACACATTTCTTGTATTGG 180  
QY 216 TTCTCGAGACGAGGACATCTCCTCAGCTCTGATGATTGATGTCACCCCTGCA 275  
Db 181 TTCTCGAGAGGCGGCGGAGCTCTCCTCACTCTGATATCGGATGTCACACCTTGGC 240  
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAAATC 335

Db 241 TCCGGAGTCCAGACAGGTTTCAGTGGCAGTGGGTCCAGGAAGTCTTTCACACTGAGAGTC 300  
QY 336 AGTAGAGTGAAGCTGAGGATGTGGGTGTATTTACTGTCAACACTTGTAGAGTATCCA 395  
Db 301 AGTAGAGTGGAGGCTGAGGATGTGGGTGTATTTACTGTATGCAACATCTAGAATATCCT 360  
QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433  
Db 361 TTCACGTTCCGCTCGGGACCAAGCTGGAGCTGAAACG 398

## RESULT 12

US-08-450-809-2  
; Sequence 2, Application US/08450809  
; Patent No. 6506881  
; GENERAL INFORMATION:  
; APPLICANT: Adair et al.  
; TITLE OF INVENTION: Anti-HMFG Antibodies and  
; TITLE OF INVENTION: Procedures for their Production  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6506881ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,809  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/948,541B  
; FILING DATE: 9/22/92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Joanne Longo Feeney  
; REGISTRATION NUMBER: 35,134  
; REFERENCE/DOCKET NUMBER: CELL-0004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 399  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-450-809-2

Query Match 63.2%; Score 276.4; DB 4; Length 399;  
Best Local Similarity 80.9%; Pred. No. 9.4e-84;  
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCGGGGGTCATTATGTTCTGGATCTCTGAGTCAGTGGG 95  
Db 1 ATGAGGTGCTAGCTGAGTTCTCTGGGGGCTGTTGCTCTGGATCCCTGGAGCCATTGGG 60  
QY 96 GATATTGTGATACCCAGGATGAACCTCCAAATCTCTGTCACCTCTCGGAGATCAGTTTCC 155  
Db 61 GATATTGTGATGACTCAGGCTGACCCCTCTGTTCTGTCACCTCTCGGAGATCATTATCC 120  
QY 156 ATCTCTCGAGGCTTAGTAAGAGTCTCCTGATAAGGATGGGAAGACATACCTTGAATTGG 215  
Db 121 ATTTCTCGAGGCTTAGTAAGAGTCTCCTTCATAGTATGGGACACATTTCTTGTATTGG 180  
QY 216 TTCTCGAGAGACGAGGACATCTCCTCAGCTCTGATGATTGATGTCACCCCTGCA 275

Db 181 TTCCTGCAGAGGCCAGCCAGTCTCCCTCAACTCTGTATATATCGGATGTCCAACTTGGC 240  
Qy 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTCACCTTGGAAATC 335  
Db 241 TCCGAGTCCACAGACAGTTTCAGTGGCAGTGGGTTCAGGAAGTCTTTCACACTGAGATC 300  
Qy 336 AGTAGAGTGAAGGCTGAGGATGGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA 395  
Db 301 AGTAGAGTGGAGGCTGAGGATGGGTGTGTATTTACTGTATGCAACATCTAGAATATCCT 360  
Qy 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAACA 431  
Db 361 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAACA 336

## RESULT 13

US-08-483-749A-3  
; Sequence 3, Application US/08483749A  
; Patent No. 6054561  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
; CITY: EMERYVILLE  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,749A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL B.  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0508.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 336 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..336

## US-08-483-749A-3

Query Match 57.1%; Score 249.6; DB 3; Length 336;  
Best Local Similarity 83.9%; Pred. No. 1.1e-74;  
Matches 282; Conservative 0; Mismatches 54; Indels 0; Gaps 0;  
Qy 96 GATATTGTGATACCCAGGATGACTCTCAATCTGTCTCACTTCGAGNATCAGTTTCC 155  
Db 1 GATATTGTGATACCCAGGATGACTCTCAATCTGTCTCACTTCGAGNATCAGTTTCC 60  
Qy 156 ATCTCTGCAGGCTAGTAGAGTCTCTGTATAGGATGGGAGACATACCTTGAATTGG 215  
Db 61 ATCTCTGCAGGCTAGTAGAGTCTCTGTATAGGATGGGAGACATACCTTGTATTGG 120  
Qy 216 TTTCTGCAGAGACAGGACAAATCTCTCAGCTCTCTGATGTATTTGATGTCCACCCGTGCA 275  
Db 121 TTTCTGCAGAGGCGAGGCGAGTCTCTCAGCTCTCTGATATATCGGATGTCCAACTTGGC 180

Qy 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTCACCTTGGAAATC 335  
Db 181 TCAGGAGTCCACAGACAGTTTCAGTGGCAGTGGGTTCAGGAAGTCTTTCACACTGAGATC 240  
Qy 336 AGTAGAGTGAAGGCTGAGGATGGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA 395  
Db 241 AGTAGAGTGGAGGCTGAGGATGGGTGTGTATTTACTGTATGCAATATCTAGAATATCCT 300  
Qy 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAACA 431  
Db 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAACA 336

## RESULT 14

US-09-406-532-13  
; Sequence 13, Application US/09406532A  
; Patent No. 6365154  
; GENERAL INFORMATION:  
; APPLICANT: Connie L. Erickson-Miller  
; APPLICANT: Stephen D. Holmes  
; APPLICANT: James D. Winkler  
; TITLE OF INVENTION: TIE2 Agonist Antibodies  
; FILE REFERENCE: P50843  
; CURRENT APPLICATION NUMBER: US/09/406,532A  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: 60/102,098  
; PRIOR FILING DATE: 1998-09-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 339  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(339)  
; OTHER INFORMATION: 13H10 light chain v region  
US-09-406-532-13

Query Match 56.8%; Score 248.4; DB 3; Length 339;  
Best Local Similarity 83.4%; Pred. No. 2.9e-74;  
Matches 282; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 96 GATATTGTGATACCCAGGATGACTCTCAATCTGTCTCACTTCGAGNATCAGTTTCC 155  
Db 1 GATATTGTGATGACTCAGGCTGCACCTCTGTACCTGTCTCTCGGAGTGCAGTATCC 60  
Qy 156 ATCTCTGCAGGCTAGTAGAGTCTCTGTATAGGATGGGAGACATACCTTGAATTGG 215  
Db 61 ATCTCTGCAGGCTAGTAGAGTCTCTGTATAGGATGGGAGACATACCTTGTATTGG 120  
Qy 216 TTTCTGCAGAGACAGGACAAATCTCTCAGCTCTCTGATGTATTTGATGTCCACCCGTGCA 275  
Db 121 TTTCTGCAGAGGCGAGGCGAGTCTCTCAGCTCTCTGATATATCGGATGTCCAACTTGGC 180  
Qy 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTCACCTTGGAAATC 335  
Db 181 TCAGGAGTCCACAGACAGTTTCAGTGGCAGTGGGTTCAGGAAGTCTTTCACACTGAGATC 240  
Qy 336 AGTAGAGTGAAGGCTGAGGATGGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA 395  
Db 241 AGTAGAGTGGAGGCTGAGGATGGGTGTGTATTTACTGTATGCAACGCTCTAGAATATCCT 300  
Qy 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAACA 433  
Db 301 TTCACGTTCCGAGGGGGGACCAAGCTGGAAATAAACA 338

## RESULT 15

US-10-000-489-7  
; Sequence 7, Application US/10000489  
; Patent No. 6794363

```

; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Jpatent
; SEQ ID NO 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; NAME/KEY: CDS
; LOCATION: 32..748
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; NAME/KEY: polyA_signal
; LOCATION: 928..933
; NAME/KEY: polyA_site
; LOCATION: 953..968
; US-10-000-489-7

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Query Match	56.5%	Score 247;	DB 4;	Length 968;
Best Local Similarity	75.4%;	Pred. No. 1.5e-73;		
Matches 307; Conservative 0;	Mismatches 100;	Indels 0;	Gaps 0;	
Qy	30	CTCACCATGAGGTTCCTCTGTTTCAGTTCTCGGGGTGCTTATGTCTTGGATCTCTGGAGTC	89	
Db	26	CTCACATGAGGTCCTCTGCTCAGTCTCTGGGGTCTTAATGCTCTGGTCTCTGGATCC	85	
Qy	90	AGTGGGATATTGTGATAACCCAGATGAATCTTCCAATCTGTCACTTCTTGGAGAAATCA	149	
Db	86	AGTGGGATATTGTGATGAATCAGTCTCCAATCTTCTGCCCCTCAGCCCTGGAGAGCG	145	
Qy	150	GTTTCCATCTCTGCAGTCTAGTAAGAGTCTCTGTATAGGATGGGAACACATACTTG	209	
Db	146	GCCTCCATCTCTGCAGTCTAGTCAGAGCTCTCTGCATGTTCAAGGGTCCAATATTTG	205	
Qy	210	AATTGGTTTCTGCAGAGACCAGGACAATCTCCTCAGTCTCTGTATGTATTGTATGTCACC	269	
Db	206	GATTGGTACCACAGAGCCAGGCGAGTCTCCACAACCTCTGATATACTTGGTTCATAAT	265	
Qy	270	CGTGATCAGAGTCTCAGACCGTTTATGGCAGTGGGTGAGGCACGATTTCACCTGT	329	
Db	266	CGGCGCTCCGGGGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGCACAGATTTCAACTG	325	
Qy	330	GAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTATTACTGTCAACAACCTGTAGAC	389	
Db	326	AAATCAGTAGAGTGAGGCTGAGGATGTGGGTATTACTGCATCAGAGCTCAACA	385	
Qy	390	TATCCATTCACTGCTCGCTCGGGGACAAAGTTTGGAAATAAACCTGAC	436	
Db	386	ACTCCATTCACTTTCCGCCCTCGGACAGAGTGGATCAACAGCGAAC	432	

Search completed: April 18, 2005, 21:13:06  
Job time : 85.297 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:59:59 ; Search time 13.8372 Seconds  
(without alignments)  
48.674 Million cell updates/sec

Title: US-09-674-716B-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	74	2	Ig kappa chain V r
2	31	100.0	112	2	Ig kappa chain V r
3	31	100.0	113	1	Ig kappa chain V r
4	31	100.0	120	1	Ig kappa chain pre
5	27	87.1	104	2	conserved hypother
6	27	87.1	234	2	hypothetical prote
7	27	87.1	342	2	flagellar motor sw
8	27	87.1	409	2	probable beta-keto
9	27	87.1	409	2	probable beta-keto
10	27	87.1	760	2	minichromosome mal
11	27	87.1	842	2	hypothetical prote
12	27	87.1	845	1	replication licens
13	27	87.1	1401	2	MAP kinase kinase
14	26	83.9	112	2	hypothetical prote
15	26	83.9	313	2	probable transcrip
16	26	83.9	341	1	NADH2 dehydrogenas
17	26	83.9	810	2	probable pona, pro
18	26	83.9	1453	2	collagen alpha 1(I
19	26	83.9	1464	1	collagen alpha 1(I
20	25	80.6	177	2	hypothetical prote
21	25	80.6	212	2	agglutinin isolect
22	25	80.6	212	2	agglutinin isolect
23	25	80.6	326	2	T26647
24	25	80.6	341	2	WD repeat protein
25	25	80.6	390	2	protein T22H9.4 [i
26	25	80.6	511	2	dopamine receptor
27	25	80.6	532	2	malate synthase (E
28	25	80.6	565	2	probable type II D
29	25	80.6	627	2	conserved hypother

ALIGNMENTS

RESULT 1

G30538  
IG kappa chain V region (253.15E2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 16-Aug-1996  
C;Accession: G30538  
R;Clafin, J.L.; Berry, J.  
J. Immunol. 141, 4012-4019, 1988  
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pne  
A;Reference number: A30534; MUID:89035545; PMID:3141511  
A;Accession: G30538  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr  
A;Molecule type: mRNA  
A;Residues: 1-74 <CUA>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 74;  
Best Local Similarity 100.0%; Pred. No. 0.78; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 24 LMSTRAS 30  
|||||

RESULT 2

KVMS16  
IG kappa chain V region (M167) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 09-Jul-2004  
C;Accession: A01908  
R;Rudikoff, S.; Potter, M.  
Biochemistry 17, 2703-2707, 1978  
A;Title: Kappa-Chain variable region from M167, a phosphorylcholine binding myeloma pro  
A;Reference number: A01908; MUID:79000273; PMID:95160  
A;Accession: A01908  
A;Molecule type: protein  
A;Residues: 1-112 <RUD>  
A;Cross-references: UNIPROT:P01626  
C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-95/Domain: immunoglobulin homology <IMM>  
F;23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61

RESULT 3  
 KWS51  
 Ig kappa chain V region (M511) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 09-Jul-2004  
 C:Accession: A01910  
 R:Appella, E.  
 Mol. Immunol. 17, 711-718, 1980  
 A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine  
 A:Reference number: A01910; MUID:81052016; PMID:6776396  
 A:Accession: A01910  
 A:Molecule type: protein  
 A:Residues: 1-113 <APP>  
 A:Cross-references: UNIPROT:P01628  
 C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-95/Domain: immunoglobulin homology <IMM>  
 F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61

RESULT 4  
 KWS67  
 Ig kappa chain precursor V region (VK167) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
 C:Accession: A01909  
 R:Selsing, E.; Storb, U.  
 Cell 25, 47-58, 1981  
 A:Title: Somatic mutation of immunoglobulin light-chain variable-region genes.  
 A:Reference number: A01909; MUID:82002223; PMID:6791832  
 A:Accession: A01909  
 A:Molecule type: DNA  
 A:Residues: 1-120 <SEL>  
 A:Cross-references: UNIPROT:P01627  
 A>Note: the sequence was determined from the germline gene  
 C:Genetics:  
 A:Introns: 17/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>  
 F:36-115/Domain: immunoglobulin homology <IMM>  
 F:43-113/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 75 LMSTRAS 81

RESULT 5  
 E69832

conserved hypothetical protein yhgB - Bacillus subtilis  
 N:Alternate names: hypothetical protein y (pbpF 5' region)  
 C:Species: Bacillus subtilis  
 C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C:Accession: E69832; C40614  
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 330, 249-256, 1997  
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser  
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrak, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.  
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377  
 A:Accession: E69832  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-104 <KUN>  
 A:Cross-references: UNIPROT:P38048; GB:Z99109; GB:AL009126; NID:G2633260; PIDN:CAB12849.  
 A:Experimental source: strain 168  
 R:Popham, D.L.; Setlow, P.  
 J. Bacteriol. 175, 4870-4876, 1993  
 A:Title: Cloning, nucleotide sequence, and regulation of the Bacillus subtilis pbpF gene  
 A:Reference number: A40614; MUID:93328693; PMID:8335642  
 A:Accession: C40614  
 A:Molecule type: DNA  
 A:Residues: 1-67 <POP>  
 A:Cross-references: GB:L10630  
 C:Genetics:  
 A:Gene: yhgB

Query Match 87.1%; Score 27; DB 2; Length 104;  
 Best Local Similarity 85.7%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 Db 38 LMSTRAS 44

RESULT 6  
 S50468  
 hypothetical protein YER010c - yeast (Saccharomyces cerevisiae)  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: S50468  
 R:Dietrich, F.S.  
 submitted to the EMBL Data Library, December 1994  
 A:Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda  
 A:Reference number: S50433  
 A:Accession: S50468  
 A:Molecule type: DNA  
 A:Residues: 1-234 <DIE>  
 A:Cross-references: UNIPROT:P40011; EMBL:U18778; NID:G603592; PID:G603602; GSPDB:GN00005  
 C:Genetics:  
 A:Gene: MIPS:YER010c  
 A:Cross-references: SGD:S0000812  
 A:Map position: 5R

Query Match 87.1%; Score 27; DB 2; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 6  
 Db 102 LMSTRAS 107





A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-842 <LEI>  
A;Cross-references: UNIPROT:Q19852; EMBL:U42834; NID:g1125756; PID:g1125758; PIDN:AAA839  
C;Genetics:  
A;Gene: CBSP:F28B4.2  
A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2  
F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>  
Query Match 87.1%; Score 27; DB 2; Length 842;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 MSTRAS 7  
DB 650 MSTRAS 655  
RESULT 12  
S34027  
replication licensing factor MCM7 [validated] - yeast (Saccharomyces cerevisiae)  
N;Alternate names: cell division control protein CDC47; protein YBR1441; protein YBR202W  
C;Species: Saccharomyces cerevisiae  
C;Date: 13-Aug-1999 #sequence revision 13-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: S34027; S46074; S34925; S56049  
R;Jacquet, M.  
submitted to the EMBL Data Library, January 1993  
A;Reference number: S34022  
A;Accession: S34027  
A;Molecule type: DNA  
A;Residues: 1-845 <JAC>  
A;Cross-references: UNIPROT:P38132; EMBL:Z21487; NID:g311665; PIDN:CAA79689.1; PID:g3116  
R;Bussereau, F.; Demolis, N.; Jacquet, M.; Mallet, L.  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S46054  
A;Accession: S46074  
A;Molecule type: DNA  
A;Residues: 1-845 <BUS>  
A;Cross-references: EMBL:Z36071; NID:g536576; PIDN:CAA85166.1; PID:g536577; GSPDB:GN0000  
R;Bussereau, F.; Mallet, L.; Gaillon, L.; Jacquet, M.  
Yeast 9, 797-806, 1993  
A;Title: Yeast Sequencing Reports. A 12.8 Kb segment, on the right arm of chromosome II  
A;Reference number: S34925; MUID:93377417; PMID:8368014  
A;Accession: S34925  
A;Molecule type: DNA  
A;Residues: 407-620 <BU2>  
A;Cross-references: EMBL:Z21487  
R;Dalton, S.  
submitted to the EMBL Data Library, September 1994  
A;Description: Cdc47 and Cdc54 belong to a family of proteins essential for initiation o  
A;Reference number: S56049  
A;Accession: S56049  
A;Molecule type: DNA  
A;Residues: 1-551, 'G', 553-555, 'TLN', 559-573, 'Y', 575-845 <DAL>  
A;Cross-references: EMBL:U14730; NID:g608168; PIDN:AAA86309.1; PID:g608169  
C;Comment: The complex of six MCM proteins is one of several proteins that must be bound  
phosphorylated and dissociate from the chromatin.  
C;Genetics:  
A;Gene: SGD:CDG47; MIPS:YBR202w  
A;Cross-references: SGD:S0000406; MIPS:YBR202w  
A;Map position: 2R  
C;Complex: The predominant form is a heterohexamer of MCM2 (PIR:S45757), MCM3 (PIR:A3637  
Component of replication licensing factor.  
C;Function:  
A;Description: MCM7 is a component of the replication licensing factor that permits DNA  
C;Superfamily: replication licensing factor MCM7; MCM homology  
C;Keywords: cell cycle control; DNA replication initiation; heterohexamer; nucleus; phos  
F;227-719/Domain: MCM homology <MCM>  
Query Match 87.1%; Score 27; DB 1; Length 845;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTRAS 7  
DB 300 MSTRAS 305  
RESULT 13  
T39225  
MAP kinase kinase - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 16-Aug-2004  
C;Accession: T39225  
R;Churcher, C.M.; Gentles, S.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, August 1997  
A;Reference number: Z21837  
A;Accession: T39225  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-1401 <CHU>  
A;Cross-references: UNIPROT:O14299; EMBL:Z98763; PIDN:CAB11500.1; GSPDB:GN000066; SPDB:SP  
A;Experimental source: strain 972h-; cosmid c9G1  
C;Genetics:  
A;Gene: SPDB:SPAC9G1.02  
A;Map position: 1  
C;Superfamily: protein kinase homology  
Query Match 87.1%; Score 27; DB 2; Length 1401;  
Best Local Similarity 85.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 LMSTRAS 7  
DB 81 LMSTRAS 87  
RESULT 14  
E95905  
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymB  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: E95905  
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo  
A;Reference number: A95842; MUID:21396508; PMID:11481431  
A;Accession: E95905  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-112 <KUR>  
A;Cross-references: UNIPROT:Q92W36; GB:AL591985; PIDN:CAC48909.1; PID:g15140382; GSPDB:G  
A;Experimental source: strain 1021, megaplasmid pSymB  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.,  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
A;Contents: annotation  
C;Genetics:  
A;Gene: Smb20530  
A;Genome: plasmid  
Query Match 83.9%; Score 26; DB 2; Length 112;  
Best Local Similarity 71.4%; Pred. No. 23;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LMSTRAS 7  
DB 5 LMSTRAS 11  
RESULT 15

D96028

Probable transcription activator of the pca operon, LysR family protein [imported] - Sin  
 C;Species: Sinorhizobium meliloti  
 C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
 C;Accession: D96028  
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo  
 A;Reference number: A95842; MUID:21396508; PMID:11481431  
 A;Accession: D96028  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-313 <KUR>  
 A;Cross-references: UNIPROT:Q92TL9; GB:AL591985; PIDN:CAC49892.1; FID:g15141380; GSPDB:Q  
 A;Experimental source: strain 1021, megaplasmid pSymB  
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
 L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
 A;Reference number: A96039; MUID:21368234; PMID:11474104  
 A;Contents: annotation  
 C;Genetics:  
 A;Gene: pcaQ; SMD20580  
 A;Genome: plasmid

Query Match 83.9%; Score 26; DB 2; Length 313;

Best Local Similarity 85.7%; Pred. No. 64;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 199 LMPTRAS 205

Search completed: April 18, 2005, 14:23:23

Job time : 15.8372 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:57:43 ; Search time 63.6512 Seconds  
(without alignments)  
56.316 Million cell updates/sec

Title: US-09-674-716B-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	112	1 KV2A MOUSE	P01626 mus musculus
2	31	100.0	113	1 KV2C MOUSE	P01628 mus musculus
3	31	100.0	120	1 KV2B MOUSE	P01627 mus musculus
4	28	90.3	177	2 O63ME2	O63me2 burkholderi
5	28	90.3	301	2 O6C0S1	O6c0s1 yarrowia li
6	28	90.3	847	2 Q7UWT5	Q7uwt5 rhodospirill
7	27	87.1	104	1 YHGB BACSU	P38048 bacillus su
8	27	87.1	124	2 O8EEB9	O8eeb9 shewanella
9	27	87.1	226	2 Q7SHG3	Q7shg3 neurospora
10	27	87.1	226	2 Q7MHJ0	Q7mhj0 vibrio vuln
11	27	87.1	234	1 YEK0 YEAST	P40011 saccharomyc
12	27	87.1	235	2 Q6CQK7	Q6cqk7 kluyveromyc
13	27	87.1	238	2 Q75AA2	Q75aa2 ashbya goss
14	27	87.1	255	2 Q6BWC8	O6bwc8 debaryomyc
15	27	87.1	342	2 Q9PII0	Q9pii0 campylobact
16	27	87.1	409	2 Q6KDF2	O6kdf2 escherichia
17	27	87.1	409	2 Q8FJL5	O8fjl5 escherichia
18	27	87.1	409	2 Q8X5U5	Q8x5u5 escherichia
19	27	87.1	454	2 Q6BRP6	Q6brf6 debaryomyc
20	27	87.1	505	2 Q7UQF6	Q7uqf6 rhodospirill
21	27	87.1	541	2 Q868T1	O868t1 anopheles g
22	27	87.1	544	2 Q8BX14	O8bx14 mus musculus
23	27	87.1	558	2 Q63P50	O63p50 burkholderi
24	27	87.1	579	2 Q7YF69	Q7yfe9 cryptospori
25	27	87.1	657	2 Q8BLC8	O8blc8 mus musculus
26	27	87.1	760	1 MCM7 SCHPO	O75001 schizosacch
27	27	87.1	803	2 Q6BWN6	O6bwn6 debaryomyc
28	27	87.1	812	2 Q6FJL2	O6fjl2 candida gla
29	27	87.1	813	2 Q75A77	Q75a77 ashbya goss
30	27	87.1	825	2 Q7QTK8	Q7qtk8 giardia lam
31	27	87.1	826	2 Q6CM41	O6cm41 kluyveromyc

32	27	87.1	845	1	CC47 YEAST	P38132 saccharomyc
33	27	87.1	860	2	Q19852	Q19852 caenorhabdi
34	27	87.1	981	2	Q7NFT8	Q7nft8 gloeobacter
35	27	87.1	1024	2	Q9ESJ5	O9esj5 mus musculu
36	27	87.1	1031	2	Q6DID0	O6did0 mus musculu
37	27	87.1	1049	2	Q9XBP6	Q9xbp6 myxococcus
38	27	87.1	1141	2	Q8LJJ7	O8ljj7 oryza sativ
39	27	87.1	1401	1	WIS4 SCHPO	O14299 schizosacch
40	26	83.9	82	2	Q6H2X9	O6h2x9 sus scrofa
41	26	83.9	112	2	Q92W36	Q92w36 rhizobium m
42	26	83.9	114	2	Q862S4	O862s4 bos taurus
43	26	83.9	174	2	Q6GV12	O6gv12 oryctolagus
44	26	83.9	193	1	RS3A SULTO	O975f8 sulfolobus
45	26	83.9	212	2	Q862R9	Q862r9 bos taurus

ALIGNMENTS

RESULT 1  
KV2A\_MOUSE  
ID KV2A\_MOUSE STANDARD; PRT; 112 AA.  
AC P01626;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-II region MOPC 167.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79000273; PubMed=99160;  
RA Rudikoff S., Potter M.;  
RT "Kappa Chain variable region from M167, a phosphorylcholine binding  
myeloma protein.";  
RL Biochemistry 17:2703-2707(1978).  
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
binds phosphorylcholine. The sequence of the V region of the heavy  
chain has also been determined.  
CC PIR; A01908; KVM516.  
DR HSSP; Q8KOF8; 1KN2.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF000047; ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 39 Complementarity-determining-1.  
FT DOMAIN 40 54 Framework-2.  
FT DOMAIN 55 61 Complementarity-determining-2.  
FT DOMAIN 62 93 Framework-3.  
FT DOMAIN 94 102 Complementarity-determining-3.  
FT DOMAIN 103 112 Framework-4.  
FT DISULFID 23 93 By similarity.  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
|||||  
Db 55 LMSTRAS 61

RESULT 2  
KV2C\_MOUSE STANDARD; PRT; 113 AA.  
ID KV2C\_MOUSE  
AC P01628;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396; DOI=10.1016/0161-5890(80)90140-6;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine.
DR PIR; A01910; KVM51.
DR HSP; Q8K0F8; IKN2.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 123 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 55 LMSTRAS 61

RESULT 3
KV2B MOUSE STANDARD; PRT; 120 AA.
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VKappa167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=G2002223; PubMed=6791832; DOI=10.1016/0092-8674(81)90230-0;
RA Selsing E.; Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region
RT genes.";
RL Cell 25:47-58(1981).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).

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DR EMBL; J00562; AAA39032.1; -.
DR EMBL; X02415; AAA39051.1; -.
DR PIR; A01909; KVM567.
DR HSP; P01751; INOB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 120 Ig kappa chain V-II region VKappa167.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 59 Complementarity-determining-1.
FT DOMAIN 60 74 Framework-2.
FT DOMAIN 75 81 Complementarity-determining-2.
FT DOMAIN 82 113 Framework-3.
FT DOMAIN 114 120 Complementarity-determining-3.
FT DISULFID 43 113 By similarity.
SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 75 LMSTRAS 81

RESULT 4
Q63ME2 PRELIMINARY; PRT; 177 AA.
AC Q63ME2;
DT 25-OCT-2004 (TREMELrel. 28, Created)
DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
DE Putative exported protein.
GN ORFName=BPS0715;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=X96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.P., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagsels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinovitch E., Ruthford K., Sanders M., Simmonds M.,
RA Songvilailai S., Stevens K., Tumapa S., Vesatichavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571966; CAH38175.1; -.
SQ SEQUENCE 177 AA; 18847 MW; 1F6B18829392ADD5 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 177;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 126 LMSTRAS 132

RESULT 5

```

```

O6COS1
ID Q6COS1 PRELIMINARY; PRT; 301 AA.
AC Q6COS1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similarities with gpP40011 Saccharomyces cerevisiae YER010c.
GN ORFNames=YALI0F22209g;
OS Yarrowia lipolytica CLIB99;
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marek C., Neuveglise C., Talia E.,
RA Barnay S., Brangeul L., Aigie M., Anthouard V., Babour A., Barbe V.,
RA Boistrame A., Boyer J., Beckerich J.M., Beyne E., Bleykasten C.,
RA Despons L., Fabre J., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
[2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genoscops;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR382132; CAG78552.1; -
DR InterPro; IPR005493; Methyltransf_6.
DR Pfam; PF03737; Methyltransf_6; 1_-
SQ SEQUENCE 301 AA; 32405 MW; 85580D97B610B3E5 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 301;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 159 LMSTRAN 165

RESULT 6
O7UWTS PRELIMINARY; PRT; 847 AA.
ID Q7UWTS
AC Q7UWTS;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB1802;
OS Rhodospirillum rubrum;
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
OS Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlensner H., Anann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp. strain 1.";

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RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294135; CAD72277.1; -
DR InterPro; IPR011445; DUF1550.
DR Pfam; PF07584; DUF1550; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 847 AA; 89847 MW; 437EF2BCED0B2812 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 847;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 177 LMATRAS 183

RESULT 7
YHGB BACSU STANDARD; PRT; 104 AA.
ID YHGB BACSU
AC P38048;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein yhgb.
GN Names=yhgb; OrderedLocusNames=BSU10090;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98240224; PubMed=9579061;
RA Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,
RA Wedler H., Venema G., Bron S.;
RT "The 172 kb prfA-addAB region from 83 degrees to 97 degrees of the
RT Bacillus subtilis chromosome contains several dysfunctional genes, the
RT glyB marker, many genes encoding transporter proteins, and the
RT ubiquitous hit gene.";
RL Microbiology 144:859-875(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Tognoni K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Takenaru K., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vasearotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzengger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus

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RT subtitlis";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-67 FROM N.A.
RC STRAIN=168;
RX MEDLINE=93328693; PubMed=8335642;
RA Fopham D.L., Setlow P.;
RT "Cloning, nucleotide sequence, and regulation of the Bacillus subtilis
RT pbpf gene, which codes for a putative class A high-molecular-weight
RT penicillin-binding protein.";
RL J. Bacteriol. 175:4870-4876(1993).
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DR EMBL; Y14083; CAA74515.1; -
DR EMBL; Z99109; CAB12849.1; -
DR EMBL; L10630; AAA71940.2; -
DR PIR; E69832; E69832.
DR Subtilisin; BG10426; yhgB.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 104 AA; 11998 MW; 6B44CD77B52FDD968 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 104;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 38 LMSTRCS 44

RESULT 8
ID Q8EEB9 PRELIMINARY; PRT; 124 AA.
AC Q8EEB9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adhesion-related protein.
GN OrderedLocusNames=SO2467;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Teapin A., Scott J., Beanan M.J.,
RA Brinkac L.N., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Unayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealsen K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015688; AAN55499.1; -
DR TIGR; SO2467; -
KW Complete proteome.
SQ SEQUENCE 124 AA; 13061 MW; D77E2F6F42DEF735 CRC64;

Query Match 87.1%; Score 27; DB 2; Length 124;
Best Local Similarity 85.7%; Pred. No. 58;

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Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 83 LMGTRAS 89

RESULT 9
ID Q7SHG3 PRELIMINARY; PRT; 226 AA.
AC Q7SHG3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU02941.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Renman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnere S.,
RA Kamal M., Kanysseilis M., Maucelli E., Bielke C., Rudd S., Frisman D.,
RA Kratsofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Piamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mammhaupt G., Eboile D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000003; EAA36387.1; -
DR InterPro; IPR005493; Methyltransf_6.
DR Pfam; PF03737; Methyltransf_6; 1.
KW Hypothetical protein.
SQ SEQUENCE 226 AA; 24727 MW; 76485DFDC959D50D CRC64;

Query Match 87.1%; Score 27; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRA 6
Db 100 LMSTRA 105

RESULT 10
ID Q7MHJ0 PRELIMINARY; PRT; 226 AA.
AC Q7MHJ0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Xanthosine triphosphate pyrophosphatase.
GN OrderedLocusNames=VW2879;
OS Vibrio vulnificus (strain VJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=14656965; DOI=10.1101/gr.1295503;
RX

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RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,  
 Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,  
 Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;  
 "Comparative genome analysis of *Vibrio vulnificus*, a marine  
 pathogen.";  
 RL Genome Res. 13:2577-2587(2003).  
 CC -I- SIMILARITY: Belongs to the HAM1 NTPase family.  
 DR EMBL; AP005341; BAC95643.1; -;  
 DR HSSP; P52061; IK7K.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR InterPro; IPR002637; Hamip\_like.  
 DR Pfam; PF01725; Hamip\_like; 1.  
 DR TIGRfams; TIGR00042; Hamip\_like; 1.  
 KW Complete proteome; Hydrolase.  
 SQ SEQUENCE 226 AA; 24762 MW; 65E34589230DBCEA CRC64;  
 Query Match 87.1%; Score 27; DB 2; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 MSTRAS 7  
 DB 1 MSTRAS 6  
 RESULT 11  
 YEKO YEAST STANDARD; PRT; 234 AA.  
 ID YEKO YEAST STANDARD; PRT; 234 AA.  
 AC P40011;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Hypochemical 25.6 kDa protein in NTP2-SRP1 intergenic region.  
 GN OrderedLocustNames=YER010C;  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RX MEDLINE-97313264; PubMed-9169868;  
 RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,  
 Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,  
 Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,  
 Hunnicke-Smith S., Hymen R.W., Kayser A., Komp C., Lashkari D., Lew H.,  
 Lin D., Mossdale D., Nakahara K., Namath A., Norgren R., Oefner P.,  
 Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,  
 Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;  
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome V.";  
 RL Nature 387:78-81(1997).  
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 DR EMBL; U18776; AAB64543.1; -;  
 DR FIR; S50468; S50468.  
 DR GERMOnline; 139090; -;  
 DR SGD; S00000812; YER010C.  
 DR InterPro; IPR005493; Methyltransf\_6.  
 DR Pfam; PF03737; Methyltransf\_6; 1.  
 KW Hypochemical protein.  
 SQ SEQUENCE 234 AA; 25563 MW; EC109F224240F980 CRC64;  
 Query Match 87.1%; Score 27; DB 1; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6  
 DB 102 LMSTRA 107  
 RESULT 12  
 Q6COX7 PRELIMINARY; PRT; 235 AA.  
 ID Q6COX7;  
 AC Q6COX7;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Similar to sp|P40011 Saccharomyces cerevisiae YER010c singleton.  
 GN ORFNames=KLLA0D134429;  
 OS Kluyveromyces lactis NRRL Y-1140.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=284590;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL Y-1140;  
 RG Genolevures;  
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,  
 Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
 Boissrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,  
 Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
 Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 Zeniun-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
 Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
 Wincker P., Souciet J.L.;  
 RT "Genome evolution in yeasts.";  
 RL Nature 430:35-44(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL Y-1140;  
 RA Genoscope;  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR382124; CAH00758.1; -;  
 DR InterPro; IPR005493; Methyltransf\_6.  
 DR Pfam; PF03737; Methyltransf\_6; 1.  
 SQ SEQUENCE 235 AA; 25766 MW; A2ED50D9CC4F7057 CRC64;  
 Query Match 87.1%; Score 27; DB 2; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LMSTRA 6  
 DB 103 LMSTRA 108  
 RESULT 13  
 Q75AA2 PRELIMINARY; PRT; 238 AA.  
 ID Q75AA2;  
 AC Q75AA2;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ADRO16Cp.  
 GN ORFNames=ADRO16C;  
 OS *Ashbya gossypii* (Yeast) (Eremothecium gossypii).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.  
 OX NCBI\_TaxID=33169;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 10895;

RA Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,  
 RA Philippsen P.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE016817; RA051936.1; -;  
 DR AGD; AD01616; -;  
 DR InterPro; IPR005493; Methyltransf.6.  
 DR Pfam; PF03737; Methyltransf.6; 1\_  
 SQ SEQUENCE 238 AA; 25785 MW; 2981918CF8A8761C CRC64;

Query Match 87.1%; Score 27; DB 2; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6  
 |||||  
 Db 102 LMSTRA 107

## RESULT 14

Q6BWC8 PRELIMINARY; PRT; 255 AA.  
 AC Q6BWC8;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Similar to CA2357|IPF8957 Candida albicans IPF8957 unknown  
 DE function.  
 GN ORFNames=DEHA0B12584g;  
 OS Debaryomyces hansenii CBS767.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.  
 OX NCBI\_TaxID=284592;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CBS767;  
 RG Genolevures;

RA Dujon B., Sherman D., Fischer G., Durkens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
 RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,  
 RA Wincker P., Souciet J.L.;  
 RT "Genome evolution in yeasts";  
 RL Nature 430:35-44(2004).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CBS767;  
 RA Genoscope;  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR382134; CAG85495.1; -;  
 DR InterPro; IPR005493; Methyltransf.6.  
 DR Pfam; PF03737; Methyltransf.6; 1\_  
 SQ SEQUENCE 255 AA; 27450 MW; C8FF0F6527033F1C CRC64;

Query Match 87.1%; Score 27; DB 2; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6  
 |||||  
 Db 117 LMSTRA 122

## RESULT 15

Q9PII0

ID Q9PII0 PRELIMINARY; PRT; 342 AA.  
 AC Q9PII0;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Flagellar motor switch protein.  
 GN Name=flig; OrderedLocName=Cj0319;  
 OS Campylobacter jejuni.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=197;  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=NCTC 11168;  
 RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;  
 RA Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,  
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,  
 RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,  
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,  
 RA Whitehead S., Barrell B.G.;  
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni  
 RT reveals hypervariable sequences";  
 RL Nature 403:665-668(2000).  
 DR EMBL; AL139074; CAB72786.1; -;  
 DR PIR; C81451; C81451.  
 DR HSP; Q9WY63; 1QC7.  
 DR GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.  
 DR GO; GO:0003774; F:motor activity; IEA.  
 DR GO; GO:0006935; P:chemotaxis; IEA.  
 DR GO; GO:0001539; P:ciliary or flagellar motility; IEA.  
 DR InterPro; IPR000090; Flg\_Motor\_Flig.  
 DR InterPro; IPR011002; Flig\_like.  
 DR Pfam; PF01706; Flig\_C; 1.  
 DR PRINTS; PR00954; FLGMOTORFLIG.  
 DR TIGRFAMS; TIGR00207; flig; 1.  
 KW Complete proteome; Flagellum.  
 SQ SEQUENCE 342 AA; 38429 MW; ED4D214417C1524C CRC64;

Query Match 87.1%; Score 27; DB 2; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTRAS 7  
 |||||  
 Db 289 MSTRAS 294

Search completed: April 19, 2005, 14:21:52  
 Job time : 66.6512 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:32:07 ; Search time 73.7442 Seconds  
(without alignments)  
36.712 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1980s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	2 AAW39825	Aw39825 Light cha
2	31	100.0	7	2 AAW39822	Aw39822 Light cha
3	31	100.0	7	2 AAW39819	Aw39819 Light cha
4	31	100.0	7	3 AAY32255	Aay32255 Light cha
5	31	100.0	100	4 AAE06969	Aae06969 Mouse ger
6	31	100.0	100	8 ADQ89254	Adq89254 Mouse imm
7	31	100.0	113	2 AAW39803	Aw39803 Variable
8	31	100.0	113	2 AAW39886	Aw39886 Light cha
9	31	100.0	113	2 AAW39802	Aw39802 Variable
10	31	100.0	113	2 AAW39882	Aw39882 Light cha
11	31	100.0	113	2 AAW39804	Aw39804 Variable
12	31	100.0	116	3 AAY32262	Aay32262 Humanised
13	31	100.0	145	3 AAY32261	Aay32261 Mouse ant
14	31	100.0	248	7 ADG32323	Adg32323 Mouse scf
15	31	100.0	317	7 ADG32360	Adg32360 Precursor
16	28	90.3	7	2 AAW39816	Aw39816 Light cha
17	28	90.3	113	2 AAW39801	Aw39801 Variable
18	28	90.3	274	2 AAW39899	Aw39899 Single ch
19	28	90.3	407	8 ADN17638	Adn17638 Bacterial
20	28	90.3	979	7 ADB64292	Adb64292 Human pro
21	27	87.1	7	2 AAW39876	Aw39876 Light cha
22	27	87.1	68	4 AAU64213	Aau64213 Propionib
23	27	87.1	68	6 ABM60732	Abm60732 Propionib
24	27	87.1	119	4 ABU00425	Abu00425 Human nov
25	27	87.1	123	4 AAU54742	Aau54742 Propionib

26	27	87.1	123	6	ABM51261	Abm51261 Propionib
27	27	87.1	131	2	AAR12232	Aar12232 Mouse Mab
28	27	87.1	132	2	AAR12354	Aar12354 Light (ka
29	27	87.1	140	4	AAM95756	Aam95756 Human rep
30	27	87.1	218	5	ABG77402	Abg77402 Selected
31	27	87.1	218	5	ABJ11304	Abj11304 Yeast sel
32	27	87.1	342	6	ABU26357	Abu26357 Protein e
33	27	87.1	409	4	ABBS2717	Abbs2717 Escherich
34	27	87.1	760	8	ADS44134	Ads44134 Bacterial
35	27	87.1	809	5	ABP73372	Abp73372 Candida a
36	27	87.1	845	6	ABR53640	Abr53640 Protein s
37	27	87.1	845	7	ADK64136	Adk64136 Disease t
38	27	87.1	845	8	ADN18834	Adn18834 Bacterial
39	27	87.1	1401	8	ADN19524	Adn19524 Bacterial
40	26	83.9	77	4	AAU39838	Aau39838 Propionib
41	26	83.9	77	6	ABM36357	Abm36357 Propionib
42	26	83.9	115	4	AAU14133	Aau14133 Peptide #
43	26	83.9	115	4	ABB33078	Abb33078 Peptide #
44	26	83.9	115	4	AAM26539	Aam26539 Peptide #
45	26	83.9	115	4	ABB27906	Abb27906 Human pep

#### ALIGNMENTS

##### RESULT 1

AAW39825

ID AAW39825 standard; peptide; 7 AA.

XX AC AAW39825;

XX AC AAW39825;

DT 16-JUN-1998 (first entry)

XX DE Light chain CDR2 of catalytic antibody 12H1.

XX DE Variable domain; lambda light chain; catalytic antibody; degradation;

KW cocaine; cocaine transition state analogue; TSA; benzoic acid;

KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

KW overdose; addiction.

XX OS Mus sp.

XX PN W09749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX PT New catalytic antibodies able to decompose cocaine, single-chain  
PT analogues - used to treat cocaine overdose and addiction, required in far  
PT smaller doses than antibodies that antagonise cocaine by simply binding.  
XX PS Claim 17; Page 83; 147pp; English.

CC AAW39824-26 represent the sequences of the light chain complementarity  
CC determining regions (CDRs) of the catalytic antibody 12H1, which is able  
CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
CC were prepared and used to immunise mice for production of hybridomas.  
CC Catalytic antibodies were identified by their capacity to release 3H-  
CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified  
CC using TSA2, and has a per minute kcat of 0.16. The antibodies reduce the  
CC concentration of cocaine in a subject, and are used particularly for the  
CC treatment of an overdose. They are also used for treating addiction (by  
CC reducing the in vivo concentration that can be achieved)

```

SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
Db       1 LMSTRAS 7

RESULT 2
AAW39822
ID      AAW39822 standard; peptide; 7 AA.
XX
AC      AAW39822;
XX
DT      16-JUN-1998 (first entry)
XX
DE      Light chain CDR2 of catalytic antibody 2A10.
XX
KW      Variable domain; lambda light chain; catalytic antibody; degradation;
KW      cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW      phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW      overdose; addiction.
XX
OS      Mus sp.
XX
PN      WO9749800-A1.
XX
PD      31-DEC-1997.
XX
PF      25-JUN-1997; 97WO-US010965.
XX
PR      25-JUN-1996; 96US-00672345.
XX
PA      (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI      Landry DW;
XX
DR      WPI; 1998-077166/07.
XX
PT      New catalytic antibodies able to decompose cocaine, single-chain
PT      analogues - used to treat cocaine overdose and addiction, required in far
PT      smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS      Claim 15; Page 82; 147pp; English.
XX
CC      AAW39821-23 represent the sequences of the light chain complementarity
CC      determining regions (CDRs) of the catalytic antibody 2A10, which is able
CC      to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC      were prepared and used to immunise mice for production of hybridomas.
CC      Catalytic antibodies were identified by their capacity to release 3H-
CC      benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
CC      using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC      transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
CC      The antibodies reduce the concentration of cocaine in a subject, and are
CC      used particularly for the treatment of an overdose. They are also used
CC      for treating addiction (by reducing the in vivo concentration that can be
CC      achieved)
XX
SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
Db       1 LMSTRAS 7

RESULT 3
AAW39819
ID      AAW39819 standard; peptide; 7 AA.
XX
AC      AAW39819;
XX
DT      16-JUN-1998 (first entry)
XX
DE      Light chain CDR2 of catalytic antibody 6A12.
XX
KW      Variable domain; lambda light chain; catalytic antibody; degradation;
KW      cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW      phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW      overdose; addiction.
XX
OS      Mus sp.
XX
PN      WO9749800-A1.
XX
PD      31-DEC-1997.
XX
PF      25-JUN-1997; 97WO-US010965.
XX
PR      25-JUN-1996; 96US-00672345.
XX
PA      (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI      Landry DW;
XX
DR      WPI; 1998-077166/07.
XX
PT      New catalytic antibodies able to decompose cocaine, single-chain
PT      analogues - used to treat cocaine overdose and addiction, required in far
PT      smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS      Claim 13; Page 81; 147pp; English.
XX
CC      AAW39818-20 represent the sequences of the light chain complementarity
CC      determining regions (CDRs) of the catalytic antibody 6A12, which is able
CC      to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC      were prepared and used to immunise mice for production of hybridomas.
CC      Catalytic antibodies were identified by their capacity to release 3H-
CC      benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified
CC      using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC      transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072.
CC      The antibodies reduce the concentration of cocaine in a subject, and are
CC      used particularly for the treatment of an overdose. They are also used
CC      for treating addiction (by reducing the in vivo concentration that can be
CC      achieved)
XX
SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
Db       1 LMSTRAS 7

RESULT 4
AAW32255
ID      AAW32255 standard; peptide; 7 AA.
XX
AC      AAW32255;
XX
DT      15-FEB-2000 (first entry)
XX
DE      Light chain CDR L2 of mouse anti-CD23 MAb C11.
XX
KW      CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
KW      monoclonal antibody; chimeric antibody; humanised antibody;
KW      complementarity determining region; CDR; autoimmune disease;

```

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.

OS Mus musculus.  
 XX  
 XX WO9958679-A1.  
 XX  
 XX PD 18-NOV-1999.  
 XX  
 XX PF 07-MAY-1999; 99WO-GB001434.  
 XX  
 XX PR 09-MAY-1998; 98GB-00009839.  
 XX  
 XX PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 XX PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 XX WPI: 2000-053101/04.  
 DR N-PSDB; AAZ34749.  
 DR  
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 XX  
 XX Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 2 (CDR L2)  
 CC of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11  
 CC (see also AAY32262). The invention provides altered antibodies, such as  
 CC chimeric or humanised antibodies, which comprise sufficient of the amino  
 CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to  
 CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis.  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents

XX Sequence 7 AA;  
 SQ  
 Query Match 100.0%; Score 31; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 |||||  
 Db 1 LMSTRAS 7

RESULT 5  
 AAE06969  
 ID AAE06969 standard; protein; 100 AA.  
 XX  
 XX AAE06969;  
 AC  
 XX 16-OCT-2001 (first entry)  
 DT  
 XX Mouse germline kappa light chain variable (VK) region, 167/24.

DE Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 XX neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;

KW multiple sclerosis; atherosclerosis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; VK; kappa light chain variable region.

XX Mus sp.  
 XX WO200157226-A1.  
 XX  
 XX PD 09-AUG-2001.  
 XX  
 XX PF 02-FEB-2001; 2001WO-US003537.  
 XX  
 XX PR 03-FEB-2000; 2000US-00497625.  
 XX  
 XX PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
 XX WPI: 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
 PT disorder in a patient, comprises a binding specificity for CCR2, and a  
 PT non-human antigen binding region and human immunoglobulin.  
 XX  
 XX Disclosure; Page 151; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding  
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
 CC comprising an antigen binding region of non-human origin and at least a  
 CC portion of an immunoglobulin of human origin. The humanised antibodies  
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They  
 CC are useful for inhibiting or treating HIV infection. The proteins of the  
 CC invention are useful for inhibiting leukocyte trafficking, for treating  
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune  
 CC disorders such as rheumatoid arthritis and multiple sclerosis,  
 CC atherosclerosis and atherosclerosis, and for inhibiting restenosis. They  
 CC are useful in therapy or diagnosis, and in the manufacture of a  
 CC medicament for treating CCR-2 mediated disease. They are also useful for  
 CC treating allergy, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and IgE-mediated allergic reaction, shock,  
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
 CC associated with vascular intervention, including angioplasty and/or stent  
 CC placement in a mammal. Humanised antibodies are also useful for  
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated  
 CC with vascular intervention. The present sequence is mouse germline kappa  
 CC light chain variable (VK) region, 167/24

XX Sequence 100 AA;  
 SQ  
 Query Match 100.0%; Score 31; DB 4; Length 100;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 |||||  
 Db 55 LMSTRAS 61

RESULT 6  
 ADQ89254  
 ID ADQ89254 standard; protein; 100 AA.  
 XX  
 XX ADQ89254;  
 AC  
 XX 21-OCT-2004 (first entry)  
 DT  
 XX Mouse immunoglobulin protein #14.  
 DE  
 XX Mouse; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;

KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;  
 KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
 KW anti-HIV; virucide; antiarteriosclerotic.  
 XX Mus musculus.  
 OS US2004151721-A1.  
 XX  
 PN 05-AUG-2004.  
 XX  
 PD 10-DEC-2003; 2003US-00733563.  
 XX  
 PF 19-OCT-2001; 2001US-0350166P.  
 XX  
 PR 26-JUN-2002; 2002US-0392364P.  
 PR  
 PR 17-OCT-2002; 2002US-00272899.  
 XX  
 XX (OKEE/) O'KEEFE T.  
 PA (PONA/) PONATH P.  
 PA  
 XX O'keefe T, Ponath P;  
 PI  
 XX WPI; 2004-580175/56.  
 DR  
 XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
 PT useful for diagnosing and/or treating inflammatory or autoimmune  
 PT diseases, and HIV infection.  
 XX  
 XX Example 2; SEQ ID NO 32; 128pp; English.  
 PS  
 XX The invention relates to humanised immunoglobulin heavy and light chains  
 CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
 CC immunoglobulin or its antigen binding fragment comprising the chains. The  
 CC humanised immunoglobulin or its antigen binding fragment preferably  
 CC comprises two heavy chains and two light chains. The humanised  
 CC immunoglobulin and its heavy and light chains are useful for the  
 CC diagnosis, prevention and/or treatment of diseases or conditions  
 CC associated with aberrant expression or activity of the CCR2 polypeptide,  
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
 CC infection and atherosclerosis. This sequence represents a mouse  
 CC immunoglobulin protein of the invention.  
 XX  
 XX  
 SQ Sequence 100 AA;  
 Query Match 100.0%; Score 31; DB 8; Length 100;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61  
 RESULT 7  
 AAW39803  
 ID AAW39803 standard; protein; 113 AA.  
 XX  
 AC AAW39803;  
 XX  
 DT 16-JUN-1998 (first entry)  
 DE  
 DE Variable domain of the Kappa light chain of catalytic antibody 12H1.  
 XX  
 XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9749800-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 DE New catalytic antibodies able to decompose cocaine, single-chain

PF 25-JUN-1997; 97WO-US010965.  
 XX  
 PR 25-JUN-1996; 96US-00672345.  
 XX  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 XX Landry DW;  
 PI  
 XX WPI; 1998-077166/07.  
 DR P-PSDB; AAV09802.  
 DR  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 XX Claim 18; Page 73; 147pp; English.  
 PS  
 XX AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the Kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808  
 CC represents the heavy chain) was identified using TSA2, and has a per  
 CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine  
 CC in a subject, and are used particularly for the treatment of an overdose.  
 CC They are also used for treating addiction (by reducing the in vivo  
 CC concentration that can be achieved)  
 XX  
 XX Sequence 113 AA;  
 SQ  
 Query Match 100.0%; Score 31; DB 2; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 Db 55 LMSTRAS 61  
 RESULT 8  
 AAW39886  
 ID AAW39886 standard; protein; 113 AA.  
 XX  
 AC AAW39886;  
 XX  
 DT 18-JUN-1998 (first entry)  
 DE  
 DE Light chain of the catalytic antibody 6A12.  
 XX  
 XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9749800-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 DE 25-JUN-1997; 97WO-US010965.  
 XX  
 XX 25-JUN-1996; 96US-00672345.  
 PR  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX Landry DW;  
 PI  
 XX WPI; 1998-077166/07.  
 DR N-PSDB; AAV09793.  
 DR  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT

PT analogues - used to treat cocaine overdose and addiction, required in far  
 XX smaller doses than antibodies that antagonise cocaine by simply binding.  
 PS Disclosure; Fig 19; 147pp; English.

CC The present sequence represents the light chain of a catalytic antibody  
 CC which is capable of degrading cocaine. A series of cocaine transition  
 CC state analogues (TSAs) were prepared and used to immunise mice for  
 CC production of hybridomas. Catalytic antibodies were identified by their  
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
 CC antibodies reduce the concentration of cocaine in a subject, and are used  
 CC particularly for the treatment of an overdose. They are also used for  
 CC treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX SQ Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
 Db 55 LMSTRAS 61

RESULT 9  
 AAW39802  
 ID AAW39802 standard; protein; 113 AA.

XX AC AAW39802;

XX DT 16-JUN-1998 (first entry)

XX DE Variable domain of the Kappa light chain of catalytic antibody 6A12.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 XX smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Claim 14; Page 72; 147pp; English.

XX SS AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 6A12 antibody (AAW39807  
 CC represents the heavy chain) was identified using TSA1, which is an  
 CC immunogenic conjugate of a phosphate monoester transition state analogue.  
 CC Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the

CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)  
 XX SQ Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
 Db 55 LMSTRAS 61

RESULT 10

AAW39882

ID AAW39882 standard; protein; 113 AA.

XX AC AAW39882;

XX DT 16-JUN-1998 (first entry)

XX DE Light chain of the catalytic antibody 2A10.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX N-PSDB; AAV09789.

XX PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 XX smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Disclosure; Fig 21; 147pp; English.

XX SS The present sequence represents the light chain of a catalytic antibody  
 CC which is capable of degrading cocaine. A series of cocaine transition  
 CC state analogues (TSAs) were prepared and used to immunise mice for  
 CC production of hybridomas. Catalytic antibodies were identified by their  
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
 CC antibodies reduce the concentration of cocaine in a subject, and are used  
 CC particularly for the treatment of an overdose. They are also used for  
 CC treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX SQ Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
 Db 55 LMSTRAS 61





Qy 1 LMSTRAS 7  
 Db 55 LMSTRAS 61

RESULT 13  
 ID AAY32261 standard; protein; 145 AA.  
 XX AC AAY32261;  
 XX DT 15-FEB-2000 (first entry)  
 XX DE Mouse anti-CD23 Mab C11 light chain variable region.  
 XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.  
 XX OS Mus musculus.

Key Location/Qualifiers  
 Region 55..70  
 FT /note= "CDR L1"  
 Region 83..92  
 FT /note= "CDR L2"  
 Region 125..134  
 FT /note= "CDR L3"

XX W09958679-A1.  
 XX 18-NOV-1999.  
 XX 07-MAY-1999; 99WO-GB001434.  
 XX 09-MAY-1998; 98GB-00009839.  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 WPI; 2000-053101/04.  
 DR N-PSDB; AAZ34746.

Cell receptor specific antibodies useful for treating e.g. arthritis,  
 diabetes, multiple sclerosis and psoriasis.  
 Claim 8; Fig 2; 8lpp; English.

This sequence represents the light chain variable region (VL) of murine  
 anti-CD23 (FCERII) monoclonal antibody C11. The invention provides  
 altered antibodies, such as chimeric or humanised antibodies (see  
 AAY32262 and AAY32263), which comprise sufficient of the amino acid  
 sequences of the C11 light and heavy chain complementarity determining  
 regions (see AAY32254-59) to render them capable of binding to the CD23  
 type II molecule expressed on haematopoietic cells. The antibodies are  
 used to block soluble CD23 formation in human therapy, for the treatment  
 of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 bronchitis) or diabetes (particularly type I diabetes), and B-cell  
 malignancies (claimed). They are also useful for studying interactions

CC between CD23 and various ligands and determining the binding agents  
 XX  
 SQ Sequence 145 AA;

Query Match 100.0%; Score 31; DB 3; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
 Db 86 LMSTRAS 92

## RESULT 14

ADG32323  
 ID ADG32323 standard; protein; 248 AA.

XX AC ADG32323;  
 XX DT 26-FEB-2004 (first entry)

XX DE Mouse scFV VDM1 antibody targeted against V\_dahliae SeqID 32.  
 XX mouse; murine; scFV; anti-fungal peptide; APP; scFV; disease resistant;  
 KW transgenic; plant; fungal infection; antibody;  
 KW pathogen-specific antibody; fungicidal; agriculture.

XX OS Mus sp.

PN W02003089475-A2.  
 XX 30-OCT-2003.

XX 14-APR-2003; 2003WO-BP003852.

XX 22-APR-2002; 2002EP-00008929.

XX 28-MAY-2002; 2002EP-00011807.

XX (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;  
 WPI; 2003-854088/79.

DR N-PSDB; ADG32298.

XX New fusion protein comprising an anti-fungal protein or peptide and an  
 antibody fragment, useful in agriculture and horticulture for producing  
 Ascomyceta-resistant transgenic plants, plant cells or plant tissues.  
 Example 13; SEQ ID NO 32; 47pp; English.

This invention relates to a novel fusion protein comprising an anti-  
 fungal protein or peptide (APP) and an antibody fragment (scFV).  
 Specifically, it refers to APPs recognizing an epitope of an Ascomyceta  
 and a cellular targeting sequence, which can be used to generate disease  
 resistant transgenic plants that are protected against fungal infection.  
 Accordingly, a method is described for antibody based resistance in  
 plants such that the undesirable and expensive chemical controls often  
 used in agriculture are not required. The present invention provides  
 antibodies, recombinant antibodies and fragments thereof, as well as  
 fusion proteins that can be used as pathogen-specific antibodies targeted  
 to different plant cell compartments. As such, these fungicidal agents  
 confer a broad spectrum of disease resistance in both economically  
 important crops and ornamental plants. This polypeptide is an antibody  
 used in an exemplification of the invention.

XX SQ Sequence 248 AA;

Query Match 100.0%; Score 31; DB 7; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7

Job time : 76.7442 secs

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Db      189 LMSTRAS 195
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RESULT 15
ADG32360
ID ADG32360 standard; protein; 317 AA.
XX
AC ADG32360;
XX
DT 26-FEB-2004 (first entry)
XX
DE Precursor fusion protein of AFP AG-scfv VDM1 SeqID 69.
XX
KW scfV; anti-fungal peptide; AFP; scfV; disease resistant; transgenic;
XX plant; fungal infection; antibody; pathogen-specific antibody;
XX fungicidal; agriculture; mouse; chimeric; murine.
XX
OS Chimeric.
OS Synthetic.
OS Apeargillus giganteus.
OS Mus musculus.
XX
PN WO2003089475-A2.
XX
PD 30-OCT-2003.
XX
PF 14-APR-2003; 2003WO-EP003852.
XX
PR 22-APR-2002; 2002EP-0008929.
XX
PR 28-MAY-2002; 2002EP-00011807.
XX
PA (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;
XX
DR WPI; 2003-854088/79.
XX
DR N-PSDB; ADG32349.
XX
XX New fusion protein comprising an anti-fungal protein or peptide and an
FT antibody fragment, useful in agriculture and horticulture for producing
FT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.
XX
PS Disclosure; SEQ ID NO 69; 47pp; English.
XX
CC This invention relates to a novel fusion protein comprising an anti-
CC fungal protein or peptide (AFP) and an antibody fragment (scfV).
CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta
CC and a cellular targeting sequence, which can be used to generate disease
CC resistant transgenic plants that are protected against fungal infection.
CC Accordingly, a method is described for antibody based resistance in
CC plants such that the undesirable and expensive chemical controls often
CC used in agriculture are not required. The present invention provides
CC antibodies, recombinant antibodies and fragments thereof, as well as
CC fusion proteins that can be used as pathogen-specific antibodies targeted
CC to different plant cell compartments. As such, these fungicidal agents
CC confer a broad spectrum of disease resistance in both economically
CC important crops and ornamental plants. This polypeptide is a precursor
CC fusion protein of the order [AFP - linker - antibody fragment] of the
CC invention.
XX
SQ Sequence 317 AA;
Query Match 100.0%; Score 31; DB 7; Length 317;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMSTRAS 7
|||||
Db 258 LMSTRAS 264

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Search completed: April 18, 2005, 14:15:14

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:22:17 ; Search time 52.907 Seconds  
(without alignments)  
43.975 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	10	US-09-940-727B-23
2	31	100.0	7	10	US-09-940-727B-26
3	31	100.0	7	10	US-09-940-727B-29
4	31	100.0	100	9	US-09-840-459-32
5	31	100.0	100	16	US-10-766-773-32
6	31	100.0	100	16	US-10-766-610-32
7	31	100.0	100	16	US-10-733-563-32
8	31	100.0	113	10	US-09-940-727B-6
9	31	100.0	113	10	US-09-940-727B-7
10	31	100.0	113	10	US-09-940-727B-8
11	31	100.0	113	10	US-09-940-727B-104
12	31	100.0	113	10	US-09-940-727B-108
13	31	100.0	113	10	US-09-940-727B-112

14	29	93.5	63	15	US-10-424-599-191879	Sequence 191879,
15	28	90.3	7	10	US-09-940-727B-20	Sequence 20, Appl
16	28	90.3	113	10	US-09-940-727B-5	Sequence 5, Appl
17	28	90.3	113	10	US-09-940-727B-100	Sequence 100, App
18	28	90.3	276	15	US-10-425-114-49630	Sequence 49630, A
19	28	90.3	280	10	US-09-940-727B-119	Sequence 119, App
20	28	90.3	407	15	US-10-369-493-291	Sequence 291, App
21	28	90.3	979	15	US-10-104-047-2446	Sequence 2446, Ap
22	27	87.1	7	10	US-09-940-727B-80	Sequence 80, Appl
23	27	87.1	102	15	US-10-424-599-198627	Sequence 198627,
24	27	87.1	140	10	US-09-764-891-4114	Sequence 4114, Ap
25	27	87.1	342	15	US-10-282-122A-54281	Sequence 54281, A
26	27	87.1	409	14	US-10-238-075-835	Sequence 835, App
27	27	87.1	760	15	US-10-369-493-22564	Sequence 22564, A
28	27	87.1	809	14	US-10-032-585-7209	Sequence 7209, Ap
29	27	87.1	845	15	US-10-369-493-1487	Sequence 1487, Ap
30	27	87.1	1141	16	US-10-437-963-106873	Sequence 106873,
31	27	87.1	1401	15	US-10-369-493-2177	Sequence 2177, Ap
32	26	83.9	115	9	US-09-864-761-33844	Sequence 33844, A
33	26	83.9	133	15	US-10-104-047-2464	Sequence 2464, Ap
34	26	83.9	220	15	US-10-139-794-201	Sequence 201, App
35	26	83.9	246	15	US-10-366-125-13	Sequence 13, Appl
36	26	83.9	258	15	US-10-139-794-81	Sequence 81, Appl
37	26	83.9	347	16	US-10-437-963-151641	Sequence 151641,
38	26	83.9	364	16	US-10-437-963-110408	Sequence 110408,
39	26	83.9	420	16	US-10-468-091-24	Sequence 24, Appl
40	26	83.9	441	14	US-10-106-698-6367	Sequence 6367, Ap
41	26	83.9	449	9	US-09-925-301-884	Sequence 884, App
42	26	83.9	531	16	US-10-437-963-110409	Sequence 110409,
43	26	83.9	611	15	US-10-424-599-204138	Sequence 204138,
44	26	83.9	672	15	US-10-425-114-60058	Sequence 60058, A
45	26	83.9	810	9	US-09-712-363-281	Sequence 281, App

#### ALIGNMENTS

RESULT 1  
US-09-940-727B-23  
; Sequence 23, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940, 727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-23

Query Match 100.0%; Score 31; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
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Db 1 LMSTRAS 7

RESULT 2  
US-09-940-727B-26  
; Sequence 26, Application US/09940727B

**Tue Apr 19 06:15:04 2005**

APPLICANT:	O'Keefe, Theresa	APPLICANT:	O'Keefe, Theresa
TITLE OF INVENTION:	HUMANIZED ANTI-CCR2 ANTIBODIES AND METHODS OF USE THEREFOR	TITLE OF INVENTION:	ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE:	1855.1052-012	FILE REFERENCE:	0575/51400-B
CURRENT APPLICATION NUMBER:	US/09/840,459	CURRENT APPLICATION NUMBER:	US/09/940,727B
CURRENT FILING DATE:	2001-02-02	CURRENT FILING DATE:	2002-09-04
PRIOR APPLICATION NUMBER:	PCT/US01/03537	PRIOR APPLICATION NUMBER:	PCT/US97/10965
PRIOR FILING DATE:	2001-02-02	PRIOR FILING DATE:	1997-06-25
PRIOR APPLICATION NUMBER:	09/497,625	PRIOR APPLICATION NUMBER:	08/672,345
PRIOR FILING DATE:	2000-02-03	PRIOR FILING DATE:	1996-06-25
PRIOR APPLICATION NUMBER:	09/359,193	PRIOR APPLICATION NUMBER:	08/672,345
PRIOR FILING DATE:	1999-07-22	PRIOR FILING DATE:	1996-06-25
PRIOR APPLICATION NUMBER:	09/121,781	PRIOR APPLICATION NUMBER:	08/672,345
PRIOR FILING DATE:	1998-07-23	PRIOR APPLICATION NUMBER:	08/672,345
NUMBER OF SEQ ID NOS:	107	NUMBER OF SEQ ID NOS:	121
SOFTWARE:	FastSeq for Windows Version 3.0	SOFTWARE:	PatentIn version 3.1
SEQ ID NO 32		SEQ ID NO 26	
LENGTH:	100	LENGTH:	7
TYPE:	PRT	TYPE:	PRT
ORGANISM:	Mus musculus	ORGANISM:	mouse
US-09-840-459-32		US-09-940-727B-26	
Query Match	100.0%; Score 31; DB 9; Length 100;	Query Match	100.0%; Score 31; DB 10; Length 7;
Best Local Similarity	100.0%; Pred. No. 8.6;	Best Local Similarity	100.0%; Pred. No. 1.3e+06;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 LMSTRAS 7	QY	1 LMSTRAS 7
Db	55 LMSTRAS 61	Db	1 LMSTRAS 7
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US-10-766-773-32		US-09-940-727B-29	
Sequence 32, Application US/10766773		Sequence 29, Application US/09940727B	
Publication No. US20040126851A1		Publication No. US2003007793A1	
GENERAL INFORMATION:		GENERAL INFORMATION:	
APPLICANT: Larosa, Gregory J.		APPLICANT: Landry, Donald W.	
APPLICANT: Horvath, Christopher		APPLICANT: Landry, Donald W.	
APPLICANT: Newman, Walter		APPLICANT: Landry, Donald W.	
APPLICANT: Jones, S. Tarran		APPLICANT: Landry, Donald W.	
APPLICANT: O'Brien, Siobhan H.		APPLICANT: Landry, Donald W.	
APPLICANT: O'Keefe, Theresa		APPLICANT: Landry, Donald W.	
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND METHODS OF USE THEREFOR		TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY	
FILE REFERENCE: 1855.1052-028		FILE REFERENCE: 0575/51400-B	
CURRENT APPLICATION NUMBER: US/10/766,773		CURRENT APPLICATION NUMBER: US/09/940,727B	
CURRENT FILING DATE: 2004-01-27		CURRENT FILING DATE: 2002-09-04	
PRIOR APPLICATION NUMBER: 09/497,625		PRIOR APPLICATION NUMBER: 09/214,095	
PRIOR FILING DATE: 2000-02-03		PRIOR FILING DATE: 1998-12-28	
PRIOR APPLICATION NUMBER: 09/359,193		PRIOR APPLICATION NUMBER: PCT/US97/10965	
PRIOR FILING DATE: 1999-07-22		PRIOR APPLICATION NUMBER: PCT/US97/10965	
PRIOR APPLICATION NUMBER: 09/121,781		PRIOR APPLICATION NUMBER: PCT/US97/10965	
PRIOR FILING DATE: 1998-07-23		PRIOR APPLICATION NUMBER: PCT/US97/10965	
NUMBER OF SEQ ID NOS: 106		PRIOR APPLICATION NUMBER: PCT/US97/10965	
SOFTWARE: FastSeq for Windows Version 3.0		PRIOR APPLICATION NUMBER: PCT/US97/10965	
SEQ ID NO 32		NUMBER OF SEQ ID NOS: 121	
LENGTH:	100	SOFTWARE: PatentIn version 3.1	
TYPE:	PRT	SEQ ID NO 29	
ORGANISM:	Mus musculus	LENGTH:	7
US-10-766-773-32		TYPE:	PRT
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Best Local Similarity	100.0%; Pred. No. 8.6;	US-09-940-727B-29	
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QY	1 LMSTRAS 7	Best Local Similarity	100.0%; Pred. No. 1.3e+06;
Db	55 LMSTRAS 61	Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-766-610-32		Db	1 LMSTRAS 7
Sequence 32, Application US/10766610		RESULT 4	
		US-09-840-459-32	
		Sequence 32, Application US/09840459	
		Patent No. US20020150576A1	
		GENERAL INFORMATION:	
		APPLICANT: Larosa, Gregory J.	
		APPLICANT: Horvath, Christopher	
		APPLICANT: Newman, Walter	
		APPLICANT: Jones, S. Tarran	
		APPLICANT: O'Brien, Siobhan H.	

Publication No. US20040132980A1  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran H.  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-029  
CURRENT APPLICATION NUMBER: US/10/766,610  
CURRENT FILING DATE: 2004-01-27  
PRIOR APPLICATION NUMBER: 09/840,459  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-766-610-32

Query Match 100.0%; Score 31; DB 16; Length 100;  
Best Local Similarity 100.0%; Pred. No. 8.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

## RESULT 7

US-10-733-563-32  
Sequence 32, Application US/10733563  
Publication No. US20040151721A1  
GENERAL INFORMATION:  
APPLICANT: O'Keefe, Theresa  
APPLICANT: Ponath, Paul  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
METHODS OF USE THEREOF  
FILE REFERENCE: 10448-213001  
CURRENT APPLICATION NUMBER: US/10/733,563  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: US 10/272,899  
PRIOR FILING DATE: 2002-10-17  
PRIOR APPLICATION NUMBER: US 60/392,364  
PRIOR FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: US 60/350,166  
PRIOR FILING DATE: 2001-10-19  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-733-563-32

Query Match 100.0%; Score 31; DB 16; Length 100;  
Best Local Similarity 100.0%; Pred. No. 8.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

RESULT 8  
US-09-940-727B-6  
Sequence 6, Application US/09940727B  
Publication No. US20030077793A1  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald W  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 0575/51400-B  
CURRENT APPLICATION NUMBER: US/09/940,727B  
CURRENT FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: 09/214,095  
PRIOR FILING DATE: 1998-12-28  
PRIOR APPLICATION NUMBER: PCT/US97/10965  
PRIOR FILING DATE: 1997-06-25  
PRIOR APPLICATION NUMBER: 08/672,345  
PRIOR FILING DATE: 1996-06-25  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 113  
TYPE: PRT  
ORGANISM: mouse  
US-09-940-727B-6

Query Match 100.0%; Score 31; DB 10; Length 113;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

## RESULT 9

US-09-940-727B-7  
Sequence 7, Application US/09940727B  
Publication No. US20030077793A1  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald W  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 0575/51400-B  
CURRENT APPLICATION NUMBER: US/09/940,727B  
CURRENT FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: 09/214,095  
PRIOR FILING DATE: 1998-12-28  
PRIOR APPLICATION NUMBER: PCT/US97/10965  
PRIOR FILING DATE: 1997-06-25  
PRIOR APPLICATION NUMBER: 08/672,345  
PRIOR FILING DATE: 1996-06-25  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 113  
TYPE: PRT  
ORGANISM: mouse  
US-09-940-727B-7

Query Match 100.0%; Score 31; DB 10; Length 113;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

## RESULT 10

US-09-940-727B-8  
Sequence 8, Application US/09940727B  
Publication No. US20030077793A1  
GENERAL INFORMATION:

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; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-8

Query Match          100.0%; Score 31; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
Db      55 LMSTRAS 61

RESULT 11
US-09-940-727B-104
; Sequence 104, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-104

Query Match          100.0%; Score 31; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
Db      55 LMSTRAS 61

RESULT 12
US-09-940-727B-108
; Sequence 108, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
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; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-108

Query Match          100.0%; Score 31; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
Db      55 LMSTRAS 61

RESULT 13
US-09-940-727B-112
; Sequence 112, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-112

Query Match          100.0%; Score 31; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
Db      55 LMSTRAS 61

RESULT 14
US-10-424-599-191879
; Sequence 191879, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191879
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_15287C.1.pep
; US-10-424-599-191879

Query Match          93.5%; Score 29; DB 15; Length 63;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 24 IMSTRAS 30

RESULT 15
US-09-940-727B-20
; Sequence 20, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
; US-09-940-727B-20

Query Match          90.3%; Score 28; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRSS 7

Search completed: April 18, 2005, 14:54:40
Job time : 53.907 secs
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:01:43 ; Search time 19.0465 seconds  
(without alignments)  
27.435 Million cell updates/sec

Title: US-09-674-716B-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	2	US-08-672-345C-23
2	31	100.0	7	2	US-08-672-345C-26
3	31	100.0	7	2	US-08-672-345C-29
4	31	100.0	7	3	US-09-214-095D-23
5	31	100.0	7	3	US-09-214-095D-26
6	31	100.0	7	3	US-09-214-095D-29
7	31	100.0	100	4	US-08-840-459-32
8	31	100.0	100	4	US-09-497-625A-32
9	31	100.0	113	2	US-08-672-345C-6
10	31	100.0	113	2	US-08-672-345C-7
11	31	100.0	113	2	US-08-672-345C-8
12	31	100.0	113	2	US-08-672-345C-96
13	31	100.0	113	2	US-08-672-345C-97
14	31	100.0	113	2	US-08-672-345C-98
15	31	100.0	113	3	US-09-214-095D-6
16	31	100.0	113	3	US-09-214-095D-7
17	31	100.0	113	3	US-09-214-095D-8
18	31	100.0	113	3	US-09-214-095D-104
19	31	100.0	113	3	US-09-214-095D-108
20	31	100.0	113	3	US-09-214-095D-112
21	28	90.3	7	2	US-08-672-345C-20
22	28	90.3	7	3	US-09-214-095D-20
23	28	90.3	113	2	US-08-672-345C-5
24	28	90.3	113	2	US-08-672-345C-95
25	28	90.3	113	3	US-09-214-095D-5
26	28	90.3	113	3	US-09-214-095D-100
27	28	90.3	280	3	US-09-214-095D-119

28	27	87.1	7	2	US-08-672-345C-80	Sequence 80, Appl
29	27	87.1	7	3	US-09-214-095D-80	Sequence 80, Appl
30	27	87.1	234	4	US-09-538-092-230	Sequence 230, App
31	27	87.1	249	4	US-09-248-796A-14685	Sequence 14685, A
32	27	87.1	331	4	US-09-248-796A-18673	Sequence 18673, A
33	27	87.1	451	4	US-09-502-540-15550	Sequence 15550, A
34	26	83.9	250	3	US-09-029-348-14	Sequence 14, Appl
35	26	83.9	1341	3	US-08-963-825-18	Sequence 18, Appl
36	26	83.9	1341	3	US-09-500-811-18	Sequence 18, Appl
37	26	83.9	1341	3	US-09-570-573-18	Sequence 18, Appl
38	26	83.9	1341	3	US-09-548-608-18	Sequence 18, Appl
39	26	83.9	1461	4	US-09-585-887-9	Sequence 9, Appl
40	26	83.9	1461	4	US-09-289-578-9	Sequence 9, Appl
41	26	83.9	1464	4	US-09-331-347C-21	Sequence 21, Appl
42	25	80.6	51	4	US-09-270-767-34317	Sequence 34317, A
43	25	80.6	51	4	US-09-270-767-49534	Sequence 49534, A
44	25	80.6	130	4	US-09-252-991A-27521	Sequence 27521, A
45	25	80.6	221	4	US-09-248-796A-20200	Sequence 20200, A

ALIGNMENTS

RESULT 1  
US-08-672-345C-23  
; Sequence 23, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Durham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-23

Query Match 100.0%; Score 31; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred.No. 4.1e+05; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;

QY 1 LMSTRAS 7  
Db 1 LMSTRAS 7

RESULT 2

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US-08-672-345C-26
; Sequence 26, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-26

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 4
US-09-214-095D-23
; Sequence 23, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-23

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 5
US-09-214-095D-26
; Sequence 26, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-26

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 3
US-08-672-345C-29
; Sequence 29, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-29

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 3
US-08-672-345C-29
; Sequence 29, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
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QY 1 LMSTRAS 7  
|||||||  
Db 1 LMSTRAS 7

RESULT 6  
US-09-214-095D-29  
; Sequence 29, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214, 095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-29

Query Match 100.0%; Score 31; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
|||||||  
Db 1 LMSTRAS 7

RESULT 7  
US-09-840-459-32  
; Sequence 32, Application US/09840459  
; Patent No. 6698550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-840-459-32

Query Match 100.0%; Score 31; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
|||||||  
Db 55 LMSTRAS 61

RESULT 8  
US-09-497-625A-32  
; Sequence 32, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-497-625A-32

Query Match 100.0%; Score 31; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
|||||||  
Db 55 LMSTRAS 61

RESULT 9  
US-08-672-345C-6  
; Sequence 6, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-672-345C-6

Query Match 100.0%; Score 31; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

## RESULT 10

US-08-672-345C-7  
; Sequence 7, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-672-345C-7

Query Match 100.0%; Score 31; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

## RESULT 11

US-08-672-345C-8  
; Sequence 8, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas

; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-672-345C-8

Query Match 100.0%; Score 31; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

## RESULT 12

US-08-672-345C-96  
; Sequence 96, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 96:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid

US-08-672-345C-96

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-672-345C-96

Query Match 100.0%; Score 31; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

## RESULT 13

US-08-672-345C-97  
Sequence 97, Application US/08672345C  
Patent No. 5948658

GENERAL INFORMATION:  
APPLICANT: Landry Donald, W.  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper and Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,345C  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-672-345C-97

Query Match 100.0%; Score 31; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

## RESULT 14

US-08-672-345C-98  
Sequence 98, Application US/08672345C  
Patent No. 5948658

GENERAL INFORMATION:  
APPLICANT: Landry Donald, W.  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,345C  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-672-345C-98

Query Match 100.0%; Score 31; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

## RESULT 15

US-09-214-095D-6  
Sequence 6, Application US/09214095D  
Patent No. 6280987

GENERAL INFORMATION:  
APPLICANT: Landry, Donald  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 51400-A-PCT-US  
CURRENT APPLICATION NUMBER: US/09/214,095D  
CURRENT FILING DATE: 1999-07-19  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 113  
TYPE: PRT  
ORGANISM: Murinae gen. sp.  
US-09-214-095D-6

Query Match 100.0%; Score 31; DB 3; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7  
Db 55 LMSTRAS 61

Search completed: April 18, 2005, 14:25:26  
Job time : 20.0465 secs

*This Page Blank (uspto)*

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 14:49:23 ; Search time 42 Seconds  
(without alignments)  
16.036 Million cell updates/sec

Title: US-09-674-716B-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	45.2	3	3 I50412	Gene p20K protein
2	13	41.9	6	2 A11490	pyruvate kinase (E
3	12	38.7	5	2 I40469	dnazX-like protein
4	12	38.7	6	2 I51434	H4 histone - Afric
5	12	38.7	6	2 PT0518	T-cell receptor be
6	11	35.5	5	2 B31836	20K protein - Rick
7	11	35.5	5	2 H44817	34.5K structural p
8	11	35.5	5	2 F44817	34.5K structural p
9	11	35.5	5	4 A58728	serrawettin W2 - S
10	11	35.5	7	2 S42620	aggrekan - bovine
11	10	32.3	5	2 A37114	hypoxanthine phosph
12	10	32.3	5	2 PT0295	Ig heavy chain CRD
13	10	32.3	5	2 PT0577	T-cell receptor be
14	10	32.3	5	2 PT0700	T-cell receptor be
15	10	32.3	5	2 S69237	surface protein te
16	10	32.3	5	2 PT0565	T-cell receptor be
17	10	32.3	6	2 A37765	hypothetical prote
18	10	32.3	6	2 S14159	paraspasal crystal
19	10	32.3	6	2 B26206	alpha-1,4-glucan-p
20	10	32.3	7	2 A46474	Fc epsilon RIib -
21	10	32.3	7	2 A34026	acetylcholinestera
22	10	32.3	7	2 B33541	hypothetical prote
23	10	32.3	7	4 I55382	hypothetical pepti
24	9	29.0	3	3 I78890	tyrosine protein k
25	9	29.0	5	2 S70154	URF2 protein - Xan
26	9	29.0	5	2 I40702	primase - Citrobac
27	9	29.0	5	2 B37325	pap fibmbrial regul
28	9	29.0	5	2 T14910	hypothetical prote
29	9	29.0	5	2 PT0695	T-cell receptor be

30	9	29.0	5	2 PT0686	T-cell receptor be
31	9	29.0	6	2 B34835	dnAA protein - Pse
32	9	29.0	6	2 I49808	D-SP2.5 region - m
33	9	29.0	6	2 PT0643	T-cell receptor be
34	9	29.0	6	2 A41946	T-cell receptor ga
35	9	29.0	6	2 I49421	laminin B1 - weste
36	9	29.0	6	2 PC4127	hypothetical 6 pro
37	9	29.0	6	4 S15596	orf 3 rara 5'-regi
38	9	29.0	7	2 S25266	pilE protein - Esc
39	9	29.0	7	2 S38516	mabinlin II chain
40	9	29.0	7	2 E61491	seed protein wa-5
41	9	29.0	7	2 PT0520	T-cell receptor be
42	9	29.0	7	2 PN0649	pullulanase (EC 3.
43	9	29.0	7	2 S45311	microcin C7 - Esch
44	9	29.0	7	2 A28340	myomodulin - Calif
45	9	29.0	7	2 S33244	neuromodulatory pe

ALIGNMENTS

RESULT 1

I50412  
Gene p20K protein - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: I50412  
R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.  
J. Biol. Chem. 268, 8131-8139, 1993  
A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken  
A;Reference number: A46643; MUID:93216790; PMID:8463325  
A;Accession: I50412  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <MAO>  
A;Cross-references: GB:I02537; NID:G212616; PID:G212617  
C;Genetics:  
A;Gene: p20K

Query Match 45.2%; Score 14; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4  
DB 1 MST 3

RESULT 2

A11490  
pyruvate kinase (EC 2.7.1.40) - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 03-Mar-1995  
C:Accession: A11490  
R;Hjeltnquist, G.; Andersson, J.; Edlund, B.; Engstrom, L.  
Biochem. Biophys. Res. Commun. 61, 559-563, 1974  
A;Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate kinase p  
A;Reference number: A11490; MUID:75127438; PMID:4375589  
A;Accession: A11490  
A;Molecule type: protein  
A;Residues: 1-6 <HJE>  
A;Experimental source: liver  
C;Keywords: glycolysis; phosphotransferase

Query Match 41.9%; Score 13; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RAS 7  
DB 3 RAS 5

```

RESULT 3
I40469
dnazX-like protein - Bacillus subtilis (fragment)
C:Species: Bacillus subtilis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40469
R;Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
Mol. Gen. Genet. 215, 478-482, 1989
A;Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
A;Reference number: I40469; MUID:89218958; PMID:2468993
A;Accession: I40469
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: UNIPROT:P09122; EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g43762
C;Genetics:
A;Start codon: GTG

Query Match 38.7%; Score 12; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTR 6
|||
Db 1 MSYQA 5

RESULT 4
I51434
H4 histone - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51434
R;Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
Nucleic Acids Res. 12, 4939-4958, 1984
A;Title: Are there major developmentally regulated H4 gene classes in Xenopus?
A;Reference number: I51391; MUID:84247348; PMID:6330691
A;Accession: I51434
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-6 <WO>
A;Cross-references: GB:K02304; NID:g214227; PIDN:AAA49738.1; PID:g555517

Query Match 38.7%; Score 12; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MSTR 5
|||
Db 1 MSGR 4

RESULT 5
PT0518
T-cell receptor beta chain V-D-J region (100-4B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0518
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0518
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 38.7%; Score 12; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
B31836
20K protein - Rickettsia rickettsii (fragment)
C:Species: Rickettsia rickettsii
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C:Accession: B31836
R;Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A;Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii
A;Reference number: A91885; MUID:89008059; PMID:3139629
A;Accession: B31836
A;Molecule type: DNA
A;Residues: 1-5 <AND>
A;Cross-references: GB:J03371; NID:g152455; PIDN:AAD15030.1; PID:g4262874

Query Match 35.5%; Score 11; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 MSTR 6
|||
Db 1 MDTNS 5

RESULT 7
H44817
34.5K structural protein - Leuconostoc oenos phage P32 (fragment)
C:Species: Leuconostoc oenos phage P32
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: H44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: H44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70332)

Query Match 35.5%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4
|||
Db 1 MAT 3

RESULT 8
F44817
34.5K structural protein - Leuconostoc oenos phage P54 (fragment)
C:Species: Leuconostoc oenos phage P54
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: F44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: F44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70335)

Query Match 35.5%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4
|||

```



Db 1 MAT 3

# RESULT 9

A58728  
Serrawattin W2 - Serratia marcescens  
C;Species: Serratia marcescens  
C;Date: 10-Feb-1998 #sequence\_revision 12-Feb-1998 #text\_change 12-Feb-1998  
C;Accession: A58728  
R;Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.  
J. Bacteriol. 174, 1769-1776, 1992  
A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and  
A;Reference number: A58728; MUID:92193260; PMID:1548227

A;Accession: A58728  
A;Status: unencoded polypeptide  
A;Molecule type: protein  
A;Residues: 1-5 <MAT>  
A;Experimental source: strain NS 25  
C;Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation  
C;Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencoded  
F;1/Modified site: D-leucine (Ileu) #status experimental  
F;4/Modified site: D-phenylalanine (Phe) #status experimental  
F;1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status experimental

Query Match 35.5%; Score 11; DB 4; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4  
Db 1 LST 3

# RESULT 10

S42620  
aggreccan - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
C;Accession: S42620  
R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.  
Matrix Biol. 14, 171-179, 1994  
A;Title: Aggreccan in bovine tendon.  
A;Reference number: S42620; MUID:94340214; PMID:7520336  
A;Accession: S42620  
A;Molecule type: protein  
A;Residues: 1-7 <VOG>  
A;Experimental source: flexor tendon  
C;Keywords: cartilage

Query Match 35.5%; Score 11; DB 2; Length 7;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Indels 1; Gaps 0;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTR 5  
Db 3 IVSPR 7

# RESULT 11

A37114  
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragment)  
C;Species: Schistosoma mansoni  
C;Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 23-Jun-1993  
C;Accession: A37114  
R;Luan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.  
J. Biol. Chem. 265, 13528-13532, 1990  
A;Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Further  
A;Reference number: A37114; MUID:90337955; PMID:2199439  
A;Accession: A37114  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <YUA>

C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 32.3%; Score 10; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4  
Db 1 MSS 3

# RESULT 12

PT0295  
Ig heavy chain CRD3 region (clone 5-91) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0295  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0295  
A;Molecule type: DNA  
A;Residues: 1-5 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 32.3%; Score 10; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TR 5  
Db 3 TR 4

# RESULT 13

PT0577  
T-cell receptor beta chain V-D-J region (141-IBC) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0577; PT0574  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0577  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-IBC  
A;Accession: PT0574  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FE2>  
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1Q  
C;Keywords: T-cell receptor

Query Match 32.3%; Score 10; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STR 5  
Db 2 SSR 4

# RESULT 14

PT0700  
T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0700

R;Peeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0700  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 32.3%; Score 10; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STR 5  
|:  
Db 2 SSR 4

RESULT 15  
S69237  
surface protein tetraabrachion heavy chain - Staphylothermus marinus (fragment)  
C;Species: Staphylothermus marinus  
C;Date: 04-Dec-1997 #sequence\_revision 04-Dec-1997 #text\_change 17-Mar-1999  
C;Accession: S69237  
R;Peters, J.; Nitsch, M.; Kuehlmoergen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh  
J. Mol. Biol. 245, 385-401, 1995  
A;Title: Tetraabrachion: a filamentous archaeobacterial surface protein assembly of unusua  
A;Reference number: S69237; MUID:95139068; PMID:7837271  
A;Accession: S69237  
A;Molecule type: protein  
A;Residues: 1-5 <PET>  
A;Experimental source: strain F1, DSM 3639  
C;Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 32.3%; Score 10; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMS 3  
|:  
Db 3 LLS 5

Search completed: April 18, 2005, 15:02:19  
Job time : 43 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:25:50 ; Search time 182 Seconds  
(without alignments)  
19.695 Million cell updates/sec

Title: US-09-674-716B-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	14	45.2	7	1 GFRP MOUSE	P99025 mus musculus
2	11	35.5	5	1 BIOA CITFR	P13071 citrobacter
3	11	35.5	6	2 P82541	P82541 spinacia ol
4	11	35.5	7	1 UC24 MAIZE	P80630 zea mays (m
5	10	32.3	6	1 VP19 HHV1K	P23210 human herpe
6	10	32.3	7	2 Q65578	Q65578 bovine herp
7	9	29.0	4	1 ILME SEPOF	P83568 sepiia offic
8	9	29.0	6	1 PYF1 PENNO	P84005 penaeus mon
9	9	29.0	7	1 UH11 RAT	P56576 rattus norv
10	9	29.0	7	1 WWA1 ACHFU	P35919 achatina fu
11	9	29.0	7	1 WWA2 ACHFU	P35920 achatina fu
12	9	29.0	7	1 WWA3 ACHFU	P35921 achatina fu
13	9	29.0	7	2 P83492	P83492 bionectria
14	9	29.0	7	2 Q8MFY6	Q8MFY6 taraxacum (
15	9	29.0	7	2 Q95945	Q95945 saccharomyc
16	9	29.0	7	2 P93233	P93233 lycopersico
17	9	29.0	7	2 P70804	P70804 azotobacter
18	9	29.0	7	2 Q8KMS3	Q8KMS3 klebsiella
19	9	29.0	7	2 Q47505	Q47505 escherichia
20	8	25.8	5	2 Q99007	Q99007 hordeum vul
21	8	25.8	7	1 CIA_ENTFA	P11932 enterococcu
22	7	22.6	4	1 TUFT_HUMAN	P01858 homo sapien
23	7	22.6	6	2 P82181	P82181 spinacia ol
24	7	22.6	6	2 P82182	P82182 spinacia ol
25	7	22.6	7	1 IGAO DACDE	P06294 dactylium d
26	7	22.6	7	2 Q34028	Q34028 sphingomona
27	7	22.6	7	2 Q47029	Q47029 enterobacte
28	6	19.4	4	1 DCMS_PSECH	P19918 pseudomonas
29	6	19.4	4	1 FFKA ANTEL	P58705 anthopleura
30	6	19.4	5	1 BIOB CITFR	P12997 citrobacter
31	6	19.4	5	1 PRCT_CARMA	P67857 carcinus ma

32	6	19.4	5	1 PRCT LIMPO	P67858 limulus pol
33	6	19.4	5	1 PRCT PERAM	P67859 periplaneta
34	6	19.4	5	1 PSK DAUCA	P58261 daucus caro
35	6	19.4	5	2 P83073	P83073 bacillus ce
36	6	19.4	6	1 TRPI_PSEPU	P36414 pseudomonas
37	6	19.4	6	1 UN06_CLOPA	P81351 clostridium
38	6	19.4	6	2 P83533	P83533 lactobacill
39	6	19.4	7	1 CCFL_ENTFA	P20104 enterococcu
40	6	19.4	7	1 CHO1_ALCSP	P16101 alcaligenes
41	6	19.4	7	2 Q15897	Q15897 homo sapien
42	6	19.4	7	2 Q15903	Q15903 homo sapien
43	6	19.4	7	2 Q8NH77	Q8NH77 homo sapien
44	6	19.4	7	2 Q8TAQ4	Q8TAQ4 homo sapien
45	6	19.4	7	2 Q9BRY4	Q9BRY4 homo sapien

## ALIGNMENTS

## RESULT 1

ID	GFRP_MOUSE	STANDARD;	PRT;	7 AA.
AC	P99025;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).			
GN	Name=Gchfr; Synonyms=Gfrp;			
OS	Mus musculus (Mouse)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE			
RC	TISSUE=liver;			
RA	Sanchez J.-C., Rouge V., Prutiger S., Hughes G., Yan J.X.,			
RA	Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;			
RL	Submitted (AUG-1998) to Swiss-Prot.			
CC	-!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP			
CC	cyclohydrolase I. This inhibition is reversed by L-phenylalanine			
CC	(By similarity).			
CC	-!- SUBUNIT: Homodimer (By similarity).			
DR	SWISS-2DPAGE; P99025; MOUSE.			
KW	Direct protein sequencing.			
FT	INIT MET 0 0			
FT	NON_TER 7 7			
SQ	SEQUENCE 7 AA; 806 MW; 71BSB057273B4700 CRC64;			

Query Match 45.2%; Score 14; DB 1; Length 7;  
Best Local Similarity 75.0%; Pred. NO. 1.6e+06;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMST 4  
Db 4 List 7

## RESULT 2

ID	BIOA_CITFR	STANDARD;	PRT;	5 AA.
AC	P13071;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase			
DE	(SC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA			
DE	aminotransferase) (Fragment).			
GN	Name=bioA;			
OS	Citrobacter freundii.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Citrobacter.			
OX	NCBI_TaxID=546;			
RN	[1]			

RP SEQUENCE FROM N.A.  
RX MEDLINE=89006280; PubMed=2971595; DOI=10.1016/0378-1119(88)90397-6;  
RA Shiuan D., Campbell A.;  
RT "transcriptional regulation and gene arrangement of *Escherichia coli*,  
RT *Citrobacter freundii* and *Salmonella typhimurium* biotin operons.";   
RL Gene 67:203-211(1988).  
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-diaminononanoate.  
CC -1- COFACTOR: Pyridoxal phosphate.  
CC -1- PATHWAY: Biotin biosynthesis.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent aminotransferase family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M21922; -, NOT\_ANNOTATED\_CDS.  
CC DR PIR; I40697; I40697.  
CC DR InterPro; IPR005814; Aminotrans\_3.  
CC DR PROSITE; PS00600; AA\_TRANSFER\_CLASS\_3; PARTIAL.  
CC KW Aminotransferase; Biotin biosynthesis; Pyridoxal phosphate;  
CC FT Transferase.  
CC FT NON\_TER  
CC SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;  
CC  
CC Query Match 35.5%; Score 11; DB 1; Length 5;  
CC Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
CC Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 2 MST 4  
CC | |  
CC 1 MTT 3  
CC  
CC Db  
CC  
CC RESULT 3  
CC P82541 PRELIMINARY; PRT; 6 AA.  
CC AC P82541;  
CC DT 01-OCT-2000 (TREMBlrel. 15, Created)  
CC DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
CC DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
CC DE Chloroplast 30S ribosomal protein S19 beta (fragment).  
CC OS Spinacia oleracea (Spinach).  
CC OG Chloroplast  
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
CC OC Caryophyllales; Amaranthaceae; Spinacia.  
CC NCBI\_TaxID=3562;  
CC RN [1]  
CC RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
CC RC STRAIN=cv. ALMARO; TISSUE=Leaf;  
CC RX MEDLINE=20435797; PubMed=10874039; DOI=10.1074/jbc.M004350200;  
CC RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;  
CC RT "The plastid ribosomal proteins. Identification of all the proteins in the small subunit of an organelle ribosome (chloroplast).";  
CC RL J. Biol. Chem. 37:28455-28465(2000).  
CC CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.  
CC CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.  
CC CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
CC CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.  
CC CC -1- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.  
CC CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PT. S19 BETA FORM IS THE MINOR BASIC FORM.  
CC CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 kDa.  
CC CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
CC GO; GO:0009507; C:chloroplast; IEA.

DR GO; GO:0019843; F:rRNA binding; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR InterPro; IPR002222; RIBOSOMAL\_S19.  
DR PROSITE; PS00323; RIBOSOMAL\_S19; PARTIAL.  
KW Chloroplast; Ribosomal protein; rRNA-binding.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;  
CC  
CC Query Match 35.5%; Score 11; DB 2; Length 6;  
CC Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
CC Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 4 TRA 6  
CC | |  
CC 1 TRS 3  
CC  
CC Db  
CC  
CC RESULT 4  
CC UC24\_MAIZE STANDARD; PRT; 7 AA.  
CC ID UC24\_MAIZE  
CC AC P80630;  
CC DT 01-OCT-1996 (Rel. 34, Created)  
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)  
CC DT 05-JUL-2004 (Rel. 44, Last annotation update)  
CC DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 447) (fragment).  
CC OS Zea mays (Maize).  
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
CC OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
CC NCBI\_TaxID=4577;  
CC RN [1]  
CC RP SEQUENCE  
CC RC TISSUE=Coleoptile;  
CC RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
CC RT Pernollet J.-C., Zivy M., de Vienne D.;  
CC RT "The maize two dimensional gel protein database: towards an integrated genome analysis program";  
CC RL Theor. Appl. Genet. 93:997-1005(1996).  
CC CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.0, its MW is: 30.0 kDa.  
CC CC Maize-2DPAGE; P80630; COLEOPTILE.  
CC DR MaizeDB; 123956; -.  
CC KW Direct protein sequencing.  
CC FT NON\_TER  
CC FT NON\_TER  
CC SQ SEQUENCE 7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;  
CC  
CC Query Match 35.5%; Score 11; DB 1; Length 7;  
CC Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
CC Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
CC  
CC QY 3 STRAS 7  
CC | |  
CC 1 STAKS 5  
CC  
CC Db  
CC  
CC RESULT 5  
CC VP19\_HHV1K STANDARD; PRT; 6 AA.  
CC ID VP19\_HHV1K  
CC AC P23210;  
CC DT 01-NOV-1991 (Rel. 20, Created)  
CC DT 01-NOV-1991 (Rel. 20, Last sequence update)  
CC DT 05-JUL-2004 (Rel. 44, Last annotation update)  
CC DE Capsid assembly and DNA maturation protein (Virion protein UL38) (Capsid protein VP19C) (fragment).  
CC GN Name=UL38;  
CC OS Human herpesvirus 1 (strain KOS) (HHV-1) (Human herpes simplex virus 1).  
CC OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
CC OC Alphaherpesvirinae; Simplexvirus.  
CC OX NCBI\_TaxID=10306;  
CC RN [1]

SEQUENCE FROM N.A.  
 RP MEDLINE=91101287; PubMed=1846198;  
 RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,  
 RA Silverstein S., Wagner E.K.;  
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the  
 RT expression of UL38, a true late gene involved in capsid assembly.";  
 RL J Virol. 65:769-786(1991).  
 CC -!- FUNCTION: Component of the basal layer in which the capsids are  
 CC embedded. Binds DNA.  
 CC  
 CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; M57646; AAA45830.1; -;  
 KW Capsid assembly; Coat protein; DNA-binding.  
 FT NON TER 6  
 SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;  
 Query Match 32.3%; Score 10; DB 1; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 MST 4  
 Db | |  
 1 MKT 3  
 RESULT 6  
 Q65578 PRELIMINARY; PRT; 7 AA.  
 AC Q65578;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Bovine herpesvirus 1.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID=10320;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=Cooper;  
 RX MEDLINE=95313343; PubMed=7793062;  
 RA Vicek C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,  
 RA Letcworth G.J., Schwytzer M.;  
 RT "Nucleotide sequence analysis of a 30-kb region of the bovine  
 RT herpesvirus 1 genome which exhibits a colinear gene arrangement with  
 RT the UL21 to UL4 genes of herpes simplex virus.";  
 RL Virology 210:100-108(1995).  
 DR EMBL; Z48053; CAA88130.1; -;  
 KW Hypothetical protein.  
 FT NON TER 1  
 SEQUENCE 7 AA; 758 MW; 6DD33455B1F1B1C0 CRC64;  
 Query Match 32.3%; Score 10; DB 2; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 STRA 6  
 Db | |  
 4 SNKA 7  
 RESULT 7  
 ID ILME\_SEPOF STANDARD; PRT; 4 AA.  
 AC P83568;

DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pheromone peptide ILME.  
 OS Sepia officinalis (Common cuttlefish).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
 OX NCBI\_TaxID=6610;  
 RN [1]  
 RN SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS  
 RP SPECTROMETRY.  
 RC TISSUE=Egg;  
 RX MEDLINE=20403899; PubMed=10944467; DOI=10.1006/bbrc.2000.3286;  
 RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;  
 RT "TIME: a waterborne pheromonal peptide released by the eggs of Sepia  
 RT officinalis.";  
 RL Biochem. Biophys. Res. Commun. 275:217-222(2000).  
 RN [2]  
 RN SEQUENCE.  
 RP TISSUE=Egg;  
 RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;  
 RA Zatylny C., Marvin L., Gagnon J., Henry J.;  
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-  
 RT attracting peptide.";  
 RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).  
 CC -!- FUNCTION: Has myotropic activity targeting the genital tract.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg (EC2).  
 CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.  
 KW Direct protein sequencing; Pheromone.  
 SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;  
 Query Match 29.0%; Score 9; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LM 2  
 Db | |  
 2 LM 3  
 RESULT 8  
 ID PYFI\_PENMO STANDARD; PRT; 6 AA.  
 AC P84005;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DE Peptide tyrosine phenylalanine 1 (Pem-PYFI).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RN SEQUENCE, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.  
 RP TISSUE=Eveatalk;  
 RX PubMed=12431727; DOI=10.1016/S0196-9781(02)00176-6;  
 RA Sithigongul P., Pupum J., Krungkarn C., Longyant S., Panchan N.,  
 RA Chaiwisuthangkura P., Sithigongul W., Petsom A.;  
 RT "Four novel PYFs: members of NPY/PP peptide superfamily from the  
 RT eveatalk of the giant tiger prawn Penaeus monodon.";  
 RL Peptides 23:1895-1906(2002).  
 CC -!- FUNCTION: May act as a neurotransmitter, neuromodulator or  
 CC neurohormone.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Limited to neuronal cell bodies, neuronal  
 CC processes and sinus gland.  
 CC -!- MASS SPECTROMETRY: MW=801.5; METHOD=MALDI; RANGE=1-6; NOTE=Ref.1.  
 CC -!- SIMILARITY: Belongs to the NPY family.  
 DR Interpro; IPR001955; Pancreatic hormn.  
 DR PROSITE; PS00265; PANCREATIC\_HORMONE\_1; PARTIAL.  
 DR PROSITE; PS50276; PANCREATIC\_HORMONE\_2; PARTIAL.

KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 6 6 Phenylalanine amide (Potential).  
 SQ SEQUENCE 6 AA; 802 MW; 69D417740DC46000 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RA 6  
 DB 1 RA 2

RESULT 9  
 UH11\_RAT  
 ID UH11\_RAT STANDARD; PRT; 7 AA.  
 AC P56576;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Unknown protein from 2D-PAGE of heart tissue (Spot P11) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RC SEQUENCE  
 RP STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to Swiss-Prot.  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 8.5, its MW is: 42 kDa.  
 KW Direct protein sequencing.  
 FT NON\_TER 2 2 S or A.  
 FT UNSURE 7 7  
 SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STR 5  
 DB 2 SAR 4

RESULT 10  
 WWA1\_ACHF  
 ID WWA1\_ACHF STANDARD; PRT; 7 AA.  
 AC P35919;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Wamide-1.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RC SEQUENCE  
 RP TISSUE=Ganglion;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
 RT ganglia of the African giant snail, Achatina fulica.";  
 RL FEBS Lett. 323:104-108(1993).  
 CC -1- FUNCTION: Exhibits modulatory effects on the peripheral nervous  
 CC system. Inhibits activity on a central neuron.  
 DR PIR; S33245; S33245.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 7 7 Tryptophan amide.  
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MS 3  
 DB 4 MS 5

RESULT 11  
 WWA2\_ACHF  
 ID WWA2\_ACHF STANDARD; PRT; 7 AA.  
 AC P35920;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Wamide-2.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RC SEQUENCE  
 RP TISSUE=Ganglion;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
 RT ganglia of the African giant snail, Achatina fulica.";  
 RL FEBS Lett. 323:104-108(1993).  
 DR PIR; S33246; S33246.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 7 7 Tryptophan amide.  
 SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MS 3  
 DB 4 MS 5

RESULT 12  
 WWA3\_ACHF  
 ID WWA3\_ACHF STANDARD; PRT; 7 AA.  
 AC P35921;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Wamide-3.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RC SEQUENCE  
 RP TISSUE=Ganglion;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
 RT ganglia of the African giant snail, Achatina fulica.";  
 RL FEBS Lett. 323:104-108(1993).  
 DR PIR; S33244; S33244.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 7 7 Tryptophan amide.  
 SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MS 3  
 DB 4 MS 5

QY 2 MS 3  
Db 4 MS 5

## RESULT 13

ID P83492 PRELIMINARY; PRT; 7 AA.  
AC P83492;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).  
OS Bionectria ochroleuca (Gliocladium roseum).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocrymectididae; Hypocreales; Bionectriaceae; Bionectria.  
OX NCBI\_TaxID=29856;  
[1]  
RN SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.  
RC STRAIN=Gr87;  
RA Zhao M., Zhang K.;  
RL Submitted (DEC-2002) to Swiss-Prot.  
CC -!- FUNCTION: Acts as a serine protease.  
CC -!- SUBCELLULAR LOCATION: Secreted  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0004252; F:serine-type endopeptidase activity; NAS.  
DR InterPro: IPR000209; Pept S8 S53.  
DR PROSITE: PS00136; SUBTILASE ASP; PARTIAL.  
DR PROSITE: PS00137; SUBTILASE\_HIS; PARTIAL.  
DR PROSITE: PS00138; SUBTILASE\_SER; PARTIAL.  
KW Hydrolase; Serine protease.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 688 MW; 776DD455A6C1ADB0 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;  
Best Local Similarity 20.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7  
Db 1 ATQSN 5

## RESULT 14

ID Q8MEY6 PRELIMINARY; PRT; 7 AA.  
AC Q8MEY6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE PbaA (Fragment).  
GN Name=pbaA;  
OS Taraxacum (sect. Dioszegia) sp. 4310Hnew.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;  
OC Taraxacum; unclassified Taraxacum.  
OX NCBI\_TaxID=154248;  
[1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RA Mes T.H.M.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY015477; AA021591.1; -  
DR GO: GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 675 MW; 687451B5A76DDB70 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;

QY 3 ST 4  
Db 4 ST 5

## RESULT 15

ID Q95945 PRELIMINARY; PRT; 7 AA.  
AC Q95945;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Inside intron 5 (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=D273-10B;  
RX MEDLINE=81069885; PubMed=6254986;  
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;  
RT "Assembly of the mitochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit 1 of yeast cytochrome oxidase."  
RL J. Biol. Chem. 255:11927-11941(1980).  
DR EMBL; V00694; CAA24066.1; -  
DR GO: GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RA 6  
Db 1 RA 2

Search completed: April 18, 2005, 15:00:45  
Job time : 185 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:23:45 ; Search time 167 Seconds  
(without alignments)  
16.212 Million cell updates/sec

Title: US-09-674-716B-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 121728

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	2 AAW39825	Aaw39825 Light cha
2	31	100.0	7	2 AAW39822	Aaw39822 Light cha
3	31	100.0	7	2 AAW39819	Aaw39819 Light cha
4	31	100.0	7	3 AAY32255	Aay32255 Light cha
5	28	90.3	7	2 AAW39816	Aaw39816 Light cha
6	27	87.1	7	2 AAW39876	Aaw39876 Light cha
7	22	71.0	7	5 AAU70329	Aau70329 Human int
8	20	64.5	7	7 ADJ32068	Adj32068 Human int
9	19	61.3	4	3 AAY81430	Aay81430 Amino aci
10	19	61.3	7	2 AAY06840	Aay06840 Peptide S
11	19	61.3	7	2 AAY05015	Aay05015 Tumour an
12	19	61.3	7	5 ABP62370	Abp62370 Human imm
13	19	61.3	7	5 ABP62382	Abp62382 Human imm
14	19	61.3	7	5 ABP62364	Abp62364 Human imm
15	19	61.3	7	7 ADC82748	Adc82748 CDR regio
16	19	61.3	7	8 ADN08646	Adn08646 Corton wi
17	19	61.3	7	8 ADP47259	Adp47259 Human pho
18	19	61.3	7	8 ADP47256	Adp47256 Human pho
19	19	61.3	7	8 ADS52415	Ads52415 Fab targe
20	18	58.1	6	4 AAB35205	Aab35205 Retrovira
21	18	58.1	7	2 AAR46961	Aar46961 Peptide f
22	18	58.1	7	2 AAR76083	Aar76083 Mab 55.1
23	18	58.1	7	2 AAW31179	Aaw31179 Hepatitis
24	18	58.1	7	2 AAY05016	Aay05016 Tumour an
25	18	58.1	7	3 AAY95223	Aay95223 Anti-plat

26	18	58.1	7	5 ABP62377	Abp62377 Human imm
27	18	58.1	7	5 ABG77536	Abg77536 Targettin
28	18	58.1	7	7 ADC82750	Adc82750 CDR regio
29	18	58.1	7	7 ADJ72439	Adj72439 VL chain
30	18	58.1	7	8 ADL93628	Adl93628 Human CD4
31	18	58.1	7	8 ADL93550	Adl93550 Human CD4
32	18	58.1	7	8 ADP47068	Adp47068 Murine li
33	18	58.1	7	8 ADP47070	Adp47070 Murine li
34	18	58.1	7	8 ADP47292	Adp47292 Human pho
35	18	58.1	7	8 ADP47253	Adp47253 Human pho
36	18	58.1	7	8 ADP47252	Adp47252 Human pho
37	18	58.1	7	8 ADS52373	Ads52373 Fab targe
38	18	58.1	7	8 ADS52403	Ads52403 Fab targe
39	17	54.8	6	2 AAW95268	Aaw95268 Anti-prog
40	17	54.8	7	2 AAR30157	Aar30157 MAb GAH v
41	17	54.8	7	2 AAR57966	Aar57966 MAb NFS2
42	17	54.8	7	2 AAR50317	Aar50317 MAb NFS2
43	17	54.8	7	2 AAR57964	Aar57964 MAb NFS2
44	17	54.8	7	2 AAR54108	Aar54108 Humanised
45	17	54.8	7	2 AAR98485	Aar98485 Anti-IL-5

ALIGNMENTS

RESULT 1  
AAW39825  
ID AAW39825 standard; peptide; 7 AA.  
AC AAW39825;  
XX  
DT 16-JUN-1998 (first entry)  
XX  
DE Light chain CDR2 of catalytic antibody 12H1.  
XX  
KW Variable domain; lambda light chain; catalytic antibody; degradation;  
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
KW overdose; addiction.  
XX  
OS Mus sp.  
XX  
PN WO9749800-A1.  
XX  
PD 31-DEC-1997.  
XX  
PF 25-JUN-1997; 97WO-US010965.  
XX  
PR 25-JUN-1996; 96US-00672345.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Landry DW;  
XX  
WP1; 1998-077166/07.  
XX  
PT New catalytic antibodies able to decompose cocaine, single-chain  
PT analogues - used to treat cocaine overdose and addiction, required in far  
PT smaller doses than antibodies that antagonise cocaine by simply binding.  
XX  
PS Claim 17; Page 83; 147pp; English.  
XX  
CC AAW39824-26 represent the sequences of the light chain complementarity  
CC determining regions (CDRs) of the catalytic antibody 12H1, which is able  
CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
CC were prepared and used to immunise mice for production of hybridomas.  
CC Catalytic antibodies were identified by their capacity to release 3H-  
CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified  
CC using TSA2, and has a per minute Kcat of 0.16. The antibodies reduce the  
CC concentration of cocaine in a subject, and are used particularly for the  
CC treatment of an overdose. They are also used for treating addiction (by  
XX reducing the in vivo concentration that can be achieved)

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SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
Db       1 LMSTRAS 7

RESULT 2
AAW39822
ID      AAW39822 standard; peptide; 7 AA.
AC      AAW39822;
XX      16-JUN-1998 (first entry)
DT      16-JUN-1998 (first entry)
DE      Light chain CDR2 of catalytic antibody 2A10.
XX      Variable domain; lambda light chain; catalytic antibody; degradation;
KW      cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW      phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW      overdose; addiction.
XX      Mus sp.
OS      WO9749800-A1.
XX      31-DEC-1997.
PD      25-JUN-1997; 97WO-US010965.
PF      25-JUN-1997; 96US-00672345.
PR      (UYCO ) UNIV COLUMBIA NEW YORK.
XX      Landry DW;
XX      WPI; 1998-077166/07.
XX      New catalytic antibodies able to decompose cocaine, single-chain
PT      analogues - used to treat cocaine overdose and addiction, required in far
PT      smaller doses than antibodies that antagonise cocaine by simply binding.
XX      Claim 15; Page 82; 147pp; English.
XX      AAW39821-23 represent the sequences of the light chain complementarity
CC      determining regions (CDRs) of the catalytic antibody 2A10, which is able
CC      to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC      were prepared and used to immunise mice for production of hybridomas.
CC      Catalytic antibodies were identified by their capacity to release 3H-
CC      benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
CC      using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC      transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
CC      The antibodies reduce the concentration of cocaine in a subject, and are
CC      used particularly for the treatment of an overdose. They are also used
CC      for treating addiction (by reducing the in vivo concentration that can be
CC      achieved)
XX      SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
Db       1 LMSTRAS 7

RESULT 3
AAW39822
ID      AAW39822 standard; peptide; 7 AA.
AC      AAW39822;
XX      16-JUN-1998 (first entry)
DT      16-JUN-1998 (first entry)
DE      Light chain CDR2 of catalytic antibody 2A10.
XX      Variable domain; lambda light chain; catalytic antibody; degradation;
KW      cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW      phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW      overdose; addiction.
XX      Mus sp.
OS      WO9749800-A1.
XX      31-DEC-1997.
PD      25-JUN-1997; 97WO-US010965.
PF      25-JUN-1997; 96US-00672345.
PR      (UYCO ) UNIV COLUMBIA NEW YORK.
XX      Landry DW;
XX      WPI; 1998-077166/07.
XX      New catalytic antibodies able to decompose cocaine, single-chain
PT      analogues - used to treat cocaine overdose and addiction, required in far
PT      smaller doses than antibodies that antagonise cocaine by simply binding.
XX      Claim 15; Page 82; 147pp; English.
XX      AAW39821-23 represent the sequences of the light chain complementarity
CC      determining regions (CDRs) of the catalytic antibody 2A10, which is able
CC      to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC      were prepared and used to immunise mice for production of hybridomas.
CC      Catalytic antibodies were identified by their capacity to release 3H-
CC      benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
CC      using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC      transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
CC      The antibodies reduce the concentration of cocaine in a subject, and are
CC      used particularly for the treatment of an overdose. They are also used
CC      for treating addiction (by reducing the in vivo concentration that can be
CC      achieved)
XX      SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
Db       1 LMSTRAS 7

RESULT 4
AAW39822
ID      AAW39822 standard; peptide; 7 AA.
AC      AAW39822;
XX      15-FEB-2000 (first entry)
DT      15-FEB-2000 (first entry)
DE      Light chain CDR L2 of mouse anti-CD23 MAB C11.
XX      CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
KW      monoclonal antibody; chimeric antibody; humanised antibody;
KW      complementarity determining region; CDR; autoimmune disease;

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AAW39819
ID      AAW39819 standard; peptide; 7 AA.
AC      AAW39819;
XX      16-JUN-1998 (first entry)
DT      16-JUN-1998 (first entry)
DE      Light chain CDR2 of catalytic antibody 6A12.
XX      Variable domain; lambda light chain; catalytic antibody; degradation;
KW      cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW      phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW      overdose; addiction.
XX      Mus sp.
OS      WO9749800-A1.
XX      31-DEC-1997.
PD      25-JUN-1997; 97WO-US010965.
PF      25-JUN-1997; 96US-00672345.
PR      (UYCO ) UNIV COLUMBIA NEW YORK.
XX      Landry DW;
XX      WPI; 1998-077166/07.
XX      New catalytic antibodies able to decompose cocaine, single-chain
PT      analogues - used to treat cocaine overdose and addiction, required in far
PT      smaller doses than antibodies that antagonise cocaine by simply binding.
XX      Claim 13; Page 81; 147pp; English.
XX      AAW39818-20 represent the sequences of the light chain complementarity
CC      determining regions (CDRs) of the catalytic antibody 6A12, which is able
CC      to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC      were prepared and used to immunise mice for production of hybridomas.
CC      Catalytic antibodies were identified by their capacity to release 3H-
CC      benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified
CC      using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC      transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072.
CC      The antibodies reduce the concentration of cocaine in a subject, and are
CC      used particularly for the treatment of an overdose. They are also used
CC      for treating addiction (by reducing the in vivo concentration that can be
CC      achieved)
XX      SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
Db       1 LMSTRAS 7

RESULT 4
AAW39822
ID      AAW39822 standard; peptide; 7 AA.
AC      AAW39822;
XX      15-FEB-2000 (first entry)
DT      15-FEB-2000 (first entry)
DE      Light chain CDR L2 of mouse anti-CD23 MAB C11.
XX      CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
KW      monoclonal antibody; chimeric antibody; humanised antibody;
KW      complementarity determining region; CDR; autoimmune disease;

```

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.

XX Mus musculus.  
 OS  
 XX  
 XX WO9958679-A1.  
 PN  
 XX  
 XX 18-NOV-1999.  
 PD  
 XX  
 XX 07-MAY-1999; 99WO-GB001434.  
 PF  
 XX  
 XX 09-MAY-1998; 98GB-00009839.  
 PR  
 XX  
 XX (GLAX ) GLAXO GROUP LTD.  
 PA  
 XX  
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 PI  
 XX  
 XX WPI; 2000-053101/04.  
 DR  
 XX  
 XX N-PSDB; AAZ34749.  
 DR

XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 PT  
 XX  
 XX

PS Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 2 (CDR L2)  
 CC of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11  
 CC (see also AAY32262). The invention provides altered antibodies, such as  
 CC chimeric or humanised antibodies, which comprise sufficient of the amino  
 CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to  
 CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 |||||  
 Db 1 LMSTRAS 7

RESULT 5  
 AAW39816  
 ID AAW39816 standard; peptide; 7 AA.

XX AAW39816;

XX 16-JUN-1998 (first entry)

XX Light chain CDR2 of catalytic antibody 3B9.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX Mus sp.  
 OS  
 XX WO9749800-A1.  
 PN  
 XX  
 XX 31-DEC-1997.  
 PD  
 XX  
 XX 25-JUN-1997; 97WO-US010965.  
 PF  
 XX  
 XX 25-JUN-1996; 96US-00672345.  
 PR  
 XX  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX Claim 11; Page 80; 147pp; English.

XX AAW39815-17 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX Sequence 7 AA;

Query Match 90.3%; Score 28; DB 2; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 |||||  
 Db 1 LMSTRSS 7

RESULT 6  
 AAW39876  
 ID AAW39876 standard; peptide; 7 AA.

XX AAW39876;

XX 16-JUN-1998 (first entry)

XX Light chain CDR2 of a catalytic antibody capable of degrading cocaine.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX Mus sp.

XX Key Location/Qualifiers  
 FH Misc-difference 6 /note= "not specified"  
 FT

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.  
 PR (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA Landry DW;  
 PI  
 XX WPI; 1998-077166/07.  
 XX  
 XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 XX Claim 10; Page 5; 147pp; English.  
 XX  
 CC AAW39875-77 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of a catalytic antibody which is capable of  
 CC degrading cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. These antibodies were found to have  
 CC CDRs of the present sequence. The antibodies reduce the concentration of  
 CC cocaine in a subject, and are used particularly for the treatment of an  
 CC overdose. They are also used for treating addiction (by reducing the in  
 CC vivo concentration that can be achieved)  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 87.1%; Score 27; DB 2; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 DB | : | | | |  
 1 LMSTRXS 7  
 RESULT 7  
 AAU70329  
 ID AAU70329 standard; peptide; 7 AA.  
 AC AAU70329;  
 XX  
 XX 14-FEB-2002 (first entry)  
 DT  
 XX Human Kappa II light chain CDR2.  
 DE  
 XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
 KW complementarity determining region; framework region; IgBP;  
 KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;  
 KW IgD; IgE; IgY; IgM; kappa; lambda; CDR.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2001183806-A1.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX 02-MAY-2001; 2001WO-US014349.  
 PF  
 XX 02-MAY-2000; 2000US-00563222.  
 PR  
 XX (EPIC-) EPICYTE PHARM INC.  
 PA  
 XX Hiatt AC, Hein MB;  
 PI  
 XX WPI; 2002-055482/07.  
 DR  
 XX Preparing immunoglobulin binding protein array in plant cells by  
 PT transforming the cells with different polynucleotides encoding binding  
 PT protein polypeptides specific to ligand, selecting plant cells for  
 PT preparing array.  
 XX

PS Disclosure; Page 14; 129pp; English.  
 XX  
 CC The invention relates to transforming a population of cells (e.g. plant  
 CC cells), comprising using a library of two different polynucleotides  
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides  
 CC that specifically bind to a ligand or form one or more disulphide bonds  
 CC with polypeptides in transfected cells, to generate an IgBP that binds to  
 CC a ligand, and transformed plant cells are selected, and preparing an IgBP  
 CC array in plant cells. At least one peptide sequence has at least 75%  
 CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,  
 CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is  
 CC useful for preparing an immunoglobulin binding protein array, preferably  
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially  
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
 CC discovery of e.g. screening assays of IgBPs having desired  
 CC characteristics. The present sequence is a mammalian immunoglobulin  
 CC derived peptide that may be incorporated into an IgBP of the invention  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 71.0%; Score 22; DB 5; Length 7;  
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LMSTRAS 7  
 DB | : | | | |  
 1 LVSNRAS 7  
 RESULT 8  
 ADJ32068  
 ID ADJ32068 standard; peptide; 7 AA.  
 XX  
 XX AC ADJ32068;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Human interferon-gamma antibody light chain CDR2 peptide SeqID22.  
 DE  
 XX antibody; antigen binding domain; interferon-gamma; INF-gamma;  
 KW antagonist antibody; antiinflammatory; immunosuppressive;  
 KW autoimmune disease; inflammatory condition; human;  
 KW complementarity determining region; CDR.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003099647-A1.  
 PN  
 XX 29-MAY-2003.  
 PD  
 XX 05-OCT-2001; 2001US-00972656.  
 PF  
 XX 05-OCT-2001; 2001US-00972656.  
 PR  
 XX (DESH/) DESHPANDE R V.  
 PA (TSAL/) TSAI M.  
 XX  
 XX Deshpande RV, Tsai M;  
 PI  
 XX WPI; 2003-696068/66.  
 DR  
 XX New antibody or antigen binding domain, or its fragment, variant or  
 PT derivative, which binds to an interferon-gamma protein, useful for  
 PT preparing a composition for preventing or treating inflammatory or  
 PT autoimmune disorders.  
 XX  
 XX Claim 14; SEQ ID NO 22; 113pp; English.  
 PS  
 XX This invention relates to a novel antibody or antigen binding domain, or  
 CC its fragment, variant or derivative, which binds to an interferon-gamma  
 CC (INF-gamma) protein, and is an antagonist antibody. The invention may be  
 CC useful for the development of compounds with an antiinflammatory or

CC immunosuppressive activity through action as interferon-gamma agonists. A  
 CC composition containing the antibody is useful for preventing or treating  
 CC an autoimmune disease and an inflammatory condition. The present sequence  
 CC is that of a peptide which represents a complementarity determining  
 CC region (CDR) of a human IFN-gamma antibody which may be part of the  
 CC invention.

XX SQ Sequence 7 AA;

Query Match 64.5%; Score 20; DB 7; Length 7;  
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
 | | | | |  
 Db 1 LASNRAS 7

RESULT 9

AA181430  
 ID AAY81430 standard; peptide; 4 AA.

XX AC AAY81430;

DT 19-JUN-2000 (first entry)

XX DE Amino acids encoded by 5' portion of pTUGAS vector SacI-HindIII region.

XX KW pTUGAS vector; Cellulomonas fimi; endoglucanase C; CBD;  
 XX KW cellulose binding domain; polysaccharide binding peptide; fusion protein;  
 XX KW recombinant protein; cell separation; affinity phase separation.

XX OS Synthetic.

XX PN US6048715-A.

XX PD 11-APR-2000.

XX PF 24-JUL-1996; 96US-00685808.

XX PR 08-JUL-1988; 88US-00216794.

XX PR 25-OCT-1990; 90US-00603987.

XX PR 08-APR-1992; 92US-00865095.

XX PR 24-MAY-1994; 94US-00249037.

XX PR 24-JUL-1995; 95US-00505860.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX PI Haynes CA, Tomme P, Kilburn DG;  
 XX DR WPI; 2000-328038/28.

XX PT Two-phase partition affinity separation system useful for separating and  
 XX PT purifying proteins comprises a phase-forming oligosaccharide polymer and  
 XX PT a phase-separation agent.

XX PS Disclosure; Fig 3A; 46pp; English.

XX CC The invention relates to a novel two-phase partition system for affinity  
 CC separation which comprises a phase-forming oligosaccharide polymer to  
 CC which a polysaccharide binding peptide (PBP) binds, and a phase  
 CC separation inducing agent. The system may be used for the separation and  
 CC purification of recombinant proteins from cell cultures. The protein of  
 CC interest is expressed in the host cell as a fusion protein with a  
 CC polysaccharide binding peptide, and the cell lysate or fermentation broth  
 CC (or other composition comprising the fusion protein) is contacted with  
 CC the phase separation system. The fusion protein partitions into the  
 CC oligosaccharide polymer phase, and can then be isolated e.g., via the use  
 CC of a solution with a low ionic strength, high pH or containing a  
 CC chaotropic agent, or by the use of chemical cleavage agents such as  
 CC cyanogen bromide. If the fusion protein has been engineered such that  
 CC there is a protease recognition site between the PBP and the protein of  
 CC interest, the protein can be cleaved from the PBP, which remains bound to

CC the oligosaccharide. Proteins that may be purified using the method of  
 CC the invention include a wide variety of medically and industrially  
 CC important proteins e.g., interleukin 2, factor X, insulin, ligninase. The  
 CC system can also be used for cell separation and/or enrichment of a  
 CC particular cell type; for example, a fusion protein comprising a PBP and  
 CC a ligand of a particular receptor can be used to isolate cells comprising  
 CC that receptor. The system is useful for concentrating a component in a  
 CC mixture, removing contaminants and for preparing solid state reagents for  
 CC diagnostic assays. Oligosaccharide polymers can be obtained inexpensively  
 CC and the water-soluble cellulosic substrates offer a new, cost-effective,  
 CC highly flexible affinity partition system for continuous purification.  
 CC Selective binding of PBP from the oligosaccharide polymer makes it  
 CC suitable for purification of a wide variety of compounds using a single  
 CC oligosaccharide polymer phase separation system. Hence it is unnecessary  
 CC to prepare separate systems for each compound to be separated. Sequences  
 CC AAY81430-Y81431 represent the amino acids sequences encoded by the 5' and  
 CC 3' portions of the SacI-HindIII region of the pTUGAS vector. DNA encoding  
 CC the Cellulomonas fimi endoglucanase C cellulose binding domain (CBD) N1  
 CC (AAY81423) was inserted between the 5' and 3' portions of the SacI-  
 CC HindIII region of the vector  
 XX SQ Sequence 4 AA;

Query Match 61.3%; Score 19; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTR 5  
 | | | | |  
 Db 1 MSTR 4

RESULT 10

AAY06840

ID AAY06840 standard; peptide; 7 AA.

XX AC AAY06840;

XX DT 25-JUN-1999 (first entry)

XX DE Peptide Seq ID No:6 of JP11089576.

XX KW AntiHBs; monoclonal antibody; Epstein Barr virus; EBV; adr type; human;  
 XX KW HBs antigen; hepatitis C.

XX OS Homo sapiens.

XX PN JP11089576-A.

XX PD 06-APR-1999.

XX PF 19-SEP-1997; 97JP-00255705.

XX PR 19-SEP-1997; 97JP-00255705.

XX PA (NISN) NISSHINBO IND INC.

XX DR WPI; 1999-281053/24.

XX PT Anti-HBs monoclonal antibody - produced without the risk of Epstein Barr  
 XX PT virus contamination.

XX PS Claim 4; Page 7; 12pp; Japanese.

XX CC The invention relates to an antiHBs monoclonal antibody having the  
 CC following properties: (A) CDR-3 of H chain variable region; (B) it  
 CC contains no Epstein Barr virus (EBV); (C) it binds at least one adr type  
 CC among human HBs antigens. The antiHBs monoclonal antibody is high in  
 CC antibody titer and has low risk of EBV contamination. It can be used to  
 CC prevent hepatitis C

XX SQ Sequence 7 AA;

Query Match 61.3%; Score 19; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7  
Db |||||:  
3 STRAT 7

## RESULT 11

AA05015  
ID RAY05015 standard; peptide; 7 AA.

AC RAY05015;

DT 16-JUN-1999 (first entry)

XX Tumour antigen antibody light chain CDR2 clone F14.

XX Tumour antigen; antibody; CDR; complementarity determining region;  
KW binding molecule identification; tumour-specific binding polypeptide;  
KW cancer therapy; light chain.

XX Homo sapiens.

XX WO9906834-A2.

XX 11-FEB-1999.

XX 04-AUG-1998; 98WO-US016280.

XX 04-AUG-1997; 97US-00905825.

XX (IXSY-) IXSYS INC.

XX Watkins JD, Huse WD, Wu H;

XX WPI; 1999-153951/13.

XX Identifying binding molecules for ligands, particularly tumour antigens -  
PT by selectively immobilising a population of binding molecules to a solid  
PT support and screening for binding to two or more ligands.

XX Claim 15; Page 57; 80pp; English.

XX This sequence represents a light chain complementarity determining region  
CC (CDR) from a tumour antigen specific antibody. The invention relates to a  
CC method for identifying a binding molecule having selective affinity for a  
CC ligand comprising: (a) selectively immobilising a diverse population of  
CC binding molecules to a solid support; (b) simultaneously contacting the  
CC diverse population immobilised on the solid support with 2 or more  
CC ligands; and (c) determining at least one binding molecule which  
CC selectively binds to one or more of the ligands. The method allows for  
CC the rapid and efficient methods for the identification of binding  
CC molecules which exhibit selective affinity for one or more ligands of  
CC interest. They are used particularly for identifying tumour-specific  
CC binding polypeptides which can be used as targeting agents for cancer  
CC therapy that minimises impact on non-tumour tissues

XX Sequence 7 AA;

Query Match 61.3%; Score 19; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7  
Db |||||:  
3 STRAT 7

## RESULT 12

ABP62370  
ID ABP62370 standard; peptide; 7 AA.

XX ABP62370;  
AC 10-OCT-2002 (first entry)  
XX Human immunopeptide to HCV E2 glycoprotein light chain CDR #47.  
XX Viricide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
KW NS3 protein; viral infection.

XX Homo sapiens.

XX WO200259340-A1.

XX 01-AUG-2002.

XX 25-JAN-2002; 2002WO-US002303.

XX 26-JAN-2001; 2001US-0264451P.

XX (SCRI ) SCRIPPS RES INST.

XX Maruyama T, Jones IM, Burton DR, Fox RI;

XX WPI; 2002-599801/64.

XX New human immunopolypeptide with binding specificity for certain envelope  
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for  
PT diagnosing or treating patients having or suspected of having HCV  
PT infection.

XX Claim 1; Fig 17; 308pp; English.

XX The present invention relates to human immunopolypeptides, produced by a  
CC phage transfected cell library. The present sequence is one such  
CC immunopolypeptide. The immunopolypeptides have binding specificity for  
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
CC virus (HCV). E2 glycoprotein is believed to be responsible for target  
CC cell binding and contains neutralising epitopes, while NS3 is thought to  
CC be involved in the replication of HCV. The immunopolypeptides are useful  
CC for diagnosing and treating a patient having or suspected to be having  
CC HCV infection

XX Sequence 7 AA;

Query Match 61.3%; Score 19; DB 5; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7  
Db |||||:  
3 STRAT 7

## RESULT 13

ABP62382  
ID ABP62382 standard; peptide; 7 AA.

XX ABP62382;

XX 10-OCT-2002 (first entry)

XX Human immunopeptide to HCV E2 glycoprotein light chain CDR #59.

XX Viricide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
KW NS3 protein; viral infection.

XX Homo sapiens.

XX WO200259340-A1.

```

PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002303.
XX
PR 26-JAN-2001; 2001US-0264451P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX WPI; 2002-599801/64.
XX
DR
XX
PT New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
PS Claim 1; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
SQ Sequence 7 AA;

Query Match 61.3%; Score 19; DB 5; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
Db ||||:
3 STRAT 7

RESULT 15
ADC82748
ID ADC82748 standard; peptide; 7 AA.
XX
AC ADC82748;
XX
DT 01-JAN-2004 (first entry)
XX
DE CDR region #13 in light chain of human Fab fragment.
XX
KW Binding molecule; selective affinity; ligand;
KW anti-immunoglobulin reagent; phage expressed antibody library;
KW tumour antigen; complementarity determining region; CDR; human disease;
KW cellular pathology; human; Fab; light chain.
XX
OS Homo sapiens.
XX
PN US2003044772-A1.
XX
PD 06-MAR-2003.
XX
PF 15-OCT-2001; 2001US-00977797.
XX
PR 04-AUG-1997; 97US-0113667P.
PR 04-AUG-1998; 98US-00129026.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Watkins JD, Huse WD, Wu H;
XX
DR WPI; 2003-625402/59.
DR N-PSDB; ADC82747.
XX
PT Identifying binding molecules having selective affinity for ligands for
PT discovering reagents for treating diseases, by contacting solid support
PT coated with anti-immunoglobulin reagent to a phage expressed antibody
PT library.
XX
PS Example 5; Page 15; 26pp; English.
XX
CC The present invention relates to a method for identifying a binding
CC molecule having selective affinity for a ligand. The method involves
CC providing a solid support coated with an anti-immunoglobulin reagent, and
CC a phage expressed antibody library, and contacting the solid support to
CC the phage expressed antibody library. The invention also discloses a
CC method for identifying an antibody having selective affinity for a
CC tumour, and a complementarity determining region (CDR) of an antibody
CC selective for a tumour antigen. The methods of the invention are useful

```

CC for identifying a binding molecule having selective affinity for a  
CC ligand, for the discovery of specific reagents for diagnosis and  
CC treatment of human diseases, for identifying binding molecules to, for  
CC example tumour cells or other cellular pathologies for the selective  
CC targeting of therapeutic agents, or for the identification of binding  
CC molecules to normal or diseased tissues for the selective targeting of,  
CC for example diagnostic agents such as imaging reagents. The methods are  
CC rapid and efficient for the identification of binding molecules which  
CC exhibit selective affinity for one or more ligands of interest. The  
CC methods allow the simultaneous screening of multiple binding molecules  
CC against multiple ligands of interest. Moreover, very little information  
CC is required regarding the identity or function of either the binding  
CC molecule or the ligand. For example diverse populations of binding  
CC molecules can be simultaneously screened against diverse populations of  
CC ligands to rapidly identify numerous molecules exhibiting a desired  
CC binding specificity. The methods provide improved sensitivity and  
CC specificity of detection through the selective immobilisation of the  
CC binding molecule population on a solid support. The present sequence  
CC represents a CDR region in the light chain of human Fab fragment.

XX

SQ Sequence 7 AA;

Query Match 61.3%; Score 19; DB 7; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7  
|||:  
Db 3 STRAT 7

Search completed: April 18, 2005, 14:57:35  
Job time : 169 secs



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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:00:54 ; Search time 130 Seconds  
(without alignments)  
17.897 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370693 residues

Total number of hits satisfying chosen parameters: 59827

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	31	100.0	7	10	US-09-940-727B-23
2	31	100.0	7	10	US-09-940-727B-23
3	31	100.0	7	10	US-09-940-727B-29
4	28	90.3	7	10	US-09-940-727B-20
5	27	87.1	7	10	US-09-940-727B-80
6	22	71.0	7	10	US-09-563-222-9
7	22	71.0	7	16	US-10-783-950-9
8	20	64.5	7	10	US-09-972-656-22
9	19	61.3	7	10	US-09-977-797A-30
10	19	61.3	7	16	US-10-396-578-66
11	19	61.3	7	17	US-10-783-311-161
12	19	61.3	7	17	US-10-783-311-185
13	19	61.3	7	17	US-10-783-311-249

14	19	61.3	7	17	US-10-783-311-329
15	19	61.3	7	17	US-10-863-729-30
16	19	61.3	7	17	US-10-863-355-6
17	19	61.3	7	17	US-10-726-332-171
18	19	61.3	7	17	US-10-726-332-174
19	18	58.1	7	10	US-09-977-797A-32
20	18	58.1	7	15	US-10-418-182-94
21	18	58.1	7	16	US-10-663-244-123
22	18	58.1	7	16	US-10-663-244-123
23	18	58.1	7	16	US-10-396-578-24
24	18	58.1	7	16	US-10-396-578-54
25	18	58.1	7	17	US-10-783-311-89
26	18	58.1	7	17	US-10-725-962-124
27	18	58.1	7	17	US-10-725-962-126
28	18	58.1	7	17	US-10-726-332-168
29	18	58.1	7	17	US-10-726-332-177
30	18	58.1	7	17	US-10-726-332-207
31	17	54.8	7	9	US-09-749-831-5
32	17	54.8	7	9	US-09-828-708-43
33	17	54.8	7	9	US-09-828-708-46
34	17	54.8	7	9	US-09-249-011A-18
35	17	54.8	7	10	US-09-563-222-15
36	17	54.8	7	10	US-09-563-222-27
37	17	54.8	7	10	US-09-972-656-15
38	17	54.8	7	10	US-09-995-529-22
39	17	54.8	7	10	US-09-995-529-22
40	17	54.8	7	11	US-09-995-529-22
41	17	54.8	7	13	US-10-146-305-10
42	17	54.8	7	14	US-10-144-644-11
43	17	54.8	7	14	US-10-071-962-19
44	17	54.8	7	14	US-10-371-404-34
45	17	54.8	7	15	US-10-156-214A-293

#### ALIGNMENTS

##### RESULT 1

US-09-940-727B-23  
; Sequence 23, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940, 727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-23

Query Match 100.0%; Score 31; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7

Db 1 LMSTRAS 7

##### RESULT 2

US-09-940-727B-26  
; Sequence 26, Application US/09940727B

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; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-26

Query Match          100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 3
US-09-940-727B-29
; Sequence 29, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-29

Query Match          100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 4
US-09-940-727B-20
; Sequence 20, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-20

Query Match          100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 5
US-09-940-727B-80
; Sequence 80, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: MISC.FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: any amino acid
US-09-940-727B-80

Query Match          87.1%; Score 27; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 6
US-09-563-222-9
; Sequence 9, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
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; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-563-222-9

Query Match

Best Local Similarity 71.0%; Score 22; DB 10; Length 7;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 1 LVSNRAS 7

RESULT 7

US-10-783-950-9

; Sequence 9, Application US/10783950

; Publication No. US20040199945A1

; GENERAL INFORMATION:

; APPLICANT: EPICYTE PHARMACEUTICALS, INC.

; APPLICANT: HIATT, ANDREW C.

; APPLICANT: HEIN, MICH B.

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

; FILE REFERENCE: 068904-0501

; CURRENT APPLICATION NUMBER: US/10/783,950

; CURRENT FILING DATE: 2004-02-19

; PRIOR APPLICATION NUMBER: US/09/563,222

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: PCT/US01/14349

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/563,222

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 182

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-783-950-9

Query Match

Best Local Similarity 71.0%; Score 22; DB 16; Length 7;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 1 LVSNRAS 7

RESULT 8

US-09-972-656-22

; Sequence 22, Application US/09972656

; Publication No. US20030099647A1

; GENERAL INFORMATION:

; APPLICANT: Deshpande, Rajendra

; APPLICANT: Tsai, Mei-Mei

; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma

; FILE REFERENCE: A-799

; CURRENT APPLICATION NUMBER: US/09/972,656

; CURRENT FILING DATE: 2001-10-05

; NUMBER OF SEQ ID NOS: 135

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 22

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-972-656-22

Query Match

Best Local Similarity 64.5%; Score 20; DB 10; Length 7;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches

5; Conservative

0; Mismatches

2; Indels

0; Gaps

QY 1 LMSTRAS 7

Db 1 LASNRAS 7

RESULT 9

US-09-977-797A-30

; Sequence 30, Application US/09977797A

; Publication No. US20030044772A1

; GENERAL INFORMATION:

; APPLICANT: Watkins, Jeffrey D.

; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren

; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules

; FILE REFERENCE: AME-06805

; CURRENT APPLICATION NUMBER: US/09/977,797A

; CURRENT FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: 09/129,026

; PRIOR FILING DATE: 1998-08-04

; PRIOR APPLICATION NUMBER: 08/905,825

; PRIOR FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 136

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 30

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-977-797A-30

Query Match

Best Local Similarity 61.3%; Score 19; DB 10; Length 7;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7

Db 3 STRAT 7

RESULT 10

US-10-396-578-66

; Sequence 66, Application US/10396578

; Publication No. US20040191260A1

; GENERAL INFORMATION:

; APPLICANT: Reiter, Yoram

; APPLICANT: Cohen, Cyril J.

; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN

; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES

; FILE REFERENCE: 25563

; CURRENT APPLICATION NUMBER: US/10/396,578

; CURRENT FILING DATE: 2003-03-26

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 66

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Sequence of complementarity determining region of Fab

; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.

US-10-396-578-66

Query Match

Best Local Similarity 61.3%; Score 19; DB 16; Length 7;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7

Db 3 STRAT 7

RESULT 11  
US-10-783-311-161  
; Sequence 161, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 161  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Light Chain amino acid sequence  
US-10-783-311-161

Query Match 61.3%; Score 19; DB 17; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7  
Db 3 STRAT 7

RESULT 12  
US-10-783-311-185  
; Sequence 185, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 185  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Light Chain amino acid sequence  
US-10-783-311-185

Query Match 61.3%; Score 19; DB 17; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7  
Db 3 STRAT 7

RESULT 13  
US-10-783-311-249  
; Sequence 249, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001

; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 249  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Light Chain amino acid sequence  
US-10-783-311-249

Query Match 61.3%; Score 19; DB 17; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7  
Db 3 STRAT 7

RESULT 14  
US-10-783-311-329  
; Sequence 329, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 329  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Light Chain amino acid sequence  
US-10-783-311-329

Query Match 61.3%; Score 19; DB 17; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7  
Db 3 STRAT 7

RESULT 15  
US-10-863-729-30  
; Sequence 30, Application US/10863729  
; Publication No. US20050013819A1  
; GENERAL INFORMATION:  
; APPLICANT: Carles-Kinch, Kelly  
; APPLICANT: Kinch, Michael S.  
; TITLE OF INVENTION: USE OF EphA4 AND MODULATOR OF EphA4 FOR CANCER  
; FILE REFERENCE: 10271-117-999  
; CURRENT APPLICATION NUMBER: US/10/863,729  
; CURRENT FILING DATE: 2004-06-07  
; PRIOR APPLICATION NUMBER: 60/476,909  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: 60/503,356  
; PRIOR FILING DATE: 2003-09-16  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CDR2 of VL region of EA44
US-10-863-729-30

Query Match      61.3%; Score 19; DB 17; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 STRAS 7
      ||||:
Db      3 STRAT 7

Search completed: April 18, 2005, 15:13:19
Job time : 131 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:48:09 ; Search time 40 Seconds  
(without alignments)  
13.064 Million cell updates/sec

Title: US-09-674-716B-5  
Perfect score: 31  
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 61165

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	2	US-08-672-345C-23
2	31	100.0	7	2	US-08-672-345C-26
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4	31	100.0	7	3	US-09-214-095D-23
5	31	100.0	7	3	US-09-214-095D-26
6	31	100.0	7	3	US-09-214-095D-29
7	28	90.3	7	2	US-08-672-345C-20
8	28	90.3	7	3	US-09-214-095D-20
9	27	87.1	7	2	US-08-672-345C-80
10	27	87.1	7	3	US-09-214-095D-80
11	22	71.0	7	4	US-09-563-222C-9
12	19	61.3	7	4	US-08-685-808-9
13	19	61.3	4	3	US-08-505-860C-9
14	18	58.1	7	1	US-08-353-400-31
15	17	54.8	6	4	US-09-424-712-36
16	17	54.8	7	1	US-08-264-093-25
17	17	54.8	7	1	US-08-467-420A-11
18	17	54.8	7	1	US-08-470-110A-11
19	17	54.8	7	1	US-08-360-125-20
20	17	54.8	7	1	US-08-667-769A-11
21	17	54.8	7	2	US-08-452-724A-34
22	17	54.8	7	2	US-08-450-578-20
23	17	54.8	7	2	US-08-940-371-11
24	17	54.8	7	2	US-09-017-628-20
25	17	54.8	7	2	US-09-014-880-20
26	17	54.8	7	3	US-09-100-409A-30
27	17	54.8	7	3	US-08-637-647-11

28. 17 54.8 7 3 US-07-987-264-5 Sequence 5, Appl  
29 17 54.8 7 4 US-08-450-363-20 Sequence 20, Appl  
30 17 54.8 7 4 US-08-453-623-34 Sequence 34, Appl  
31 17 54.8 7 4 US-09-563-222C-15 Sequence 15, Appl  
32 17 54.8 7 4 US-09-563-222C-27 Sequence 27, Appl  
33 17 54.8 7 4 US-09-467-903-20 Sequence 20, Appl  
34 17 54.8 7 4 US-09-830-748B-8 Sequence 8, Appl  
35 17 54.8 7 4 US-09-627-896B-18 Sequence 24, Appl  
36 17 54.8 7 5 PCT-US93-08435-24 Sequence 37, Appl  
37 17 54.8 7 5 PCT-US93-08435-37 Sequence 41, Appl  
38 17 54.8 7 5 PCT-US93-08435-41 Sequence 11, Appl  
39 17 54.8 7 5 PCT-US95-17082A-11 Sequence 3, Appl  
40 16 51.6 4 1 US-07-776-257-3 Sequence 6, Appl  
41 16 51.6 4 4 US-09-509-994-6 Sequence 14, Appl  
42 16 51.6 7 1 US-08-503-062-14 Sequence 90, Appl  
43 16 51.6 7 2 US-08-340-283-90 Sequence 8, Appl  
44 16 51.6 7 3 US-09-084-605B-8 Sequence 1, Appl  
45 16 51.6 7 3 US-09-174-216-1

## ALIGNMENTS

RESULT 1  
US-08-672-345C-23  
; Sequence 23, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-23

Query Match 100.0%; Score 31; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 1 LMSTRAS 7

RESULT 2

US-08-672-345C-26  
; Sequence 26, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-26

Query Match 100.0%; Score 31; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 1 LMSTRAS 7

RESULT 3  
US-08-672-345C-29  
; Sequence 29, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-29

Query Match 100.0%; Score 31; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 1 LMSTRAS 7

RESULT 4  
US-09-214-095D-23  
; Sequence 23, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 23  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-23

Query Match 100.0%; Score 31; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 1 LMSTRAS 7

RESULT 5  
US-09-214-095D-26  
; Sequence 26, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 26  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-26

Query Match 100.0%; Score 31; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 LMSTRAS 7  
Db 1 LMSTRAS 7

## RESULT 6

US-09-214-095D-29  
; Sequence 29, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-29

Query Match 100.0%; Score 31; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 1 LMSTRAS 7

## RESULT 7

US-08-672-345C-20  
; Sequence 20, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-20

Query Match 90.3%; Score 28; DB 2; Length 7;

Best Local Similarity 85.7%; Pred. No. 4.1e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 1 LMSTRAS 7

## RESULT 8

US-09-214-095D-20  
; Sequence 20, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-20

Query Match 90.3%; Score 28; DB 3; Length 7;  
Best Local Similarity 85.7%; Pred. No. 4.1e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
Db 1 LMSTRAS 7

## RESULT 9

US-08-672-345C-80  
; Sequence 80, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-80

US-08-672-345C-80

Query Match 87.1%; Score 27; DB 2; Length 7;  
Best Local Similarity 85.7%; Pred. No. 4.1e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
|||||  
DB 1 LMSTRAS 7

RESULT 10

US-09-214-095D-80  
; Sequence 80, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 80  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Murinae gen.sp.  
; FEATURE:  
; NAME/KEY: CHAIN  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: X at position 6 represents any amino acid  
US-09-214-095D-80

Query Match 87.1%; Score 27; DB 3; Length 7;  
Best Local Similarity 85.7%; Pred. No. 4.1e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
|||||  
DB 1 LMSTRAS 7

RESULT 11

US-09-563-222C-9  
; Sequence 9, Application US/09563222C  
; Patent No. 6696620  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICHAEL B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/09/563,222C  
; CURRENT FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-563-222C-9

Query Match 71.0%; Score 22; DB 4; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.1e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
|:|:|:|  
DB 1 LVSNRAS 7

Query Match 87.1%; Score 27; DB 2; Length 7;  
Best Local Similarity 85.7%; Pred. No. 4.1e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7  
|||||  
DB 1 LMSTRAS 7

RESULT 12

US-08-685-808-9  
; Sequence 9, Application US/08685808  
; Patent No. 6048715  
; GENERAL INFORMATION:  
; APPLICANT: HAYNES, CHARLES A., et al  
; TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED  
; TITLE OF INVENTION: ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RAE-VENTER LAW GROUP  
; STREET: 260 Sheridan Ave., Ste. 440  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,808  
; FILING DATE: 24-JULY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/505,860  
; FILING DATE: 24-JULY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rae-Venter, Barbara  
; REGISTRATION NUMBER: 32,750  
; REFERENCE/DOCKET NUMBER: CDDT.017.01US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 328-4400  
; TELEFAX: (650) 328-4477  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: no  
US-08-685-808-9

Query Match 61.3%; Score 19; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTR 5  
||||  
DB 1 MSTR 4

RESULT 13

US-08-505-860C-9  
; Sequence 9, Application US/08505860C  
; Patent No. 6174700  
; GENERAL INFORMATION:  
; APPLICANT: HAYNES, CHARLES A., et al  
; TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED  
; TITLE OF INVENTION: ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RAE-VENTER LAW GROUP  
; STREET: 260 Sheridan Ave., Ste. 440  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/505,860C  
;; FILING DATE: 24-JULY-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Rae-Venter, Barbara  
;; REGISTRATION NUMBER: 32,750  
;; REFERENCE/DOCKET NUMBER: CBDDT.017.000US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (650) 328-4400  
;; TELEFAX: (650) 328-4477  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: no  
;; US-08-505-860C-9

Query Match 61.3%; Score 19; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTR 5  
|||  
Db 1 MSTR 4

RESULT 14  
US-08-353-400-31  
; Sequence 31, Application US/08353400  
; Patent No. 5665357  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 37  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/353,400  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9324819.3  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9411089.7  
; FILING DATE: 03-JUN-1994  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-353-400-31

Query Match 58.1%; Score 18; DB 1; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7  
|||  
Db 3 STRTS 7

RESULT 15  
US-09-424-712-36  
; Sequence 36, Application US/09424712  
; Patent No. 6620587  
; GENERAL INFORMATION:  
; APPLICANT: TAUSSIG, Michael John  
; APPLICANT: HE, Mingyue  
; TITLE OF INVENTION: RIBOSOME COMPLEXES AS SELECTION PARTICLES FOR IN VITRO DISPLAY A  
; TITLE OF INVENTION: EVOLUTION OF PROTEINS  
; FILE REFERENCE: 37945-0017  
; CURRENT APPLICATION NUMBER: US/09/424,712  
; CURRENT FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/GB98/01564  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: GB 9804195.7  
; PRIOR FILING DATE: 1998-02-28  
; PRIOR APPLICATION NUMBER: GB 9724850.4  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: GB 9710829.4  
; PRIOR FILING DATE: 1997-05-28  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-424-712-36

Query Match 54.8%; Score 17; DB 4; Length 6;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7  
|||  
Db 2 STRS 6

Search completed: April 18, 2005, 15:01:30  
Job time : 41 secs

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G30538  
Ig kappa chain V region (253.1552) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #H  
C:Accession: G30538  
R:Clatlin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988  
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae  
A;Reference number: A30534; MUID:89035545; PMID:3141511  
A;Accession: G30538  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-74 <CIA>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 42; DB 2; Length 74;  
Best Local Similarity 88.9%; Pred. No. 0.23;  
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 QQLVEYPT 9  
| | | | | | | |  
DB 63 QQLVEYPT 71

RESULT 3  
KWS16  
Ig kappa chain V region (M167) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 09-Jul-2004  
C;Accession: A01908  
R;Rudikoff, S.; Potter, M.  
Biochemistry 17, 2703-2707, 1978  
A;Title: Kappa-Chain variable region from M167, a phosphorylcholine binding myeloma protein  
A;Reference number: A01908; MUID:79000273; PMID:99160  
A;Accession: A01908  
A;Molecule type: protein  
A;Residues: 1-112 <RUD>  
A;Cross-references: UNIPROT:P01626  
C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;16-95/Domain: immunoglobulin homology <IMM>  
F;23-93/Disulfide bonds: #status predicted

Query Match 87.5%; Score 42; DB 1; Length 112;  
Best Local Similarity 88.9%; Pred. No. 0.23;  
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 QQLVEYPT 9  
| | | | | | | |  
DB 94 QQLVEYPT 102

RESULT 4  
KWS51  
Ig kappa chain V region (M511) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 09-Jul-2004  
C;Accession: A01910  
R;Appella, E.  
Mol. Immunol. 17, 711-718, 1980  
A;Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine-binding myeloma protein  
A;Reference number: A01910; MUID:81052016; PMID:6776396  
A;Accession: A01910  
A;Molecule type: protein  
A;Residues: 1-113 <APP>  
A;Cross-references: UNIPROT:P01628  
C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;16-95/Domain: immunoglobulin homology <IMM>  
F;23-93/Disulfide bonds: #status predicted

Query Match 87.5%; Score 42; DB 1; Length 113;

Best Local Similarity 88.9%; Pred. No. 0.23;  
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 QQLVEYPT 9  
| | | | | | | |  
DB 94 QQLVEYPT 102

RESULT 5  
KWS67  
Ig kappa chain precursor V region (VK167) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
C;Accession: A01909  
R;Selsing, E.; Storb, U.  
Cell 25, 47-58, 1981  
A;Title: Somatic mutation of immunoglobulin light-chain variable-region genes.  
A;Reference number: A01909; MUID:82002223; PMID:6791832  
A;Accession: A01909  
A;Molecule type: DNA  
A;Residues: 1-120 <SEL>  
A;Cross-references: UNIPROT:P01627  
A;Note: the sequence was determined from the germline gene  
C;Genetics:  
A;Introns: 17/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>  
F;36-115/Domain: immunoglobulin homology <IMM>  
F;43-113/Disulfide bonds: #status predicted

Query Match 77.1%; Score 37; DB 1; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPT 7  
| | | | | | | |  
DB 114 QQLVEYPT 120

RESULT 6  
A85363  
Probable calmodulin-binding protein [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: A85363  
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory  
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A;Reference number: A85001; MUID:20083488; PMID:10617198  
A;Accession: A85363  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-467 <STO>  
A;Cross-references: UNIPROT:O65550; GB:NC\_001268; NID:97270002; PIDN:CAB79818.1; GSPDB:1CAB79818.1  
C;Genetics:  
A;Gene: At4g31000  
A;Map position: 4

Query Match 77.1%; Score 37; DB 2; Length 467;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 QQLVEYPT 8  
| | | | | | | |  
DB 334 QQLVEYPT 341

RESULT 7  
S36277

Ig lambda chain V region (clone alpha-FOG1-G8) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: S36277  
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MUID:93178448; PMID:7679990  
A:Accession: S36277  
A>Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-108 <GFI>  
A:Cross-references: EMBL:Z18829; NID:933417; PIDN:CAA79281.1; PID:9939910  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 36; DB 2; Length 108;  
Best Local Similarity 66.7%; Pred. No. 3.8;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
|||: |||  
Db 89 QQLISVPLT 97

RESULT 8  
T38148  
phosphatidyl synthase - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T38148  
R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z21774  
A:Accession: T38148  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-570 <PEA>  
A:Cross-references: UNIPROT:O13899; EMBL:Z99295; PIDN:CA16578.1; GSPDB:GN00066; SPDB:SH  
A:Experimental source: strain 972h-; cosmid C22A12  
C:Genetics:  
A:Gene: SPDB:SPAC22A12.08c  
A:Map position: 1  
A:Introns: 43/2; 62/2; 227/2; 483/1

Query Match 75.0%; Score 36; DB 2; Length 570;  
Best Local Similarity 77.8%; Pred. No. 23;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
|||: |||  
Db 547 QQLVEYSFT 555

RESULT 9  
B29775  
Ig kappa chain precursor V region (mouse 24.1) - shrew mouse  
C:Species: Mus pahari  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 21-Jan-2000  
C:Accession: B29775  
R:Jouvin-Marche, E.; Rudikoff, S.  
Immunogenetics 24, 191-201, 1986  
A:Title: Evolution of a V-kappa gene family  
A:Reference number: A91751; MUID:87006895; PMID:3093373  
A:Accession: B29775  
A:Molecule type: DNA  
A:Residues: 1-120 <JOU>  
A:Cross-references: GB:M15553; NID:9197470; PIDN:AAA39037.1; PID:gl97471  
A>Note: this sequence was determined from the germline gene  
C:Genetics:  
A:Introns: 17/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-120/Product: Ig kappa chain V region 24.1 #status predicted <MAT>  
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 120;  
Best Local Similarity 85.7%; Pred. No. 6.9;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7  
|||: |||  
Db 114 QQLVEYP 120

RESULT 10  
A86371  
hypothetical protein F508.25 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: A86371  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.W.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: A86371  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-480 <STO>  
A:Cross-references: UNIPROT:Q9ZUC5; GB:AE005172; NID:94056452; PIDN:AAC98025.1; GSPDB:G1  
C:Genetics:  
A:Map position: 1

Query Match 72.9%; Score 35; DB 2; Length 480;  
Best Local Similarity 85.7%; Pred. No. 30;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQLVEYPP 8  
|||: |||  
Db 269 QQLVEYPP 275

RESULT 11  
D82100  
meat protein VC2242 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C:Species: Vibrio cholerae  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: D82100  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,  
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: D82100  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-440 <HEI>  
A:Cross-references: UNIPROT:Q9KFX0; GB:AE004296; GB:AE003852; NID:99656799; PIDN:AAF953  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC2242  
A:Map position: 1  
C:Superfamily: Cell cycle protein MesJ

Query Match 70.8%; Score 34; DB 2; Length 440;  
Best Local Similarity 75.0%; Pred. No. 45;

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Matches      6;  Conservative      0;  Mismatches      2;  Indels      0;  Gaps      0;

Qy      1  QQLVEYPP 8
      ||| |||
Db      10  QQLARYPP 17

RESULT 12
D89903
hypothetical protein SALL31 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89903
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89503
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-586 <KUR>
A;Cross-references: UNIPROT:Q99UI4; GB:BA0000018; PID:g13701089; PIDN:BAB42384.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: SALL31
C;Superfamily: Halobacterium halobium 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid fer
Query Match      70.8%; Score 34; DB 2; Length 586;
Best Local Similarity 75.0%; Pred. No. 61;
Matches      6;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

Qy      2  QQLVEYPP 9
      ||| |||
Db      109  QQLLEPPT 116

RESULT 13
S76367
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Accession: S76367
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R;Kanehisa, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76367
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-722 <KAN>
A;Cross-references: UNIPROT:Q55690; EMBL:D64000; GB:AB001339; MUID:g1001484; PIDN:BAA1021
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: glycine-tRNA ligase beta chain
Query Match      70.8%; Score 34; DB 2; Length 722;
Best Local Similarity 85.7%; Pred. No. 76;
Matches      6;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  QQLVEYPP 7
      ||| |||
Db      254  EQLVEYPP 260

RESULT 14
T01906
hypothetical protein T12H20.3 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

```

```

C;Accession: T01906
R;Cotton, M.; Graves, T.; Sutterer, C.; Modde, T.
submitted to the EMBL Data Library, July 1998.
A;Description: The sequence of A. thaliana T12H20.
A;Reference number: Z14453
A;Accession: T01906
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1074 <COT>
A;Cross-references: UNIPROT:O82491; EMBL:AF080119; MUID:g3600029; PID:g3600033
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Note: T12H20.3
Query Match      70.8%; Score 34; DB 2; Length 1074;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches      5;  Conservative      2;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      2  QQLVEYPP 8
      ||| |||
Db      853  ELIEYPP 859

RESULT 15
D26317
Ig kappa chain V region (H37-84) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C;Accession: D26317
R;Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a d
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: D26317
A;Molecule type: DNA
A;Residues: 1-112 <CAT>
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
Query Match      68.8%; Score 33; DB 2; Length 112;
Best Local Similarity 75.0%; Pred. No. 17;
Matches      6;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

Qy      2  QQLVEYPP 9
      ||| |||
Db      95  QHLEYPP 102

Search completed: April 18, 2005, 14:23:25
Job time : 19.7907 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:57:43 ; Search time 81.8372 Seconds  
(without alignments)  
56.316 Million cell updates/sec

Title: US-09-674-716B-7  
Perfect score: 48  
Sequence: 1 QQLVEVPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	89.6	383	1	CYB_APILI
2	42	87.5	112	1	KV2A MOUSE
3	42	87.5	113	1	KV2C MOUSE
4	40	83.3	349	2	Q85TH4
5	39	81.2	506	2	Q87RR4
6	38	79.2	368	2	Q6PRB0
7	38	79.2	532	2	Q6LTX1
8	37	77.1	120	1	KV2B MOUSE
9	37	77.1	278	2	Q8W454
10	37	77.1	467	2	Q65550
11	37	77.1	609	2	Q8H816
12	36	75.0	84	2	Q9B313
13	36	75.0	247	2	Q9MP34
14	36	75.0	330	2	Q6YAK6
15	36	75.0	331	2	Q6YAK5
16	36	75.0	352	2	Q9XNV8
17	36	75.0	371	2	Q8M293
18	36	75.0	377	2	Q9XNV0
19	36	75.0	377	2	Q9XNV5
20	36	75.0	379	1	CYB_AKQAE
21	36	75.0	379	1	CYB_AKQJE
22	36	75.0	379	1	CYB_AKQJU
23	36	75.0	379	1	CYB_AKQKO
24	36	75.0	379	1	CYB_AKQMO
25	36	75.0	379	1	CYB_AKOPU
26	36	75.0	379	1	CYB_AKOPR
27	36	75.0	379	1	CYB_AKOSI
28	36	75.0	379	1	CYB_AKOSU
29	36	75.0	379	1	CYB_AKOTB
30	36	75.0	379	1	CYB_AKOTO
31	36	75.0	379	1	CYB_MICMI

32 36 75.0 379 2 Q8LU40  
33 36 75.0 379 2 Q8M290  
34 36 75.0 379 2 Q8M292  
35 36 75.0 379 2 Q8M294  
36 36 75.0 379 2 Q8M295  
37 36 75.0 379 2 Q8M296  
38 36 75.0 379 2 Q8M297  
39 36 75.0 379 2 Q8M299  
40 36 75.0 379 2 Q8M2A0  
41 36 75.0 379 2 Q8M2A0  
42 36 75.0 379 2 Q8M2A0  
43 36 75.0 379 2 Q8M2A0  
44 36 75.0 379 2 Q8M2A0  
45 36 75.0 379 2 Q8M2A0

#### ALIGNMENTS

##### RESULT 1

CYB\_APILI STANDARD; PRT; 383 AA.  
AC P34845;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cytochrome b.  
GN Name-MTCVB; Synonyms-COB, CYTB;  
OS Apis mellifera ligustica (Common honeybee).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apoidea; Apoidea;  
OC Apidae; Apis.  
OX NCBI\_TaxID=7469;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thorax;  
RX MEDLINE=92261310; PubMed=1533894;  
RA Crozier R.H., Crozier Y.C.;  
RT "The cytochrome b and ATPase genes of honeybee mitochondrial DNA.";  
RL Mol. Biol. Evol. 9:474-482(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thorax;  
RX MEDLINE=93114603; PubMed=8417993;  
RA Crozier R.H., Crozier Y.C.;  
RT "The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization.";  
RL Genetics 133:97-117(1993).  
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).  
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By similarity).  
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).  
CC -!- SIMILARITY: Belongs to the cytochrome b family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).  
DR EMBL; L06178; AAB96809.1; -;  
DR EMBL; M87052; -; NOT ANNOTATED\_CDS.  
DR PIR; C42622; C42622.  
DR InterPro; IPR005798; Cytb\_b6\_C.

DR InterPro; IPR005797; Cytb b6 N.  
DR Pfam; PF00032; Cytochrom B\_C; 1.  
DR Pfam; PF00033; Cytochrom B\_N; 1.  
DR PROSITE; PS1003; CYTB\_CTER; 1.  
DR PROSITE; PS1002; CYTB\_NTER; 1.  
KW Electron transport; Heme; Mitochondrion; Respiratory chain;  
KW Transmembrane.  
FT METAL 85 Iron 1 (heme b562 axial ligand).  
FT METAL 99 Iron 2 (heme b566 axial ligand).  
FT METAL 184 Iron 1 (heme b562 axial ligand).  
FT METAL 198 Iron 2 (heme b566 axial ligand).  
SQ SEQUENCE 383 AA; 45256 MW; A140A05E6053C2D5 CRC64;  
  
Query Match 89.6%; Score 43; DB 1; Length 383;  
Best Local Similarity 77.8%; Pred. No. 5.1;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QQLVEYPT 9  
Db 341 QQLIEYPT 349  
  
RESULT 2  
KV2A MOUSE  
ID KV2A MOUSE STANDARD; PRT; 112 AA.  
AC P01626;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-II region MOPC 167.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79000273; PubMed=99160;  
RA Rudikoff S., Potter M.;  
RT "Kappa Chain variable region from M167, a phosphorylcholine binding  
myeloma protein."  
RL Biochemistry 17:2703-2707(1978).  
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
binds phosphorylcholine. The sequence of the V region of the heavy  
chain has also been determined.  
DR PIR; A01908; KWS16.  
DR HSPF; Q8K0F8; 1KN2.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 39 Complementarity-determining-1.  
FT DOMAIN 40 54 Framework-2.  
FT DOMAIN 55 61 Complementarity-determining-2.  
FT DOMAIN 62 93 Complementarity-determining-3.  
FT DOMAIN 94 102 Complementarity-determining-4.  
FT DOMAIN 103 112 By similarity.  
FT DISULFID 23 93  
FT NON TER 112 112  
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;  
  
Query Match 87.5%; Score 42; DB 1; Length 112;  
Best Local Similarity 88.9%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 QQLVEYPT 9  
Db 94 QQLVEYPT 102  
  
RESULT 3  
KV2A MOUSE  
ID KV2A MOUSE STANDARD; PRT; 112 AA.  
AC P01626;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-II region MOPC 167.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79000273; PubMed=99160;  
RA Rudikoff S., Potter M.;  
RT "Kappa Chain variable region from M167, a phosphorylcholine binding  
myeloma protein."  
RL Biochemistry 17:2703-2707(1978).  
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
binds phosphorylcholine. The sequence of the V region of the heavy  
chain has also been determined.  
DR PIR; A01908; KWS16.  
DR HSPF; Q8K0F8; 1KN2.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 39 Complementarity-determining-1.  
FT DOMAIN 40 54 Framework-2.  
FT DOMAIN 55 61 Complementarity-determining-2.  
FT DOMAIN 62 93 Complementarity-determining-3.  
FT DOMAIN 94 102 Complementarity-determining-4.  
FT DOMAIN 103 112 By similarity.  
FT DISULFID 23 93  
FT NON TER 112 112  
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;  
  
Query Match 87.5%; Score 42; DB 1; Length 112;  
Best Local Similarity 88.9%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 QQLVEYPT 9  
Db 94 QQLVEYPT 102  
  
RESULT 4  
KV2C MOUSE  
ID KV2C MOUSE STANDARD; PRT; 113 AA.  
AC P01628;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-II region MOPC 511.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81052016; PubMed=6776396; DOI=10.1016/0161-5890(80)90140-6;  
RA Appella E.;  
RT "Amino acid sequence of the light chain variable region of M511, a  
phosphorylcholine-binding murine myeloma protein."  
RL Mol. Immunol. 17:711-718(1980).  
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
binds phosphorylcholine.  
DR PIR; A01910; KWS51.  
DR HSPF; Q8K0F8; 1KN2.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 39 Complementarity-determining-1.  
FT DOMAIN 40 54 Framework-2.  
FT DOMAIN 55 61 Complementarity-determining-2.  
FT DOMAIN 62 93 Complementarity-determining-3.  
FT DOMAIN 94 102 Complementarity-determining-4.  
FT DOMAIN 103 112 By similarity.  
FT DISULFID 23 93  
FT NON TER 113 113  
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;  
  
Query Match 87.5%; Score 42; DB 1; Length 113;  
Best Local Similarity 88.9%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 QQLVEYPT 9  
Db 94 QQLVEYPT 102  
  
RESULT 4  
KV2C MOUSE  
ID KV2C MOUSE STANDARD; PRT; 349 AA.  
AC P01628;  
DT 21-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DE Cytochrome b.  
GN Name=Cytb;  
OS Melipona bicolor.  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
OC Apidae; Melipona.  
OX NCBI\_TaxID=60889;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Silvestre D., Arias M.C.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBSJ databases.  
CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase  
complex (complex III or cytochrome b-c1 complex), which is a  
respiratory chain that generates an electrochemical potential  
coupled to ATP synthesis (By similarity).  
CC -1- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or  
b562) is low-potential and absorbs at about 562 nm, and heme 2 (or

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CC BH or b566) is high-potential and absorbs at about 566 nm (By
CC similarity).
CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -1- SIMILARITY: Belongs to the cytochrome b family.
DR EMBL: AF466146; AA018422.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005746; C: mitochondrial electron transport chain; IEA.
DR GO: GO:0005739; C: mitochondrion; IEA.
DR GO: GO:0016491; F: oxidoreductase activity; IEA.
DR GO: GO:0006118; P: electron transport; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR005798; Cytb_b6_C.
DR InterPro: IPR005797; Cytb_b6_N.
DR Pfam: PF00032; Cytochrom_B_C; 1.
DR Pfam: PF00033; Cytochrom_B_N; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; UNKNOWN_1.
DR PROSITE: PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane; Transport.
SQ SEQUENCE 349 AA; 41464 MW; 9B1DC3A6927DADD3 CRC64;

Query Match 83.3%; Score 40; DB 2; Length 349;
Best Local Similarity 75.08; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQLVEYPPT 9
DB |||:|||||
311 QMIEYPPT 318

RESULT 5
Q87RR4 PRELIMINARY; PRT; 506 AA.
AC Q87RR4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VP0713.
GN OrderedLocustNames=VP0713;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL: AP005075; BAC58976.1; -.
DR GO: GO:0003677; F: DNA binding; IEA.
DR GO: GO:0001556; P: two-component response regulator activity; IEA.
DR GO: GO:0000160; P: two-component signal transduction system (p. . .; IEA.
DR InterPro: IPR009059; bi_resp_regltr_C.
DR InterPro: IPR001867; Trans_reg_C.
DR Pfam: PF00486; Trans_reg_C; 1.
DR ProDom: PD000329; Trans_reg_C; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 506 AA; 57784 MW; 7B566E691D449223 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 506;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB |||:|||||
209 QQQVEYPPT 217

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## RESULT 6

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Q6PNB0 PRELIMINARY; PRT; 368 AA.
ID Q6PNB0;
AC Q6PNB0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome b.
GN Names=CyTB;
OS Steineriema carpopapseae.
OC Mitochondrion.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Steinernematidae; Steinernema.
OX NCBI_TaxID=34508;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Breton;
RA Montiel R., Medeiros J., Lucena M., Simoes N.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY591323; AAT00527.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005746; C: mitochondrial electron transport chain; IEA.
DR GO: GO:0005739; C: mitochondrion; IEA.
DR GO: GO:0016491; F: oxidoreductase activity; IEA.
DR GO: GO:0006118; P: electron transport; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR005798; Cytb_b6_C.
DR InterPro: IPR005797; Cytb_b6_N.
DR Pfam: PF00032; Cytochrom_B_C; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; UNKNOWN_1.
DR PROSITE: PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
KW Mitochondrion.
SQ SEQUENCE 368 AA; 43163 MW; 695BCB3789DBACE CRC64;

Query Match 79.2%; Score 38; DB 2; Length 368;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB |||:|||||
331 QCMVEYPPT 339

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## RESULT 7

```

Q6LTX1 PRELIMINARY; PRT; 532 AA.
ID Q6LTX1;
AC Q6LTX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein VP0713.
GN Names=VP0713; OrderedLocustNames=PBPPA0841;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RC Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR378665; CAG19254.1; -.
DR GO: GO:0003677; F: DNA binding; IEA.
DR GO: GO:0001556; P: two-component response regulator activity; IEA.
DR GO: GO:0000160; P: two-component signal transduction system (p. . .; IEA.
DR InterPro: IPR009059; bi_resp_regltr_C.
DR InterPro: IPR001867; Trans_reg_C.
DR Pfam: PF00486; Trans_reg_C; 1.
DR ProDom: PD000329; Trans_reg_C; 1.

```

KW Complete proteome: Hypothetical protein.  
SQ SEQUENCE 532 AA; 60884 MW; D863B4B91ED55249 CRC64;

Query Match 79.2%; Score 38; DB 2; Length 532;  
Best Local Similarity 66.7%; Pred. No. 70;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYFP 9  
|||:|:|  
DB 235 QQLVEYFP 243

RESULT 8  
KV2B\_MOUSE STANDARD; PRT; 120 AA.  
AC P01627;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region VKappa167 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82002223; PubMed=6791832; DOI=10.1016/0092-8674(81)90230-0;  
RA Selsing E., Storb U.;  
RT "Somatic mutation of immunoglobulin light-chain variable-region genes";  
RL Cell 25:47-58(1981).  
CC -----  
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CC -----  
CC EMBL; J00562; AAA39032.1; -;  
CC EMBL; K02415; AAA39051.1; -;  
CC PIR; A01909; KVM567.  
CC HSP; P01751; INQB.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003596; Ig\_v.  
CC Pfam; PF00047; Ig; 1.  
CC SMART; SM00406; IGV; 1.  
CC PROSITE; PS00835; IG\_LIKE; 1.  
CC Immunoglobulin V region; Signal.  
CC SIGNAL 1 20  
CC CHAIN 21 120 Ig kappa chain V-II region VKappa167.  
CC DOMAIN 21 43 Framework-1.  
CC DOMAIN 44 59 Complementarity-determining-1.  
CC DOMAIN 60 74 Framework-2.  
CC DOMAIN 75 81 Complementarity-determining-2.  
CC DOMAIN 82 113 Framework-3.  
CC DOMAIN 114 120 Complementarity-determining-3.  
CC DISULFID 43 113 By similarity.  
CC SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;

Query Match 77.1%; Score 37; DB 1; Length 120;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYFP 7  
|||:|:|  
DB 114 QQLVEYFP 120

RESULT 9  
Q8W454 PRELIMINARY; PRT; 278 AA.  
ID Q8W454

Q8W454;  
AC 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Putative calmodulin-binding protein.  
GN Name=At4g31000;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,  
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
RA Ecker J., Theologis A., Davis R.W.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,  
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
RA Ecker J., Theologis A., Davis R.W.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY062856; AAL32934.1; -;  
DR EMBL; AY114575; AAM47894.1; -;  
SQ SEQUENCE 278 AA; 31406 MW; 398DCFB65C85A836 CRC64;

Query Match 77.1%; Score 37; DB 2; Length 278;  
Best Local Similarity 75.0%; Pred. No. 58;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYFP 8  
|||:|:|  
DB 145 QQLVEYFP 152

RESULT 10  
O65550 PRELIMINARY; PRT; 467 AA.  
AC O65550;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Putative calmodulin-binding protein.  
GN Name=F6118.90; Synonyms=AT4g31000;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansong W., Hoheisel J.,  
RA Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Benes V., Rechmann S., Borkova D., Ansong W., Mewes H.W., Lemcke K.,  
RA Mayer K.F.X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RN [5]

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL022198; CA18193.1; -.  
 DR EMBL; AL161578; CAB79818.1; -.  
 DR PIR; A85363; A85363.  
 SQ SEQUENCE 467 AA; 52831 MW; 4DB1FB318D553B3D CRC64;

Query Match 77.1%; Score 37; DB 2; Length 467;  
 Best Local Similarity 75.0%; Pred. No. 96;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPP 8  
 DB 334 QHLEIYPP 341

## RESULT 11

Q8H816 ID Q8H816 PRELIMINARY; PRT; 609 AA.  
 AC Q8H816  
 DT 01-MAR-2003 (TEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein OJ1743A09.11.  
 GN Name-OJ1743A09.11;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OC NCBI\_TaxID=39947;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Sasaki C.,  
 RA Currie J., Collura K.;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC105364; AAN05331.1; -.  
 DR Gramene; Q8H816; -.  
 DR InterPro; IPR002086; Aldehyd dehydrog.  
 DR InterPro; IPR001810; F-box.  
 DR Pfam; PF00646; F-box; 1.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CVS; UNKNOWN\_1.  
 DR PROSITE; PS00181; PROX; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 609 AA; 68105 MW; AEA195731E08F07C CRC64;

Query Match 77.1%; Score 37; DB 2; Length 609;  
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPP 9  
 DB 569 QQLLEIYPP 577

## RESULT 12

Q9B313 ID Q9B313 PRELIMINARY; PRT; 84 AA.  
 AC Q9B313  
 DT 01-JUN-2001 (TEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE Cytochrome b (Fragment).  
 OS Neoceratodus forsteri (Australian lungfish).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.  
 OC NCBI\_TaxID=7892;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP Frentiu F., Ovenden J.R., Street R.;  
 RA "Australian lungfish (Neoceratodus forsteri) have low genetic  
 RT diversity at allozyme and mitochondrial loci: A conservation alert for  
 RT a living fossil?";  
 RL Conserv. Genet. 0:0-0(2001).

DR EMBL; AF344663; AAK29031.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR InterPro; IPR005798; Cytochrome b; 1.  
 DR Pfam; PF00032; Cytochrome b; 1.  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 84 AA; 9673 MW; 1E7AFAD921592DAC CRC64;

Query Match 75.0%; Score 36; DB 2; Length 84;  
 Best Local Similarity 87.5%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPP 9  
 DB 27 QPVEYPP 34

## RESULT 13

Q9MP34 ID Q9MP34 PRELIMINARY; PRT; 247 AA.  
 AC Q9MP34  
 DT 01-OCT-2000 (TEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE Cytochrome b (Fragment).  
 OS Bothriomyx meridionalis.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Formicidae; Dolichoderinae; Bothriomyx.  
 OC NCBI\_TaxID=121499;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP Chiotis M., Jermin L.S., Crozier R.H.;  
 RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase  
 CC complex (complex III or cytochrome b-c1 complex), which is a  
 CC respiratory chain that generates an electrochemical potential  
 CC coupled to ATP synthesis (By similarity).  
 CC -1- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or  
 CC b562) is low-potential and absorbs at about 562 nm, and heme 2 (or  
 CC BH or b566) is high-potential and absorbs at about 566 nm (By  
 CC similarity).  
 CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,  
 CC cytochrome c1 and the Rieske protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the cytochrome b family.  
 DR EMBL; AF146714; AAF66714.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR005798; Cytochrome b; 1.  
 DR InterPro; IPR005797; Cytochrome b; 1.  
 DR Pfam; PF00032; Cytochrome b; 1.  
 DR Pfam; PF00033; Cytochrome b; 1.  
 DR PROSITE; PS00193; CYTOCHROME B\_QO; UNKNOWN\_1.  
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;  
 KW Transmembrane; Transport.  
 FT NON TER 1  
 SQ SEQUENCE 247 AA; 29263 MW; CC68F8BA0D065B1A CRC64;

Query Match 75.0%; Score 36; DB 2; Length 247;  
 Best Local Similarity 75.0%; Pred. No. 81;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPP 9  
 DB 201 QSIYPP 208

OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea; Alaudidae;  
 OC Spizocorys.  
 OX NCBI\_TaxID=215325;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22480425; PubMed=12590762; DOI=10.1098/rspb.2002.2205;  
 RT Tieleman B.I., Williams J.B., Bloomer P.;  
 RA "Adaptation of metabolism and evaporative water loss along an aridity  
 gradient.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 270:207-214 (2003).  
 CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase  
 CC complex (complex III or cytochrome b-c1 complex), which is a  
 CC respiratory chain that generates an electrochemical potential  
 CC coupled to ATP synthesis (By similarity).  
 CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or  
 CC b562) is low-potential and absorbs at about 562 nm, and heme 2 (or  
 CC BH or b566) is high-potential and absorbs at about 566 nm (By  
 CC similarity).  
 CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,  
 CC cytochrome c1 and the Rieske protein (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome b family.  
 DR EMBL; AY165170; AA060668.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR005798; Cytb\_b6\_C.  
 DR InterPro; IPR005797; Cytb\_b6\_N.  
 DR Pfam; PF00032; Cytochrom\_B\_C; 1.  
 DR Pfam; PF00033; Cytochrom\_B\_N; 1.  
 DR PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 DR PROSITE; PS00193; CYTOCHROME\_B\_QO; UNKNOWN\_1.  
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;  
 KW Transmembrane; Transport.  
 FT NON\_TER 1  
 FT NON\_TER 331  
 SQ SEQUENCE 331 AA; 36761 MW; 91B07FFD83401CAF CRC64;  
 Query Match 75.0%; Score 36; DB 2; Length 331;  
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVPEYPT 9  
 DB 302 QPVEYPT 309  
 Search completed: April 18, 2005, 14:21:54  
 Job time : 83.8372 secs

RESULT 14  
 Q6YAK6 PRELIMINARY; PRT; 330 AA.  
 AC Q6YAK6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cytochrome b (Fragment).  
 GN Name=cytb;  
 OS Galerida magnirostris (large-billed lark).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea; Alaudidae;  
 OC Galerida.  
 OX NCBI\_TaxID=215324;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22480425; PubMed=12590762; DOI=10.1098/rspb.2002.2205;  
 RA Tieleman B.I., Williams J.B., Bloomer P.;  
 RT "Adaptation of metabolism and evaporative water loss along an aridity  
 gradient.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 270:207-214 (2003).  
 CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase  
 CC complex (complex III or cytochrome b-c1 complex), which is a  
 CC respiratory chain that generates an electrochemical potential  
 CC coupled to ATP synthesis (By similarity).  
 CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or  
 CC b562) is low-potential and absorbs at about 562 nm, and heme 2 (or  
 CC BH or b566) is high-potential and absorbs at about 566 nm (By  
 CC similarity).  
 CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,  
 CC cytochrome c1 and the Rieske protein (By similarity).  
 CC -!- SIMILARITY: Belongs to the cytochrome b family.  
 DR EMBL; AY165169; AA060667.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR005798; Cytb\_b6\_C.  
 DR InterPro; IPR005797; Cytb\_b6\_N.  
 DR Pfam; PF00032; Cytochrom\_B\_C; 1.  
 DR Pfam; PF00033; Cytochrom\_B\_N; 1.  
 DR PROSITE; PS00192; CYTOCHROME\_B\_HEME; 1.  
 DR PROSITE; PS00193; CYTOCHROME\_B\_QO; UNKNOWN\_1.  
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;  
 KW Transmembrane; Transport.  
 FT NON\_TER 1  
 FT NON\_TER 330  
 SQ SEQUENCE 330 AA; 36708 MW; 7F06BC73B311D0D5 CRC64;  
 Query Match 75.0%; Score 36; DB 2; Length 330;  
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVPEYPT 9  
 DB 301 QPVEYPT 308  
 Search completed: April 18, 2005, 14:21:54  
 Job time : 83.8372 secs

RESULT 15  
 Q6YAK5 PRELIMINARY; PRT; 331 AA.  
 AC Q6YAK5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cytochrome b (Fragment).  
 GN Name=cytb;  
 OS Spizocorys sclateri (Sclater's lark).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea; Alaudidae;  
 OC Spizocorys.

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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:32:07 ; Search time 94.8139 Seconds  
(without alignments)  
36.712 Million cell updates/sec

Title: US-09-674-716B-7  
Perfect score: 48  
Sequence: 1 QQLVYFPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	3 AAY32256	Aay32256 Light cha
2	48	100.0	116	3 AAY32262	Aay32262 Humanised
3	48	100.0	145	3 AAY32261	Aay32261 Mouse ant
4	45	93.8	19	3 AAY70804	Aay70804 Murine an
5	45	93.8	122	3 AAY70790	Aay70790 Murine an
6	45	93.8	131	2 AAR12232	Aar12232 Mouse MAB
7	45	93.8	132	2 AAR12354	Aar12354 Light (ka
8	44	91.7	9	2 AAW39823	Aaw39823 Light cha
9	44	91.7	113	2 AAW39882	Aaw39882 Light cha
10	44	91.7	113	2 AAW39804	Aaw39804 Variable
11	42	87.5	248	7 ADG32323	Adg32323 Mouse scf
12	42	87.5	317	7 ADG32360	Adg32360 Precursor
13	37	77.1	100	4 AAE06969	Aae06969 Mouse ger
14	37	77.1	100	8 ADQ89254	Adq89254 Mouse imm
15	36	75.0	9	2 AAW39817	Aaw39817 Light cha
16	36	75.0	9	8 ADR38732	Adr38732 Mouse lig
17	36	75.0	107	8 ADI22109	Adi22109 Anti-plat
18	36	75.0	113	2 AAW39803	Aaw39803 Variable
19	36	75.0	113	2 AAW39801	Aaw39801 Variable
20	36	75.0	241	2 AAW24063	Aaw24063 Human WSX
21	36	75.0	241	5 AAW90948	Aaw90948 Insulin/i
22	36	75.0	241	7 ADC08951	Adc08951 Human WSX
23	36	75.0	251	5 ABP45299	Abp45299 Human Bly
24	36	75.0	251	7 ADG96126	Adg96126 Single ch
25	36	75.0	253	5 ABP44925	Abp44925 Human Bly

26	36	75.0	253	7	ADG95752	Adg95752 Single ch
27	36	75.0	274	2	AAW39899	Aaw39899 Single ch
28	36	75.0	392	3	AAB10863	Aab10863 S11-VSGF2
29	36	75.0	510	3	AAB10864	Aab10864 S11-scVEG
30	35	72.9	112	3	AAV90813	Aay90813 2G3 hybri
31	35	72.9	126	2	AAV36951	Aay36951 Protein 1
32	35	72.9	425	6	ABM69120	Abm69120 Photothab
33	35	72.9	533	3	AAG27700	Ag27700 Arabidops
34	35	72.9	536	3	AAG27699	Ag27699 Arabidops
35	35	72.9	622	3	AAG27698	Ag27698 Arabidops
36	34	70.8	9	3	AAV92171	Aay92171 Murine l3
37	34	70.8	113	3	AAV92171	Aay92171 Murine l3
38	34	70.8	146	2	AAW28154	Aaw28154 Amino aci
39	34	70.8	440	6	ABU49487	Abu49487 Protein e
40	34	70.8	531	8	ADU86167	Adu86167 Aspergill
41	34	70.8	585	5	ABP40069	Abp40069 Staphyloc
42	34	70.8	585	8	ADS04921	Ads04921 Staphyloc
43	34	70.8	601	6	ABW73103	Abw73103 Staphyloc
44	34	70.8	604	4	AAG81648	Ag81648 S. epider
45	34	70.8	1074	8	ADJ50367	Adj50367 Oil-assoc

ALIGNMENTS

RESULT 1  
AAY32256  
ID AAY32256 standard; peptide; 9 AA.  
AC AAY32256;  
XX  
XX  
15-FEB-2000 (first entry)  
XX  
DE Light chain CDR L3 of mouse anti-CD23 MAB C11.  
XX  
KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
therapy.  
XX  
XX Mus musculus.  
OS  
XX WO9958679-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-GB001434.  
XX  
PR 09-MAY-1998; 98GB-00009839.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Bonneyfoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
XX WPI; 2000-053101/04.  
DR N-PSDB; AA234741.  
XX  
XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
diabetes, multiple sclerosis and psoriasis.  
PS  
XX Claim 1; Page 40; 81pp; English.  
XX  
CC This sequence represents complementarity determining region 3 (CDR L3)  
of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11  
(see also AAY32262). The invention provides altered antibodies, such as  
chimeric or humanised antibodies, which comprise sufficient of the amino  
acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on  
CC haematopoietic cells. The antibodies are used to block soluble CD23  
CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
CC are also useful for studying interactions between CD23 and various  
CC ligands and determining the binding agents

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
| | | | |  
Db 1 QQLVEYPFT 9

RESULT 2

AAV32262  
ID AAY32262 standard; protein; 116 AA.

AC AAY32262;

XX 15-FEB-2000 (first entry)

XX Humanised anti-CD23 Mab C11 light chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;  
XX monoclonal antibody; chimeric antibody; humanised antibody;  
XX complementarity determining region; CDR; autoimmune disease;  
XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
XX urticaria; nephrotic syndrome; glomerulonephritis;  
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
XX therapy.

OS Homo sapiens.  
OS Synthetic.

XX Key Location/Qualifiers

FT Region 1. .23  
FT Region /note= "framework region 1"  
FT Region 24. .39  
FT Region /note= "CDR 1"  
FT Region 40. .54  
FT Region /note= "framework region 2"  
FT Region 55. .61  
FT Region /note= "CDR 2"  
FT Region 62. .93  
FT Region /note= "framework region 3"  
FT Region 94. .102  
FT Region /note= "CDR 3"  
FT Region 103. .113  
FT Region /note= "framework region 4"

XX WO9958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 95WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX ) GLAXO GROUP LTD.

XX PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
XX WPI; 2000-053101/04.  
XX N-PSDB; AAZ34747.  
XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
XX diabetes, multiple sclerosis and psoriasis.  
XX Claim 9; Fig 3; 81pp; English.  
XX This sequence represents the light chain variable region (VL) of  
XX humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human  
XX framework (H5IGKVII) and the light chain complementarity determining  
XX regions (see AAY32254-56) of murine antibody C11. The DNA was constructed  
XX by splice overlap PCR. The invention provides altered antibodies, such as  
XX chimeric or humanised antibodies, which comprise sufficient of the amino  
XX acid sequences of the C11 light and heavy chain complementarity  
XX determining regions to render them capable of binding to the CD23 type II  
XX molecule expressed on haematopoietic cells. The antibodies are used to  
XX block soluble CD23 formation in human therapy, for the treatment of  
XX arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
XX sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
XX syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
XX colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
XX intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
XX versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
XX bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
XX malignancies (claimed). They are also useful for studying interactions  
XX between CD23 and various ligands and determining the binding agents  
XX SQ Sequence 116 AA;

Query Match 100.0%; Score 48; DB 3; Length 116;

Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 QQLVEYPFT 9  
| | | | |  
Db 94 QQLVEYPFT 102

RESULT 3

AAV32261

ID AAY32261 standard; protein; 145 AA.

AC AAY32261;

XX 15-FEB-2000 (first entry)

XX Mouse anti-CD23 Mab C11 light chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
XX monoclonal antibody; chimeric antibody; humanised antibody;  
XX complementarity determining region; CDR; autoimmune disease;  
XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
XX urticaria; nephrotic syndrome; glomerulonephritis;  
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
XX therapy.

XX Mus musculus.

XX Key Location/Qualifiers

FT Region 55. .70  
FT Region /note= "CDR L1"  
FT Region 83. .92  
FT Region /note= "CDR L2"  
FT Region 125. .134  
FT Region /note= "CDR L3"



PN WO9958679-A1.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PP 07-MAY-1999; 99WO-GB001434.  
 XX  
 PR 09-MAY-1998; 98GB-00009839.  
 XX  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 XX  
 DR WPI; 2000-053101/04.  
 XX  
 DR N-PSDB; AAZ34746.  
 XX  
 PT Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 XX  
 PS Claim 8; Fig 2; 8lpp; English.  
 XX  
 CC This sequence represents the light chain variable region (VL) of murine  
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides  
 CC altered antibodies, such as chimeric or humanised antibodies (see  
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions (see AAY32254-59) to render them capable of binding to the CD23  
 CC type II molecule expressed on haematopoietic cells. The antibodies are  
 CC used to block soluble CD23 formation in human therapy, for the treatment  
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 XX  
 SQ Sequence 145 AA;  
 Query Match 100.0%; Score 48; DB 3; Length 145;  
 Best Local Similarity 100.0%; Pred. NO. 0.15;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQLVEVPPT 9  
 DB 125 QQLVEVPPT 133  
 XX  
 RESULT 4  
 AAY70804  
 ID AAY70804 standard; peptide; 19 AA.  
 XX  
 AC AAY70804;  
 XX  
 DT 31-JUL-2000 (first entry)  
 XX  
 DE Murine anti-PAB-421 IDI-1 mAb light chain CDR based peptide IDI-1 L3.  
 XX  
 KW Murine, p53 protein; monoclonal antibody; mAb; PAB-421; IDI-1 L3;  
 KW light chain variable region; VL; complementarity determining region; CDR;  
 KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;  
 KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;  
 KW DNA-binding domain; anti-idiotypic antibody.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200023082-A1.  
 XX  
 PD 27-APR-2000.  
 XX  
 PP 19-OCT-1999; 99WO-US024443.  
 XX

PR 19-OCT-1998; 98US-0104816P.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Cohen IR, Rotter V, Erez-Alon N, Herkel J;  
 XX  
 DR WPI; 2000-339512/29.  
 XX  
 PT Treatment of systemic lupus erythematosus by down-regulating the  
 PT autoimmune response to the C-terminal DNA-binding domain of the p53  
 PT protein by an active compound comprising of antibodies to p53 or  
 PT fragments of p53.  
 XX  
 PS Claim 78; Fig 10; 87pp; English.  
 XX  
 CC The patent discloses a method for the treatment of systemic lupus  
 CC erythematosus (SLE) by down-regulating the autoimmune response to the C-  
 CC terminal DNA-binding domain of p53 protein by an active compound. The  
 CC present sequence is a IDI-1 L3 peptide which comprises the  
 CC complementarity determining region (CDR) of the light chain of IDI-1  
 CC monoclonal antibody (mAb). The IDI-1 mAb is an anti-idiotypic  
 CC antibody/Ab2 mAb specific for PAB-421 which is an Ab1 mAb specific to the  
 CC C-terminal DNA-binding domain of murine p53 protein. The peptide  
 CC corresponds to residues 92-110 of IDI-1 light chain variable region. It  
 CC is an example of the active compound useful in the diagnosis, prevention  
 CC and treatment of SLE in humans  
 XX  
 SQ Sequence 19 AA;  
 Query Match 93.8%; Score 45; DB 3; Length 19;  
 Best Local Similarity 88.9%; Pred. NO. 0.067;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQLVEVPPT 9  
 DB 6 QQLVEVPPT 14  
 XX  
 RESULT 5  
 AAY70790  
 ID AAY70790 standard; protein; 122 AA.  
 XX  
 AC AAY70790;  
 XX  
 DT 31-JUL-2000 (first entry)  
 XX  
 DE Murine anti-PAB-421 IDI-1 mAb light chain variable region.  
 XX  
 KW Murine, p53 protein; PAB-421; monoclonal antibody; mAb; IDI-1;  
 KW anti-idiotypic antibody; DNA-binding domain; dermatological;  
 KW immunosuppressive; antiinflammatory; autoimmune response; SLE;  
 KW systemic lupus erythematosus; diagnosis; treatment; autoantigen;  
 KW light chain variable region; VL; complementarity determining region; CDR.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 27..42  
 FT /label= CDR  
 FT /note= "Complementarity determining region"  
 FT Region 58..64  
 FT /label= CDR  
 FT /note= "Complementarity determining region"  
 FT Region 97..105  
 FT /label= CDR  
 FT /note= "Complementarity determining region"  
 XX  
 PN WO200023082-A1.  
 XX  
 PD 27-APR-2000.  
 XX  
 PP 19-OCT-1999; 99WO-US024443.  
 XX

PR 19-OCT-1998; 89US-0104816P.  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Cohen IR, Rotter V, Erez-Alon N, Herkel J;  
 DR WPI; 2000-339512/29.  
 XX  
 XX Treatment of systemic lupus erythematosus by down-regulating the  
 PT autoimmune response to the C-terminal DNA-binding domain of the p53  
 PT protein by an active compound comprising of antibodies to p53 or  
 PT fragments of p53.  
 XX  
 XX Claim 78; Fig 9; 87pp; English.  
 XX  
 CC The patent discloses a method for the treatment of systemic lupus  
 CC erythematosus (SLE) by down-regulating the autoimmune response to the C-  
 CC terminal DNA-binding domain of p53 protein by an active compound. The  
 CC present sequence is a light chain variable region of IDI-1 an anti-  
 CC idiotype antibody/Ab2 monoclonal antibody (mAb) specific for PAb-421  
 CC which is an Ab1 mAb specific to the C-terminal DNA-binding domain of  
 CC murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on  
 CC complementarity determining regions of light and heavy chain variable  
 CC regions of these antibodies, are examples of active compounds useful in  
 CC the diagnosis, prevention and treatment of SLE in humans  
 XX  
 XX Sequence 122 AA;  
 SQ  
 Query Match 93.8%; Score 45; DB 3; Length 122;  
 Best Local Similarity 88.9%; Pred. NO. 0.49;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQLVEYPPT 9  
 DB 97 QQLVEYPPT 105  
 RESULT 6  
 AAR12232 standard; protein; 131 AA.  
 ID AAR12232  
 XX AC AAR12232;  
 XX AC  
 XX 25-MAR-2003 (revised)  
 DT 19-AUG-1991 (first entry)  
 XX  
 XX Mouse MAB 2E12 L chain V region.  
 DE  
 XX HIV-1; chimera.  
 XX  
 XX Mus sp.  
 XX WO9107494-A.  
 XX  
 XX 30-MAY-1991.  
 XX  
 XX 13-NOV-1989; 89US-00433703.  
 XX  
 XX 13-NOV-1989; 89US-00433703.  
 XX  
 XX (XOMA ) XOMA CORP.  
 PA (GREC ) GREEN CROSS CORP.  
 PA (ZOMA-) ZOMA CORP.  
 XX  
 XX Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;  
 PI WPI; 1991-178106/24.  
 XX N-PSDB; AAQ12012.  
 DR  
 XX  
 XX New chimeric mouse human antibodies - used in treatment, diagnosis and  
 PT prophylaxis of HIV infections.  
 PT  
 XX Disclosure; Fig 1; 108pp; English.

XX The mouse VL gene product may be used to produce chimeric mouse-human  
 CC Abs against HIV-1 comprising human Ig constant regions and murine  
 CC variable regions. These novel sequence are useful in treatment, diagnosis  
 CC and prophylaxis of HIV infections, and may be produced by a bacterial,  
 CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct  
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 131 AA;  
 SQ  
 Query Match 93.8%; Score 45; DB 2; Length 131;  
 Best Local Similarity 88.9%; Pred. NO. 0.53;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQLVEYPPT 9  
 DB 114 QQLVEYPPT 122  
 RESULT 7  
 AAR12354  
 ID AAR12354 standard; protein; 132 AA.  
 XX AC AAR12354;  
 XX AC  
 XX 25-MAR-2003 (revised)  
 DT 15-AUG-1991 (first entry)  
 XX  
 XX Light (kappa) chain variable region of murine 2E12 immunoglobulin.  
 DE  
 XX Chimeric antibodies; immunoconjugates; HIV; AIDS.  
 KW  
 XX Mus musculus.  
 OS  
 XX WO9107493-A.  
 PN  
 XX 30-MAY-1991.  
 PD  
 XX 13-NOV-1989; 89US-00433730.  
 PF  
 XX 13-NOV-1989; 89US-00433730.  
 XX  
 XX (XOMA ) XOMA CORP.  
 PA (GREC ) GREEN CROSS CORP.  
 XX  
 XX Better MD, Horwitz AH, Ghoshdasti P, Robinson R;  
 PI WPI; 1991-178105/24.  
 XX N-PSDB; AAQ12056.  
 DR  
 XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
 PT -1 antigen from sample.  
 PT  
 XX Disclosure; Fig 1; 107pp; English.  
 PS  
 XX This is the light (kappa)- chain variable (V) region of a mouse  
 CC monoclonal antibody (MAB), 2E12, and is specific for an HIV-1 viral  
 CC antigen. It is used in the construction of a chimeric MAB comprising  
 CC heavy and light chains having murine V regions and human C regions. The  
 CC chimeric MABs are more effective than murine MAB 2E12 since they have an  
 CC increased compatibility in humans. The heavy and light chain V-regions  
 CC are joined by manipulating their respective joining (J) regions, to  
 CC generate restriction enzyme recognition sites. The chimeric MABs can be  
 CC used as immuno- conjugates, in association with e.g. toxins for HIV  
 CC treatment. They can also be used in diagnosis of HIV. See also AAQ12057-  
 CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
 CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)  
 XX  
 XX Sequence 132 AA;  
 SQ  
 Query Match 93.8%; Score 45; DB 2; Length 132;  
 Best Local Similarity 88.9%; Pred. NO. 0.54;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
 DB 114 QQLVEYPFT 122

## RESULT 8

AAW39823  
 ID AAW39823 standard; peptide; 9 AA.

XX AC AAW39823;

DT 16-JUN-1998 (first entry)

DE Light chain CDR3 of catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Claim 15; Page 82; 147pp; English.

XX CC AAW39821-23 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 2A10, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX SQ Sequence 9 AA;

Query Match 91.7%; Score 44; DB 2; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.8e+06;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9

DB 1 QQFVEYPFT 9

## RESULT 9

AAW39882  
 ID AAW39882 standard; protein; 113 AA.

XX AC AAW39882;

XX XX

DT 16-JUN-1998 (first entry)

XX Light chain of the catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX DR N-PSDB; AAV09789.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Disclosure; Fig 21; 147pp; English.

XX CC The present sequence represents the light chain of a catalytic antibody  
 CC which is capable of degrading cocaine. A series of cocaine transition  
 CC state analogues (TSAs) were prepared and used to immunise mice for  
 CC production of hybridomas. Catalytic antibodies were identified by their  
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The  
 CC antibodies reduce the concentration of cocaine in a subject, and are used  
 CC particularly for the treatment of an overdose. They are also used for  
 CC treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX SQ Sequence 113 AA;

Query Match 91.7%; Score 44; DB 2; Length 113;  
 Best Local Similarity 88.9%; Pred. No. 0.72;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9

DB 94 QQFVEYPFT 102

## RESULT 10

AAW39804  
 ID AAW39804 standard; protein; 113 AA.

XX AC AAW39804;

XX DT 16-JUN-1998 (first entry)

XX Variable domain of the Kappa light chain of catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.  
 XX  
 PR 25-JUN-1996; 96US-00672345.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Landry DW;  
 XX  
 DR WPI; 1998-077166/07.  
 XX  
 PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.  
 XX  
 PS Claim 16; Page 73-74; 147pp; English.  
 XX  
 CC AAW39801-05 represent the amino acid sequences of the variable domain of  
 CC the Kappa light chain of catalytic antibodies which are able to degrade  
 CC cocaine. A series of cocaine transition state analogues (TSAs) were  
 CC prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809  
 CC represents the heavy chain) was identified using TSA1, which is an  
 CC immunogenic conjugate of a phosphate monoester transition state analogue.  
 CC Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the  
 CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved)  
 XX  
 SQ Sequence 113 AA;  
 Query Match 91.7%; Score 44; DB 2; Length 113;  
 Best Local Similarity 88.9%; Pred. No. 0.72;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QQLVEVPFT 9  
 DB 94 QQFVEVPFT 102  
 RESULT 11  
 ADG32323  
 ID ADG32323 standard; protein; 248 AA.  
 AC ADG32323;  
 XX 26-FEB-2004 (first entry)  
 DT Mouse scFV VDM1 antibody targeted against V\_dahliae SeqID 32.  
 DE mouse; murine; scFV; anti-fungal peptide; AFP; scFV; disease resistant;  
 KW transgenic; plant; fungal infection; antibody;  
 KW pathogen-specific antibody; fungicidal; agriculture.  
 XX  
 OS Mus sp.  
 XX WO2003089475-A2.  
 XX 30-OCT-2003.  
 XX 14-APR-2003; 2003WO-EP003852.  
 XX 22-APR-2002; 2002EP-00008929.  
 XX 28-MAY-2002; 2002EP-00011807.  
 XX (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.  
 XX Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;  
 XX WPI; 2003-854088/79.  
 XX N-PSDB; ADG32298.  
 XX New fusion protein comprising an anti-fungal protein or peptide and an  
 PT antibody fragment, useful in agriculture and horticulture for producing  
 PT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.

PT New fusion protein comprising an anti-fungal protein or peptide and an  
 PT antibody fragment, useful in agriculture and horticulture for producing  
 PT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.  
 XX  
 PS Example 13; SEQ ID NO 32; 47pp; English.  
 XX  
 CC This invention relates to a novel fusion protein comprising an anti-  
 CC fungal protein or peptide (AFP) and an antibody fragment (scFV).  
 CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta  
 CC and a cellular targeting sequence, which can be used to generate disease  
 CC resistant transgenic plants that are protected against fungal infection.  
 CC Accordingly, a method is described for antibody based resistance in  
 CC plants such that the undesirable and expensive chemical controls often  
 CC used in agriculture are not required. The present invention provides  
 CC antibodies, recombinant antibodies and fragments thereof, as well as  
 CC fusion proteins that can be used as pathogen-specific antibodies targeted  
 CC to different plant cell compartments. As such, these fungicidal agents  
 CC confer a broad spectrum of disease resistance in both economically  
 CC important crops and ornamental plants. This polypeptide is an antibody  
 CC used in an exemplification of the invention.  
 XX  
 SQ Sequence 248 AA;  
 Query Match 87.5%; Score 42; DB 7; Length 248;  
 Best Local Similarity 88.9%; Pred. No. 4.2;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QQLVEVPFT 9  
 DB 228 QQLVEYPLT 236  
 RESULT 12  
 ADG32360  
 ID ADG32360 standard; protein; 317 AA.  
 AC ADG32360;  
 XX 26-FEB-2004 (first entry)  
 DT Precursor fusion protein of AFP AG-scFV VDM1 SeqID 69.  
 DE scFV; anti-fungal peptide; AFP; scFV; disease resistant; transgenic;  
 KW plant; fungal infection; antibody; pathogen-specific antibody;  
 KW fungicidal; agriculture; mouse; chimeric; murine.  
 XX  
 OS Chimeric.  
 OS Synthetic.  
 OS Aspergillus giganteus.  
 OS Mus musculus.  
 XX WO2003089475-A2.  
 XX 30-OCT-2003.  
 XX 14-APR-2003; 2003WO-EP003852.  
 XX 22-APR-2002; 2002EP-00008929.  
 XX 28-MAY-2002; 2002EP-00011807.  
 XX (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.  
 XX Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;  
 XX WPI; 2003-854088/79.  
 XX N-PSDB; ADG32349.  
 XX New fusion protein comprising an anti-fungal protein or peptide and an  
 PT antibody fragment, useful in agriculture and horticulture for producing  
 PT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.  
 XX  
 PS Disclosure; SEQ ID NO 69; 47pp; English.  
 XX

CC This invention relates to a novel fusion protein comprising an anti-fungal protein or peptide (AFP) and an antibody fragment (scFv).  
 CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta and a cellular targeting sequence, which can be used to generate disease resistant transgenic plants that are protected against fungal infection.  
 CC Accordingly, a method is described for antibody based resistance in plants such that the undesirable and expensive chemical controls often used in agriculture are not required. The present invention provides antibodies, recombinant antibodies and fragments thereof, as well as fusion proteins that can be used as pathogen-specific antibodies targeted to different plant cell compartments. As such, these fungicidal agents confer a broad spectrum of disease resistance in both economically important crops and ornamental plants. This polypeptide is a precursor fusion protein of the order [AFP - linker - antibody fragment] of the invention.

XX Sequence 317 AA;

Query Match 87.5%; Score 42; DB 7; Length 317;  
 Best Local Similarity 89.9%; Pred. No. 5.5;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9  
 |||||  
 Db 297 QQLVEYPPT 305

RESULT 13

AAE06969  
 ID AAE06969 standard; protein; 100 AA.

XX AAE06969;

DT 16-OCT-2001 (first entry)

DE Mouse germline kappa light chain variable (VK) region, 167/24.

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; VK; kappa light chain variable region.

XX Mus sp.

XX WO200157226-A1.

XX 09-AUG-2001.

PF 02-FEB-2001; 2001WO-US0003537.

XX 03-FEB-2000; 2000US-00497625.

XX (MILL-) MILLENNIUM PHARM INC.

XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
 WPI; 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin.

XX Disclosure; Page 151; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies

CC are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline kappa light chain variable (VK) region, 167/24

XX Sequence 100 AA;

Query Match 77.1%; Score 37; DB 4; Length 100;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7  
 |||||  
 Db 94 QQLVEYP 100

RESULT 14

ADQ89254

ID ADQ89254 standard; protein; 100 AA.

XX ADQ89254;

DT 21-OCT-2004 (first entry)

DE Mouse immunoglobulin protein #14.

XX Mouse; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2; inflammatory disease; autoimmune disorder; graft rejection;  
 KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
 KW anti-HIV; virucide; antiarteriosclerotic.

XX Mus musculus.

XX US2004151721-A1.

XX 05-AUG-2004.

PF 10-DEC-2003; 2003US-00733563.

XX 19-OCT-2001; 2001US-0350166P.

PR 26-JUN-2002; 2002US-0392364P.

PR 17-OCT-2002; 2002US-00272899.

XX (OKEE/) O'KEEFE T.

XX (PONA/) PONA P.

XX O'keefe T, Ponath P;

XX WPI; 2004-580175/56.

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists, useful for diagnosing and/or treating inflammatory or autoimmune diseases, and HIV infection.

XX Example 2; SEQ ID NO 32; 128pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains which have specificity for the CC-chemokine receptor 2 (CCR2) and an immunoglobulin or its antigen binding fragment comprising the chains. The

CC humanised immunoglobulin or its antigen binding fragment preferably  
 CC comprises two heavy chains and two light chains. The humanised  
 CC immunoglobulin and its heavy and light chains are useful for the  
 CC diagnosis, prevention and/or treatment of diseases or conditions  
 CC associated with aberrant expression or activity of the CCR2 polypeptide,  
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
 CC infection and atherosclerosis. This sequence represents a mouse  
 CC immunoglobulin protein of the invention.

XX Sequence 100 AA;

Query Match 77.1%; Score 37; DB 8; Length 100;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7

Db 94 QQLVEYP 100

# RESULT 15

AAW39817

ID AAW39817 standard; peptide; 9 AA.

XX AC AAW39817;

XX AC AAW39817;

DT 16-JUN-1998 (first entry)

XX Light chain CDR3 of catalytic antibody 3B9.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

PS Claim 11; Page 81; 147pp; English.

XX AAW39815-17 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified  
 CC using TSAI, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX Sequence 9 AA;

Query Match 75.0%; Score 36; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9

Db 1 QHFVDYPFT 9

Search completed: April 18, 2005, 14:15:16

Job time : 96.8139 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:22:17 ; Search time 68.0233 Seconds  
(without alignments)  
43.975 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYFPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Maximum Match 100%

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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	91.7	9	10	US-09-940-727B-27
2	44	91.7	113	10	US-09-940-727B-8
3	44	91.7	113	10	US-09-940-727B-108
4	37	77.1	100	9	US-09-840-459-32
5	37	77.1	100	16	US-10-766-773-32
6	37	77.1	100	16	US-10-766-610-32
7	37	77.1	100	16	US-10-733-563-32
8	37	77.1	609	16	US-10-437-963-104782
9	36	75.0	9	10	US-09-940-727B-21
10	36	75.0	9	16	US-10-632-706-134
11	36	75.0	113	10	US-09-940-727B-5
12	36	75.0	113	10	US-09-940-727B-7
13	36	75.0	113	10	US-09-940-727B-100

14	36	75.0	113	10	US-09-940-727B-112
15	36	75.0	241	8	US-08-779-457-50
16	36	75.0	241	17	US-10-921-710-50
17	36	75.0	251	10	US-09-880-748-1310
18	36	75.0	251	15	US-10-293-418-1310
19	36	75.0	253	10	US-09-880-748-936
20	36	75.0	253	15	US-10-293-418-936
21	36	75.0	280	10	US-09-940-727B-119
22	35	72.9	90	16	US-10-767-701-56894
23	35	72.9	298	15	US-10-425-114-71736
24	35	72.9	569	15	US-10-425-114-71735
25	34	70.8	440	15	US-10-282-122A-77411
26	34	70.8	1074	15	US-10-389-566-2371
27	33	68.8	9	16	US-10-823-253-20
28	33	68.8	79	15	US-10-425-114-44597
29	33	68.8	82	9	US-09-864-761-47635
30	33	68.8	82	15	US-10-424-599-280477
31	33	68.8	83	15	US-10-424-599-212368
32	33	68.8	105	16	US-10-823-253-30
33	33	68.8	107	10	US-09-848-798-40
34	33	68.8	107	16	US-10-823-253-25
35	33	68.8	107	16	US-10-823-253-28
36	33	68.8	107	16	US-10-823-253-32
37	33	68.8	199	15	US-10-424-599-246437
38	33	68.8	243	16	US-10-437-963-161157
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40	33	68.8	337	16	US-10-437-963-130847
41	33	68.8	368	16	US-10-333-235A-58
42	33	68.8	441	15	US-10-282-122A-45037
43	33	68.8	465	16	US-10-333-235A-59
44	33	68.8	561	15	US-10-369-493-870
45	33	68.8	726	9	US-09-973-451-10

#### ALIGNMENTS

##### RESULT 1

US-09-940-727B-27  
; Sequence 27, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-27

Query Match 91.7%; Score 44; DB 10; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.3e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

##### QY 1 QQLVEYFPFT 9

||| |||||

##### Db 1 QQFVEYFPFT 9

##### RESULT 2

US-09-940-727B-8  
; Sequence 8, Application US/09940727B

Publication No. US2003007793A1  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald W  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 0575/51400-B  
CURRENT APPLICATION NUMBER: US/09/940,727B  
CURRENT FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: 09/214,095  
PRIOR FILING DATE: 1998-12-28  
PRIOR APPLICATION NUMBER: PCT/US97/10965  
PRIOR FILING DATE: 1997-06-25  
PRIOR APPLICATION NUMBER: 08/672,345  
PRIOR FILING DATE: 1996-06-25  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 113  
TYPE: PRT  
ORGANISM: mouse  
US-09-940-727B-8

Query Match 91.7%; Score 44; DB 10; Length 113;  
Best Local Similarity 88.9%; Pred. No. 1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYFPFT 9  
Db 94 QQFVEYFPFT 102

RESULT 3  
US-09-940-727B-108  
Sequence 108, Application US/09940727B  
Publication No. US2003007793A1  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald W  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 0575/51400-B  
CURRENT APPLICATION NUMBER: US/09/940,727B  
CURRENT FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: 09/214,095  
PRIOR FILING DATE: 1998-12-28  
PRIOR APPLICATION NUMBER: PCT/US97/10965  
PRIOR FILING DATE: 1997-06-25  
PRIOR APPLICATION NUMBER: 08/672,345  
PRIOR FILING DATE: 1996-06-25  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 108  
LENGTH: 113  
TYPE: PRT  
ORGANISM: mouse  
US-09-940-727B-108

Query Match 91.7%; Score 44; DB 10; Length 113;  
Best Local Similarity 88.9%; Pred. No. 1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYFPFT 9  
Db 94 QQFVEYFPFT 102

RESULT 4  
US-09-840-459-32  
Sequence 32, Application US/09840459  
Patent No. US20020150576A1  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-840-459-32

Query Match 77.1%; Score 37; DB 9; Length 100;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYYP 7  
Db 94 QQLVEYYP 100

RESULT 5  
US-10-766-773-32  
Sequence 32, Application US/10766773  
Publication No. US20040126851A1  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-028  
CURRENT APPLICATION NUMBER: US/10/766,773  
CURRENT FILING DATE: 2004-01-27  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-766-773-32

Query Match 77.1%; Score 37; DB 16; Length 100;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYYP 7  
Db 94 QQLVEYYP 100

RESULT 6  
US-10-766-610-32  
Sequence 32, Application US/10766610



Publication No. US20040132980A1  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-029  
CURRENT APPLICATION NUMBER: US/10/766,610  
CURRENT FILING DATE: 2004-01-27  
PRIOR APPLICATION NUMBER: 09/840,459  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-766-610-32

Query Match 77.1%; Score 37; DB 16; Length 100;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYP 7  
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Db 94 QQLVEYP 100

RESULT 7  
US-10-733-563-32  
Sequence 32, Application US/10733563  
Publication No. US20040151721A1  
GENERAL INFORMATION:  
APPLICANT: O'Keefe, Theresa  
APPLICANT: Ponath, Paul  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
METHODS OF USE THEREOF  
FILE REFERENCE: 10448-213001  
CURRENT APPLICATION NUMBER: US/10/733,563  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: US 10/272,899  
PRIOR FILING DATE: 2002-10-17  
PRIOR APPLICATION NUMBER: US 60/392,364  
PRIOR FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: US 60/350,166  
PRIOR FILING DATE: 2001-10-19  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-733-563-32

Query Match 77.1%; Score 37; DB 16; Length 100;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYP 7  
| | | | |  
Db 94 QQLVEYP 100

## RESULT 8

US-10-437-963-104782  
Sequence 104782, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 104782  
LENGTH: 609  
TYPE: PRT  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_102083C.1.pap  
US-10-437-963-104782

Query Match 77.1%; Score 37; DB 16; Length 609;  
Best Local Similarity 77.8%; Pred. No. 1.2e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9  
| | | | |  
Db 569 QQLLEIPPT 577

## RESULT 9

US-09-940-727B-21  
Sequence 21, Application US/09940727B  
Publication No. US2003007793A1  
GENERAL INFORMATION:  
APPLICANT: Landry, Donald W  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 0575/51400-B  
CURRENT APPLICATION NUMBER: US/09/940,727B  
CURRENT FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: 09/214,095  
PRIOR FILING DATE: 1998-12-28  
PRIOR APPLICATION NUMBER: PCT/US97/10965  
PRIOR FILING DATE: 1997-06-25  
PRIOR APPLICATION NUMBER: 08/672,345  
PRIOR FILING DATE: 1996-06-25  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 21  
LENGTH: 9  
TYPE: PRT  
ORGANISM: mouse  
US-09-940-727B-21

Query Match 75.0%; Score 36; DB 10; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9  
| | | | |  
Db 1 QHFVDYPT 9

RESULT 10  
US-10-632-706-134

; Sequence 134, Application US/10632706  
; Publication No. US20040175385A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKS, JAMES D.  
; APPLICANT: AMERSDORFER, PETER  
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
; TITLE OF INVENTION: NEUROTOXINS  
; FILE REFERENCE: 407T-895120US  
; CURRENT APPLICATION NUMBER: US/10/632,706  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US 60/400,721  
; PRIOR FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 09/144,806  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 134  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-134

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Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9  
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DB 1 QQLISYPLT 9

RESULT 11  
US-09-940-727B-5  
; Sequence 5, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-5

Query Match 75.0%; Score 36; DB 10; Length 113;  
Best Local Similarity 66.7%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9  
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DB 94 QHEVDYPT 102

RESULT 12  
US-09-940-727B-7  
; Sequence 7, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-7

Query Match 75.0%; Score 36; DB 10; Length 113;  
Best Local Similarity 66.7%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9  
| : |||  
DB 94 QHEVDYPT 102

RESULT 13  
US-09-940-727B-100  
; Sequence 100, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 100  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-100

Query Match 75.0%; Score 36; DB 10; Length 113;  
Best Local Similarity 66.7%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9  
| : |||  
DB 94 QHEVDYPT 102

RESULT 14  
US-09-940-727B-112  
; Sequence 112, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25

Search completed: April 18, 2005, 14:54:41  
Job time : 69.0233 secs

QY 1 QQLVEYPFT 9  
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Db 94 QHFVDYPFT 102

RESULT 15

RESOLUT 15  
 US-08-779-457-50  
 ; Sequence 50, Application US/08779457  
 ; Publication No. US20020193571A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carter, Paul J.  
 ; APPLICANT: Chiang, Nancy Y.  
 ; APPLICANT: Kyung, Jin Kim  
 ; APPLICANT: Matthews, William  
 ; APPLICANT: Rodrigues, Maria L.  
 ; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES  
 ; NUMBER OF SEQUENCES: 51  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: winpatin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/779,457

AFFILIATION NUMBER: 05/06/1775-75  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/667197  
 FILING DATE: 06/20/96  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/585005  
 FILING DATE: 01/08/96  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER: 40,378  
 REFERENCE/DOCKET NUMBER: P0986P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1994  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 50:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 241 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-779-457-50

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Query Match      75.0%; Score 36; DB 8; Length 241;
Best Local Similarity 66.7%; Pred. No. 75;
Matches         6: Conservative      1: Mismatches      2: Indels

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Qy 1 00LVEYPT 9

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:01:43 ; Search time 24.4884 Seconds  
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Title: US-09-674-716B-7  
Perfect score: 48  
Sequence: 1 QQLVEVPFT 9

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	91.7	9	2	US-08-672-345C-27
2	44	91.7	9	3	US-09-214-095D-27
3	44	91.7	113	2	US-08-672-345C-8
4	44	91.7	113	2	US-08-672-345C-98
5	44	91.7	113	3	US-09-214-095D-8
6	44	91.7	113	3	US-09-214-095D-108
7	37	77.1	100	4	US-08-840-459-32
8	37	77.1	100	4	US-09-497-625A-32
9	36	75.0	9	2	US-08-672-345C-21
10	36	75.0	9	3	US-09-214-095D-21
11	36	75.0	113	2	US-08-672-345C-5
12	36	75.0	113	2	US-08-672-345C-7
13	36	75.0	113	2	US-08-672-345C-95
14	36	75.0	113	2	US-08-672-345C-97
15	36	75.0	113	3	US-09-214-095D-5
16	36	75.0	113	3	US-09-214-095D-7
17	36	75.0	113	3	US-09-214-095D-100
18	36	75.0	113	3	US-09-214-095D-112
19	36	75.0	280	3	US-09-214-095D-119
20	35	72.9	112	3	US-08-483-749A-4
21	34	70.8	9	3	US-09-406-532-20
22	34	70.8	113	3	US-09-406-532-14
23	34	70.8	585	3	US-09-134-001C-4914
24	34	70.8	604	4	US-09-710-279-390
25	33	68.8	9	1	US-08-438-123-3
26	33	68.8	11	1	US-08-438-123-11
27	33	68.8	107	3	US-09-240-274-40

28	33	68.8	108	1	US-08-468-661-3	Sequence 3, Appli
29	33	68.8	108	1	US-08-468-661-3	Sequence 3, Appli
30	33	68.8	108	1	US-08-478-857-3	Sequence 3, Appli
31	33	68.8	108	2	US-08-471-771-3	Sequence 3, Appli
32	33	68.8	108	3	US-09-130-783-3	Sequence 3, Appli
33	33	68.8	113	3	US-08-483-749A-16	Sequence 16, Appli
34	33	68.8	113	5	PCT-US93-11611-5	Sequence 5, Appli
35	33	68.8	133	1	US-08-253-877C-10	Sequence 10, Appli
36	33	68.8	133	1	US-08-253-877C-10	Sequence 28, Appli
37	33	68.8	133	2	US-08-452-164A-10	Sequence 10, Appli
38	33	68.8	133	2	US-08-452-164A-28	Sequence 28, Appli
39	33	68.8	133	3	US-08-603-024-4	Sequence 4, Appli
40	33	68.8	133	3	US-08-603-024-27	Sequence 27, Appli
41	33	68.8	133	4	US-08-450-809-23	Sequence 23, Appli
42	33	68.8	133	5	PCT-US93-11611-2	Sequence 2, Appli
43	33	68.8	133	5	PCT-US93-11611-9	Sequence 9, Appli
44	33	68.8	141	1	US-08-438-123-7	Sequence 7, Appli
45	33	68.8	437	4	US-09-252-991A-20209	Sequence 20209, A

#### ALIGNMENTS

RESULT 1  
US-08-672-345C-27  
; Sequence 27, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-27

Query Match 91.7%; Score 44; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. NO. 4.1e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEVPFT 9  
Db 1 QQFVEVPFT 9

RESULT 2

US-09-214-095D-27  
; Sequence 27, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-27

Query Match 91.7%; Score 44; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.1e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
||| |||||  
Db 1 QQFVEYPFT 9

RESULT 3  
US-08-672-345C-8  
; Sequence 8, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-672-345C-8  
; Sequence 8, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-27

Query Match 91.7%; Score 44; DB 2; Length 113;  
Best Local Similarity 88.9%; Pred. No. 0.34;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
||| |||||  
Db 94 QQFVEYPFT 102

RESULT 4  
US-08-672-345C-98  
; Sequence 98, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 98:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-98

Query Match 91.7%; Score 44; DB 2; Length 113;  
Best Local Similarity 88.9%; Pred. No. 0.34;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
||| |||||  
Db 94 QQFVEYPFT 102

RESULT 5  
US-09-214-095D-8  
; Sequence 8, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-8

Query Match 91.7%; Score 44; DB 3; Length 113;  
Best Local Similarity 88.9%; Pred. No. 0.34;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9  
||| |||||  
Db 94 QQFVEYPT 102

RESULT 6  
US-09-214-095D-108  
; Sequence 108, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 108  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Murine  
US-09-214-095D-108

Query Match 91.7%; Score 44; DB 3; Length 113;  
Best Local Similarity 88.9%; Pred. No. 0.34;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9  
||| |||||  
Db 94 QQFVEYPT 102

RESULT 7  
US-09-840-459-32  
; Sequence 32, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-840-459-32

Query Match 77.1%; Score 37; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPT 7  
||| |||||  
Db 94 QQLVEYPT 100

RESULT 8  
US-09-497-625A-32  
; Sequence 32, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-497-625A-32

Query Match 77.1%; Score 37; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPT 7  
||| |||||  
Db 94 QQLVEYPT 100

RESULT 9  
US-08-672-345C-21  
; Sequence 21, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-21

Query Match 75.0%; Score 36; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 1 QHFVDYPPT 9

RESULT 10
US-09-214-095D-21
; Sequence 21, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen.sp.
US-09-214-095D-21

Query Match 75.0%; Score 36; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 1 QHFVDYPPT 9

RESULT 11
US-08-672-345C-5
; Sequence 5, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
```

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;
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-5

Query Match 75.0%; Score 36; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 94 QHFVDYPPT 102

RESULT 12
US-08-672-345C-7
; Sequence 7, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-7

Query Match 75.0%; Score 36; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 94 QHFVDYPPT 102

RESULT 13
US-08-672-345C-95
; Sequence 95, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
```



; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 95:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-672-345C-95

Query Match 75.0%; Score 36; DB 2; Length 113;  
Best Local Similarity 66.7%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9  
Db 94 QHFVDYPPT 102

RESULT 14  
US-08-672-345C-97  
; Sequence 97, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 97:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-672-345C-97

Query Match 75.0%; Score 36; DB 2; Length 113;  
Best Local Similarity 66.7%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9  
Db 94 QHFVDYPPT 102

RESULT 15  
US-09-214-095D-5  
; Sequence 5, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Murinae gen. Sp.  
; US-09-214-095D-5

Query Match 75.0%; Score 36; DB 3; Length 113;  
Best Local Similarity 66.7%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9  
Db 94 QHFVDYPPT 102

Search completed: April 18, 2005, 14:25:26  
Job time : 24.4884 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 15:11:18 ; Search time 42 Seconds  
(without alignments)  
20.618 Million cell updates/sec

Title: US-09-674-716B-7  
Perfect score: 48  
Sequence: 1 QOLVEYPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	43.8	9	2 S66635	alpha-2-macroglobu
2	19	39.6	5	2 E60274	major protein anti
3	16	33.3	3	3 A43391	TRH-like tripeptid
4	14	29.2	4	2 PT0240	Ig heavy chain CRD
5	14	29.2	4	2 A32039	tyrosine-melanocyt
6	14	29.2	5	2 PQ0009	angiotensin-conver
7	14	29.2	6	2 JN0861	peptidyl-dipectida
8	14	29.2	7	1 A61324	dermorphin - Rohde
9	14	29.2	7	2 S36862	dermorphin (Lys-7)
10	14	29.2	7	2 S21230	dermorphin (Trp-4)
11	14	29.2	7	2 S42620	aggreccan - bovine
12	14	29.2	8	2 S66646	cardioacceleratory
13	14	29.2	9	2 B49712	ATP-binding protei
14	14	29.2	9	2 A61620	locustanyotrocin I
15	13	27.1	5	2 JS0319	subesophageal gang
16	13	27.1	6	2 A61049	halo-toxin - Pseud
17	13	27.1	6	2 I51317	bHLH transcription
18	13	27.1	7	2 E33932	Ig mu chain D regi
19	13	27.1	7	2 PX0008	glucuronosyltransf
20	13	27.1	7	4 I56695	hypothetical L2 pr
21	13	27.1	8	2 S16324	hypothetical prote
22	13	27.1	9	2 S39766	cardioactive pepti
23	13	27.1	9	2 S65433	bradykinin - horn
24	13	27.1	9	2 PT0285	Ig heavy chain CRD
25	13	27.1	9	2 S39767	cardioactive pepti
26	13	27.1	9	2 A26363	cardioactive pepti
27	13	27.1	9	2 S27233	cardioactive pepti
28	13	27.1	9	2 PT0080	60K Ca binding pro
29	13	27.1	9	2 S10784	enamelin i - bovin

30	13	27.1	9	2 I46023	growth hormone rec
31	13	27.1	9	2 A43065	hydroxyproline-3-b
32	13	27.1	9	2 S15850	vitamin D3 26-mono
33	13	27.1	9	2 A26744	bradykinin-like pe
34	13	27.1	9	2 A61057	Thr-6 bradykinin -
35	13	27.1	9	2 A60579	bradykinin-like pe
36	13	27.1	9	2 A61363	bradykinin - commo
37	13	27.1	9	2 A61358	bradykinin-like pe
38	12	25.0	5	2 B37325	pap fibrial regul
39	12	25.0	5	3 JT0870	phytosulfokine alp
40	12	25.0	7	2 S25266	pIL6 protein - Esc
41	12	25.0	7	2 A38081	amine oxidase (cop
42	12	25.0	8	2 PL0184	capsid protein VP-
43	12	25.0	8	2 B45800	serum albumin - do
44	12	25.0	8	2 D47393	neuropeptide calla
45	12	25.0	8	2 E47393	neuropeptide calla

ALIGNMENTS

RESULT 1

S66635  
alpha-2-macroglobulin isoform 1 - bovine (fragment)  
C:Species: Bos primigenius indicus (zebu cattle)  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S66635  
R:Dotmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottr  
PERS Lett. 372, 93-95, 1995  
A:Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain  
A:Reference number: S66634; MUID:96032553; PMID:7556651  
A:Accession: S66635  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <DOL>  
A:Cross-references: UNIPROT:Q7M2N8

Query Match 43.8%; Score 21; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 EYPF 8  
DB 3 EFPF 6

RESULT 2

E60274  
major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)  
C:Species: Mycobacterium tuberculosis  
C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993  
C:Accession: E60274  
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.  
Infect. Immun. 59, 372-382, 1991  
A:Title: Isolation and partial characterization of major protein antigens in the cultur  
A:Reference number: A60274; MUID:91099989; PMID:1898899  
A:Accession: E60274  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <NAG>

Query Match 39.6%; Score 19; DB 2; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 YPFT 9  
DB 2 YPIT 5

RESULT 3

A43391  
TRH-like tripeptide - alfalfa

C:Species: Medicago sativa (alfalfa)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A43391  
R:Lackey, D.B.  
J. Biol. Chem. 267, 17508-17511, 1992  
A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglu-  
A:Reference number: A43391; MUID:92388092; PMID:1517203  
A:Accession: A43391  
A:Molecule type: protein  
A:Residues: 1-3 <LAC>  
C:Keywords: amidated carboxyl end; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 16; DB 3; Length 3;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 YP 7  
Db 1 QVP 3

RESULT 4  
PT0240  
Ig heavy chain CDR3 region (clone 2-100B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0240  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0240  
A:Molecule type: DNA  
A:Residues: 1-4 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.2%; Score 14; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7  
Db 1 YP 2

RESULT 5  
A32039  
tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 18-Aug-2000  
C:Accession: A32039  
R:Horvath, A.; Kastin, A.J.  
J. Biol. Chem. 264, 2175-2179, 1989  
A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor  
A:Reference number: A32039; MUID:89123285; PMID:2563371  
A:Accession: A32039  
A:Molecule type: protein  
A:Residues: 1-4 <HOR>  
A:Experimental source: brain  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end  
F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.2%; Score 14; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7  
Db 1 YP 2

RESULT 6  
PQ0009  
angiotensin-converting enzyme inhibitor (FLP-2) - common fig  
N:Alternate names: ficus latex peptide 2  
C:Species: Ficus carica (common fig)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995  
C:Accession: PQ0009  
R:Maruyama, S.; Miyoshi, S.; Tanaka, H.  
Agric. Biol. Chem. 53, 2763-2767, 1989  
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.  
A:Reference number: PQ0008  
A:Accession: PQ0009  
A:Molecule type: protein  
A:Residues: 1-5 <MAR>  
A:Experimental source: latex  
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 29.2%; Score 14; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7  
Db 2 YP 3

RESULT 7  
JN0861  
peptidyl-diesterase A inhibitory peptide C111 - striped bonito  
C:Species: Sarda orientalis (striped bonito)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C:Accession: JN0861  
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe  
A:Reference number: JN0859; MUID:94080036; PMID:7764272  
A:Accession: JN0861  
A:Molecule type: protein  
A:Residues: 1-6 <MAT>  
A:Experimental source: liver  
C:Comment: The carboxyl end is essential for the protein's expression of angiotensin I-c  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 29.2%; Score 14; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7  
Db 3 YP 4

RESULT 8  
A61324  
dermorphin - Rohde's leaf frog  
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C:Date: 17-Jul-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C:Accession: A61324  
R:Montecucci, P.C.; De Castiglione, R.; Erspamer, V.  
Int. J. Pept. Protein Res. 17, 316-321, 1981  
A:Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Bra  
A:Reference number: A61324; MUID:82029915; PMID:7287302  
A:Accession: A61324  
A:Molecule type: protein  
A:Residues: 1-7 <MON>  
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology  
C:Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin  
F:2/Modified site: D-alanine (Ala) #status experimental  
F:6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental  
F:7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 29.2%; Score 14; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 YP 7  
DB 5 YP 6

RESULT 9  
S36662  
dermorphin (Lys-7) [validated] - two-colored leaf frog  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 10-Dec-1993 #sequence\_revision 13-Mar-1997 #text\_change 18-Aug-2000  
C;Accession: S36662  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of the  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S36662  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIG>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 29.2%; Score 14; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 YP 7  
DB 5 YP 6

RESULT 10  
S21230  
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 18-Aug-2000  
C;Accession: S21230  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of the  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S21230  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIG>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 29.2%; Score 14; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 YP 7  
DB 5 YP 6

RESULT 11  
S42620  
aggrecan - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
C;Accession: S42620  
R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.  
Matrix Biol. 14, 171-179, 1994  
A;Title: Aggrecan in bovine tendon.  
A;Reference number: S42620; MUID:94340214; PMID:7520336  
A;Accession: S42620  
A;Molecule type: protein  
A;Residues: 1-7 <VOG>

A;Experimental source: flexor tendon  
C;Keywords: cartilage

Query Match 29.2%; Score 14; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 YP 7  
DB 1 YP 2

RESULT 12  
S66646  
cardioacceleratory protein 2b - tobacco hornworm  
C;Species: Manduca sexta (tobacco hornworm)  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S66646  
R;Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderek, K.M.; Tublitz, N.J.  
FEBS Lett. 371, 311-314, 1995  
A;Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the  
A;Reference number: S66646; MUID:96013159; PMID:7556618  
A;Accession: S66646  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <HUE>  
A;Cross-references: UNIPROT:Q7M3N2

Query Match 29.2%; Score 14; DB 2; Length 8;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QLVFYP 7  
DB 1 ELYAFP 6

RESULT 13  
B49712  
ATP-binding protein p46 - dog (fragment)  
C;Species: Canis lupus familiaris (dog)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
C;Accession: B49712  
R;Nigam, S.K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.  
J. Biol. Chem. 269, 1744-1749, 1994  
A;Title: A set of endoplasmic reticulum proteins possessing properties of molecular cha  
A;Reference number: A49712; MUID:94124514; PMID:8294423  
A;Accession: B49712  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <NIG>  
C;Keywords: ATP; endoplasmic reticulum; molecular chaperone

Query Match 29.2%; Score 14; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 YP 7  
DB 5 YP 6

RESULT 14  
A61620  
locustamytropin III - migratory locust  
C;Species: Locusta migratoria (migratory locust)  
C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: A61620  
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.  
Insect Biochem. Mol. Biol. 22, 447-452, 1992  
A;Title: Isolation, identification and synthesis of locustamytropin III and IV, two ad  
A;Reference number: A61620  
A;Accession: A61620

Tue Apr 19 06:15:07 2005

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <SCH>  
A;Cross-references: UNIPROT:P41489  
C;Keywords: amidated carboxyl end: neuropeptide  
F;9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 29.2%; Score 14; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 EYPF 8  
: ||  
Db 2 QOPF 5

RESULT 15  
JS0319  
subesophageal ganglion pentapeptide - house cricket  
C;Species: Acheta domesticus (house cricket)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: JS0319  
R;Wicker, C.; Wicker, C.  
Comp. Biochem. Physiol. C 88, 185-187, 1987  
A;Title: Isolation and structure of a peptide isolated from the subesophageal ganglion  
A;Reference number: JS0319  
A;Accession: JS0319  
A;Molecule type: protein  
A;Residues: 1-5 <WIC>  
A;Cross-references: UNIPROT:P19991

Query Match 27.1%; Score 13; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PF 8  
: ||  
Db 4 PF 5

Search completed: April 18, 2005, 15:21:13  
Job time : 52 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:02:28 ; Search time 180 Seconds  
(without alignments)  
25.604 Million cell updates/sec

Title: US-09-674-716B-7  
Perfect score: 48  
Sequence: 1 QQLVEYFPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1455

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	43.8	9	2 Q7M2N8	Q7m2n8 bos indicus
2	17	35.4	8	2 Q49534	Q49534 mycoplasma
3	17	35.4	9	2 Q8WFT4	Q8wft4 diadema ant
4	16	33.3	8	2 Q9MSX1	Q9msx1 jurinea hum
5	16	33.3	8	2 Q8J35	Q8j35 ficedula hy
6	16	33.3	9	2 Q9TRU7	Q9tru7 bos taurus
7	15	31.2	8	1 ANG2 BOTJA	Q10582 bothrops ja
8	15	31.2	8	1 UPAA HUMAN	P30096 homo sapien
9	15	31.2	8	2 Q15898	Q15898 homo sapien
10	15	31.2	8	2 Q70KG9	Q70kg9 sus scrofa
11	15	31.2	8	2 Q70Y88	Q70y88 platostoma
12	15	31.2	8	2 Q6LQ05	Q6lq05 rhodobacter
13	15	31.2	8	2 Q7T282	Q7t282 geochelone
14	15	31.2	9	1 FLA2 TREHY	P80159 treponema h
15	15	31.2	9	2 Q14277	Q14277 homo sapien
16	15	31.2	9	2 Q96T78	Q96t78 homo sapien
17	15	31.2	9	2 Q65711	Q65711 berne virus
18	15	31.2	9	2 Q7SX77	Q7sx77 geochelone
19	14	29.2	8	1 AL17 CARMA	P81820 carcinus ma
20	14	29.2	8	2 P82858	P82858 puccinia re
21	14	29.2	8	2 Q6BCZ9	Q6bcz9 homo sapien
22	14	29.2	8	2 Q7M3N2	Q7m3n2 manduca sex
23	14	29.2	8	2 Q95213	Q95213 cryptotagus
24	14	29.2	8	2 Q6EX61	Q6ex61 isodon hisp
25	14	29.2	8	2 Q8GTG5	Q8gtg5 lycopersico
26	14	29.2	8	2 Q934S4	Q934s4 thiobacillu
27	14	29.2	8	2 Q98YK9	Q98yk9 human immu
28	14	29.2	9	1 AL11 CARMA	P81814 carcinus ma
29	14	29.2	9	1 LMT3 LOCM1	P41489 locusta mig
30	14	29.2	9	1 UP43 HUMAN	P30089 homo sapien
31	14	29.2	9	1 UP47 HUMAN	P30093 homo sapien

32 14 29.2 9 2 Q9UC36 Q9uc36 homo sapien  
33 14 29.2 9 2 Q7RSP2 Q7rsp2 plasmodium  
34 14 29.2 9 2 Q78337 Q78337 caloglossa  
35 14 29.2 9 2 Q81964 Q81964 caloglossa  
36 14 29.2 9 2 Q81966 Q81966 caloglossa  
37 14 29.2 9 2 Q81968 Q81968 caloglossa  
38 14 29.2 9 2 Q8HSL0 Q8hsl0 murrayella  
39 14 29.2 9 2 Q8HSL5 Q8hsl5 spyridia fi  
40 14 29.2 9 2 Q8MDU2 Q8mdu2 hypnea sp.  
41 14 29.2 9 2 Q8ME56 Q8me56 porphyra mi  
42 14 29.2 9 2 Q8ME58 Q8me58 porphyra li  
43 14 29.2 9 2 Q8W7T9 Q8wt9 bostrychia  
44 14 29.2 9 2 Q76FS7 Q76fs7 hypnea japo  
45 14 29.2 9 2 Q76FU1 Q76fu1 plocamium t

## ALIGNMENTS

## RESULT 1

Q7M2N8 PRELIMINARY; PRT; 9 AA.  
AC Q7M2N8;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DE Alpha-2-macroglobulin isoform 1 (Fragment).  
OS Bos indicus (Zebu).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9915;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=96032553; PubMed=7556651; DOI=10.1016/0014-5793(95)00960-H;  
RA Dolmer K., Jenner L.B., Jacobsen L., Andersen G.R., Koch T.J.,  
RA Thirup S., Sottrup-Jensen L., Nyborg J.;  
RT "Crystallisation and preliminary X-ray analysis of the receptor-  
RT binding domain of human and bovine alpha(2)-macroglobulin.";  
RL FEBS Lett. 372:93-95(1995).  
DR PIR; S66635; S66635.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1095 MW; 87B02DD9D769CB1A CRC64;

Query Match 43.8%; Score 21; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred.No. 1.6e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 1;

QY 5 EYPP 8  
DB 3 EYPP 6

## RESULT 2

Q49534 PRELIMINARY; PRT; 8 AA.  
AC Q49534;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE P120 (Fragment).  
GN Name=p120;  
OS Mycoplasma hominis.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2098;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=V2785;  
RA Nyvold C., Birkelund S., Christiansen G.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U22025; AAA67455.1; -.  
FT NON\_TER 1 1

SQ SEQUENCE 8 AA; 869 MW; 914457605B02C05D CRC64;

Query Match 35.4%; Score 17; DB 2; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVEYYP 7  
 :|||  
 Db 2 IVEIIP 6

RESULT 3

ID Q8WFT4 PRELIMINARY; PRT; 9 AA.  
 AC Q8WFT4;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 GN Name=COII;  
 OS Diadema antillarum.  
 OS Diadema antillarum.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Echinoidea; Diademataceae; Diadematoidea; Diadematiidae;  
 OC Diadema.  
 OC NCBI\_TaxID=105358;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=21323357; PubMed=11430656;  
 RA Lessios H.A., Kessing B.D., Pearce J.S.;  
 RT "Population structure and speciation in tropical seas: global  
 phylogeography of the sea urchin *Diadema*."  
 RL Evolution 55:955-975(2001).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=21561594; PubMed=11703875; DOI=10.1098/rspb.2001.1806;  
 RA Lessios H.A., Garrido M.J., Kessing B.D.;  
 RT "Demographic history of *Diadema antillarum*, a keystone herbivore on  
 Caribbean reefs."  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).  
 DR EMBL; AY012858; AAL33832.2;  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 9 AA; 1115 MW; EDF8DB1B173B46CA CRC64;

Query Match 35.4%; Score 17; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.6e+06;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYP 7  
 :|||  
 Db 3 QYLEEQP 9

RESULT 4

ID Q9MSX1 PRELIMINARY; PRT; 8 AA.  
 AC Q9MSX1;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE p8A (Fragment).  
 GN Name=p8A;  
 OS Jurinea humilis.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC campanulids; Asterales; Asteraceae; Carduoideae; Cardueae; Jurinea.  
 OC NCBI\_TaxID=41594;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP O'Hanlon P.C., Briese D.T.;

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF129846; AAF78138.1; -;  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 788 MW; 457451B5A76DDB10 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VEYPT 9  
 :|||  
 Db 1 IEAPT 6

RESULT 5

ID Q8JJ35 PRELIMINARY; PRT; 8 AA.  
 AC Q8JJ35;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE ATP-citrate lyase (Fragment).  
 GN Name=ACL;  
 OS Ficedula hypoleuca.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.  
 OC NCBI\_TaxID=46689;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=21918460; PubMed=11918793;  
 RA Primmer C.R., Borge T., Lindell J., Saetre G.P.;  
 RT "Single-nucleotide polymorphism characterization in species with  
 limited available sequence information: high nucleotide diversity  
 revealed in the avian genome."  
 RL Mol. Ecol. 11:603-612(2002).  
 DR EMBL; AF454211; AAM22897.1; -;  
 DR GO; GO:0016829; P:lyase activity; IEA.  
 KW Lyase.  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 981 MW; 98C77B544681AB02 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QLVYYP 7  
 :|||  
 Db 2 ETMNY 7

RESULT 6

ID Q9TRU7 PRELIMINARY; PRT; 9 AA.  
 AC Q9TRU7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE GAP-3, GTPase-activating protein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RN SEQUENCE.  
 RX MEDLINE=92112868; PubMed=1309786;  
 RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,  
 RA Burgess A.W.;  
 RT "The purification of a Rap1 GTPase-activating protein from bovine  
 brain cytosol.";



RL J. Biol. Chem. 267:1546-1553 (1992).  
 FT NON\_TER 1 1  
 KW Direct protein sequencing.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1063 MW; 89EDA77B47604B5A CRC64;  
 Query Match 33.3%; Score 16; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 VEYP 7  
 Db 4 IYP 7  
 RESULT 7  
 ANG2 BOTJA STANDARD; PRT; 8 AA.  
 AC Q10532;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Angiotensin-like peptide II (Fragment).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OC NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Plasma;  
 RX MEDLINE=96208932; PubMed=8829801; DOI=10.1016/0305-0491(95)02072-1;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the  
 plasma of the snake Bothrops jararaca."  
 RL Comp Biochem. Physiol. 113B:467-473 (1996).  
 CC -!- SIMILARITY: Belongs to the serpin family.  
 DR InterPro; IPR00215; Prot.inh.serp.in.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Direct protein sequencing; Plasma; Serpin; Vasoconstrictor.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;  
 Query Match 31.2%; Score 15; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 YPF 8  
 Db 6 HPF 8  
 RESULT 8  
 UPAA HUMAN STANDARD; PRT; 8 AA.  
 ID UPAA\_HUMAN  
 AC P30936;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Unknown protein from 2D-PAGE of plasma (Spot 36) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=9302937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing."  
 RL Electrophoresis 13:707-714 (1992).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown

CC protein is: 7, its MW is: 12 kDa.  
 DR SWISS-2DPAGE; P30096; HUMAN.  
 KW Direct protein sequencing.  
 FT NON\_TER 1 1  
 FT VARIANT 5 5  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;  
 Query Match 31.2%; Score 15; DB 1; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 LVEYP 7  
 Db 3 LTFYP 7  
 RESULT 9  
 Q15898 PRELIMINARY; PRT; 8 AA.  
 AC Q15898;  
 DT 01-NOV-1996 (TREMELrel. 01, Created)  
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
 DE Homo sapiens (clone XP6A11B) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coobang M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 arrayed cDNAs and cosmid libraries."  
 RL Hum. Mol. Genet. 0:0-0 (1995).  
 DR EMBL; L32078; AAA73888.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;  
 Query Match 31.2%; Score 15; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 YPFT 9  
 Db 3 YPIS 6  
 RESULT 10  
 Q70KG9 PRELIMINARY; PRT; 8 AA.  
 ID Q70KG9;  
 AC Q70KG9;  
 DT 05-JUL-2004 (TREMELrel. 27, Created)  
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
 DE Putative lysosomal glucocerebrosidase (EC 3.2.1.45) (Fragment).  
 GN Name=GBA;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stratil A., Wagenknecht D., Van Poucke M., Kubickova S.,  
 RA Bartschlag H., Musilova P., Rubes J., Geldermann H., Feelman L.J.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ575652; CAE06500.1; -.  
 DR EMBL; AJ575653; CAE06501.1; -.

DR EMBL; AJ575654; CAE06502.1; --  
 DR EMBL; AJ575651; CAE06499.1; --  
 DR GO; GO:0004348; F-glucosylceramidase activity; IEA.  
 DR GO; GO:0016798; F-hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005975; P-carboxylate metabolism; IEA.  
 KW Glycosidase; Hydrolase.  
 FT CHAIN 1 1  
 FT NON\_TER 8 8  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 1019 MW; 5FD40050545B5B10 CRC64;  
 Query Match 31.2%; Score 15; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VEY 6  
 Db :||  
 1 IEY 3  
 RESULT 11  
 Q70Y88 PRELIMINARY; PRT; 8 AA.  
 AC Q70Y88;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Ribosomal protein (Fragment).  
 GN Name=rpel6;  
 OS Platorstoma fimbriatum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Platorstoma.  
 OX NCBI\_TaxID=204168;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;  
 RA Paton A., Springate D.A., Siddle S., Orieno D., Grayer R., Harley M.M.,  
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;  
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)  
 based on three plastid DNA regions."  
 RL Mol. Phylogenet. Evol. 31:277-299(2004).  
 DR EMBL; AJ505368; CAD45489.1; --  
 DR GO; GO:0003735; F-structural constituent of ribosome; IEA.  
 KW Ribosomal protein.  
 FT CHAIN 1 1  
 FT NON\_TER 8 8  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 789 MW; 86786772D1BB4772 CRC64;  
 Query Match 31.2%; Score 15; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PFT 9  
 Db :||  
 2 PFT 4  
 RESULT 12  
 Q6LDQ5 PRELIMINARY; PRT; 8 AA.  
 AC Q6LDQ5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Nitrogen fixation protein (nifQ) (Fragment).  
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
 OC Rhodospirillaceae; Rhodospirillum.  
 OX NCBI\_TaxID=1061;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RT MEDLINE=89213944; PubMed=2708314;  
 RA Moreno-Vivian C., Hennecke S., Puehler A., Klipp W.;  
 RT "Open reading frame 5 (ORF5), encoding a ferredoxinlike protein, and  
 RT nifQ are cotranscribed with nifE, nifN, nifX, and ORF4 in Rhodospirillum  
 capsulatum."  
 RL J. Bacteriol. 171:2591-2598(1989).  
 DR EMBL; M26323; AAA26145.1; --  
 FT CHAIN 1 1  
 FT NON\_TER 8 8  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 890 MW; 2CC40DDDD80769CB CRC64;  
 Query Match 31.2%; Score 15; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 EYP 7  
 Db :||  
 1 EYP 3  
 RESULT 13  
 Q7T282 PRELIMINARY; PRT; 8 AA.  
 AC Q7T282;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Calmodulin (Fragment).  
 OS Geochelone nigra (Galapagos giant tortoise).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Testudines; Cryptodira; Testudinidae; Testudinidae; Geochelone.  
 OX NCBI\_TaxID=66189;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15062813; DOI=10.1016/j.ympev.2004.02.004;  
 RA Caccione A., Gentile G., Burns C., Sezzi E., Bergman W., Ruelle M.,  
 RA Saltonstall K., Powell J.R.;  
 RT "Extreme difference in rate of mitochondrial and nuclear evolution in  
 RT a large ectotherm, Galapagos tortoises."  
 RL Mol. Phylogenet. Evol. 31:794-798(2004).  
 DR EMBL; AY101722; AAM47127.1; --  
 FT CHAIN 1 1  
 FT NON\_TER 8 8  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 892 MW; 5D0769CAA041A874 CRC64;  
 Query Match 31.2%; Score 15; DB 2; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VEYP 7  
 Db :||  
 4 IDFP 7  
 RESULT 14  
 FLA2 TREHY STANDARD; PRT; 9 AA.  
 ID FLA2 TREHY  
 AC P80159;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Flagellar filament outer layer protein flaA2 (35 kDa sheath protein)  
 DE (Fragment).  
 GN Name=flaA2;  
 OS Treponema hyodysenteriae (Serpulina hyodysenteriae).  
 OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspirae.  
 OX NCBI\_TaxID=159;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=C5;  
 RX MEDLINE=93139764; PubMed=1487733;  
 RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,  
 RA van der Zeijst B.A.M., Kusters J.G.;  
 RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are

```

RT composed of two sheath proteins and three core proteins.";
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -|- FUNCTION: Component of the outer layer of the flagella.
CC -|- SUBUNIT: The flagellum consists of an outer layer composed of two
CC sheath proteins, flaA1 (44 kDa) and flaA2 (35 kDa) around a core
CC that contains three proteins flaB1 (37 kDa), flaB2 (34 kDa) and
CC flaB3 (32 kDa).
CC -|- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Direct protein sequencing; Flagellum; Periplasmic.
FT UNSURE 2 2
FT UNSURE 8 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QLVEYYPF 8
Db 1 ETVPYMF 7

RESULT 15
Q14277 PRELIMINARY; PRT; 9 AA.
AC Q14277;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RET protein short form (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94071887; PubMed=7902707;
RA Ceccherini I., Bocciardi R., Luo Y., Pasini B., Hofstra R.,
RA Takahashi M., Romeo G.;
RT "Exon structure and flanking intronic sequences of the human RET
RT proto-oncogene.";
RL Biochem. Biophys. Res. Commun. 196:1288-1295(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94366753; PubMed=8084609;
RA Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T.,
RA Bocciardi R., Nijveen H., Bolino A., Seri M., Ronchetto P., Pasini B.,
RA Bozzano M., Buys C., Romeo G.;
RT "DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
RT the ret proto-oncogene.";
RL Oncogene 9:3025-3029(1994).
DR ENBL; U11532; AAC50102.1; -.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;

Query Match 31.2%; Score 15; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VEYPT 9
Db 2 ISHAFT 7

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 Job time : 182 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:01:43 ; Search time 172 Seconds  
(without alignments)  
20.237 Million cell updates/sec

Title: US-09-674-716B-7  
Perfect score: 48  
Sequence: 1 QQLVEYFPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 330156

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	3 AAY32256	Aay32256 Light cha
2	44	91.7	9	2 AAW39823	Aaw39823 Light cha
3	36	75.0	9	2 AAW39817	Aaw39817 Light cha
4	36	75.0	9	8 ADR38732	Adr38732 Mouse lig
5	34	70.8	9	3 AAY92171	Aay92171 Murine l3
6	33	68.8	9	2 AAR30450	Aar30450 C242:l1 M
7	33	68.8	9	8 ADO43568	Ado43568 Complemen
8	33	68.8	9	8 ADO43562	Ado43562 Complemen
9	31	64.6	9	3 AAY97234	Aay97234 Complemen
10	31	64.6	9	4 AAB82708	Aab82708 VEGF anta
11	31	64.6	9	4 AAE13142	Aae13142 Humanised
12	31	64.6	9	4 AAB82896	Aab82896 Anti-huma
13	31	64.6	9	4 AAG63993	Aag63993 Complemen
14	31	64.6	9	5 AAE25954	Aae25954 Mouse ant
15	31	64.6	9	5 AAU74411	Aau74411 Light cha
16	31	64.6	9	6 ABJ26723	Abj26723 VEGF bind
17	31	64.6	9	8 ADR38200	Adr38200 Mouse VEG
18	31	64.6	9	8 ADR03426	Adr03426 Humanised
19	30	62.5	9	2 AAW39820	Aaw39820 Light cha
20	30	62.5	9	2 AAW39826	Aaw39826 Light cha
21	30	62.5	9	2 AAW59175	Aaw59175 Mouse PAF
22	30	62.5	9	7 ABO33877	Abo33877 Anti-GPI-
23	30	62.5	9	8 ADR03425	Adr03425 Humanised
24	30	62.5	9	8 ADR38731	Adr38731 Mouse lig
25	28	58.3	9	2 AAW24776	Aaw24776 Human imm

ALIGNMENTS

RESULT 1  
AAY32256  
ID AAY32256 standard; peptide; 9 AA.  
XX AAY32256;  
XX  
XX  
DT 15-FEB-2000 (first entry)  
XX  
DE Light chain CDR L3 of mouse anti-CD23 MAb C11.  
XX  
KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; Crohn's disease;  
KW Sjogren's syndrome; allergic rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
therapy.  
XX  
XX Mus musculus.  
OS  
XX  
XX WO958679-A1.  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-GB001434.  
XX  
PR 09-MAY-1998; 98GB-00009839.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
XX WPI; 2000-053101/04.  
DR N-PSDB; AA234741.  
XX  
XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
diabetes, multiple sclerosis and psoriasis.  
XX  
XX Claim 1; Page 40; 81pp; English.  
XX  
XX This sequence represents complementarity determining region 3 (CDR L3)  
of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11  
(see also AAY32262). The invention provides altered antibodies, such as  
chimeric or humanised antibodies, which comprise sufficient of the amino  
acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

26 28 58.3 9 2 AAW73171 Aaw73171 CDR3 of 1  
27 28 58.3 9 2 AAW62016 Aaw62016 Light cha  
28 28 58.3 9 2 AAW80146 Aaw80146 Light cha  
29 28 58.3 9 2 AAY28392 Aay28392 Peptide f  
30 28 58.3 9 2 AAY40428 Aay40428 Amino aci  
31 28 58.3 9 3 AAY82342 Aay82342 Humanised  
32 28 58.3 9 4 AAB83165 Aab83165 Mouse gan  
33 28 58.3 9 8 ADG39003 Adg39003 Humanised  
34 28 58.3 9 8 ADO36522 Ado36522 Human ant  
35 28 58.3 9 8 ADO36516 Ado36516 Human ant  
36 28 58.3 9 8 ADO36534 Ado36534 Human ant  
37 28 58.3 9 8 ADR03423 Adr03423 Humanised  
38 27 56.2 8 2 AAR35879 Aar35879 Hepatitis  
39 27 56.2 8 2 AAR35878 Aar35878 Hepatitis  
40 27 56.2 8 2 AAR35880 Aar35880 Hepatitis  
41 27 56.2 8 6 ADA90363 Ada90363 MS-Roche  
42 27 56.2 8 6 ADA89991 Ada89991 Anti-Abet  
43 27 56.2 8 2 AAW23435 Aaw23435 CDR-3 of  
44 27 56.2 9 2 AAW39877 Aaw39877 Light cha  
45 27 56.2 9 2 AAW89158 Aaw89158 Anti-p53

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents

XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9  
 |||||  
 Db 1 QQLVEYPPT 9

# RESULT 2

AAW39823  
 ID AAW39823 standard; peptide; 9 AA.

AC AAW39823;

DT 16-JUN-1998 (first entry)

DE Light chain CDR3 of catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

OS Mus sp.

PN WO9749800-A1.

XX 31-DEC-1997.

PF 25-JUN-1997; 97WO-US010965.

PR 25-JUN-1996; 96US-00672345.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

PS Claim 15; Page 82; 147pp; English.

XX AAW39821-23 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 2A10, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX Sequence 9 AA;

Query Match 91.7%; Score 44; DB 2; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.8e+06;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9  
 |||||  
 Db 1 QQFVEYPPT 9

# RESULT 3

AAW39817  
 ID AAW39817 standard; peptide; 9 AA.

AC AAW39817;

DT 16-JUN-1998 (first entry)

DE Light chain CDR3 of catalytic antibody 3B9.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

OS Mus sp.

PN WO9749800-A1.

XX 31-DEC-1997.

PF 25-JUN-1997; 97WO-US010965.

PR 25-JUN-1996; 96US-00672345.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

PS Claim 11; Page 81; 147pp; English.

XX AAW39815-17 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)

XX Sequence 9 AA;

Query Match 75.0%; Score 36; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9  
 |||||  
 Db 1 QQFVEYPPT 9

RESULT 4  
 ADR38732  
 ID ADR38732 standard; peptide; 9 AA.  
 XX  
 AC ADR38732;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Mouse light chain variable region CDR3 seqid 134.  
 XX  
 DE antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 KW light chain variable region; complementarity determining region; CDR3.  
 XX  
 OS Mus sp.  
 XX  
 PN US2004175385-A1.  
 XX  
 PD 09-SEP-2004.  
 XX  
 XX 01-AUG-2003; 2003US-00632706.  
 XX  
 XX 31-AUG-1998; 98US-00144886.  
 PR  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Marks JD, Amersdorfer P;  
 PI  
 XX WPI; 2004-652009/63.  
 DR  
 XX  
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 XX  
 XX Example 3; SEQ ID NO 134; 110pp; English.  
 PS  
 XX The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (II) binds to and neutralizes botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, hUC25, Ar1, Ar2, WRI(V), WRI(T), 3-1,  
 CC 3-8, 3-10 and INGL1, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse light chain variable region complementarity determining  
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 75.0%; Score 36; DB 8; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 QQLVEYPFT 9  
 |||: |||

Db 1 QQLISYPLT 9  
 RESULT 5  
 AAY92171  
 ID AAY92171 standard; peptide; 9 AA.  
 XX  
 AC AAY92171;  
 XX  
 DT 01-AUG-2000 (first entry)  
 XX  
 DE Murine 13H10 light chain variable region CDR 3.  
 XX  
 DE Light chain; variable region; complementarity determining region; CDR 3;  
 KW anti-Tie2 kinase receptor; monoclonal antibody; 1588; angiogenetic;  
 KW vascular-general; proliferative; antiischemic; cerebroprotective;  
 KW cardiant; agonist; antibody inhibition.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200018804-A1.  
 XX  
 PD 06-APR-2000.  
 XX  
 XX 28-SEP-1999; 99WO-US022428.  
 PF  
 XX 28-SEP-1998; 98US-0102098P.  
 PR  
 XX (SMIX ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Holmes SD, Erickson-Miller CL, Winkler JD;  
 PI  
 XX WPI; 2000-293114/25.  
 DR  
 XX Tie2 receptor agonist antibodies useful for promoting angiogenesis in  
 PT patients suffering from strokes and myocardial infarctions.  
 XX  
 XX Claim 20; Page 46; 50pp; English.  
 PS  
 XX AAY92169-71 are light chain CDR (complementarity determining regions)  
 CC from a novel murine anti-Tie2 kinase receptor agonist monoclonal antibody  
 CC 13H10. Tie2 is a single-transmembrane, tyrosine kinase receptor ('Tie'  
 CC stands for tyrosine kinase receptor with immunoglobulin and endothelial  
 CC growth factor (EGF) homology domain(s)). Anti-Tie2 antibodies may be  
 CC administered to enhance angiogenesis in mammals suffering from ischemic  
 CC disease, myocardial infarction or cerebral stroke or other vascular  
 CC diseases such as diabetes. It may also be used to enhance endothelial  
 CC cell survival and to promote haematopoietic or megakaryocyte cell  
 CC proliferation (claimed)  
 XX  
 SQ Sequence 9 AA;  
 Query Match 70.8%; Score 34; DB 3; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QLVEXYPT 9  
 | : |||||  
 Db 2 QRLVEYPFT 9  
 |||: |||  
 RESULT 6  
 AAR30450  
 ID AAR30450 standard; peptide; 9 AA.  
 XX  
 AC AAR30450;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 06-MAY-1993 (first entry)  
 XX  
 DE C242:11 MAB kappa chain CDR3.  
 XX

KW Kappa; Chain: heavy; complementarity determining region: CDR; Mab;  
 KW monoclonal antibody; C242:II; murine; IGG; hybridoma; cell line; spleen;  
 XX human; colonic; adenocarcinoma; myeloma; Sp2/0; antigen; endocytosis.  
 XX Synthetic.  
 XX OS  
 PN BP521842-A2.  
 XX  
 XX 07-JAN-1993.  
 PD  
 XX  
 XX 03-JUL-1992; 92EP-00850166.  
 PF  
 XX  
 XX 03-JUL-1991; 91SE-00002074.  
 PR  
 XX  
 XX (KABI ) KABI PHARMACIA AB.  
 PA (PHAA ) PHARMACIA & UPJOHN AB.  
 XX  
 XX Lindholm L, Holmgren J, Lind P;  
 PI  
 XX WPI; 1993-002345/01.  
 DR  
 XX Monoclonal antibody reacting with CA-242 antigen - obtd. by culturing  
 PT hybridoma cell line C242:II or mutants; useful for diagnosis and therapy  
 PT of pancreatic or colorectal cancers.  
 PT  
 XX  
 XX Claim 5; Page 11; 15pp; English.  
 PS  
 XX The sequences given in AAR30448-50 represent the kappa chain and AAR30451  
 CC -S3 the heavy chain complementarity determining regions (CDR) of a  
 CC monoclonal antibody (MAB), C242:II. C242:II is a monoclonal murine Ab of  
 CC IGG class produced when culturing in an appropriate medium a hybridoma  
 CC cell line obtained by fusing spleen cells from a mouse, which has been  
 CC immunised with a human colonic adenocarcinoma cell line, with the murine  
 CC myeloma cell line Sp2/0. C242:II when bound to a cell surface antigen is  
 CC capable of being endocytosed or internalised into cells. (Updated on 25-  
 CC MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 CC  
 XX  
 SQ Sequence 9 AA;  
 Query Match 68.8%; Score 33; DB 2; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QLVEYPPT 9  
 Db | : |||||  
 2 QHLEYPPT 9  
 RESULT 7  
 ADO43568  
 ID ADO43568 standard; peptide; 9 AA.  
 XX  
 AC ADO43568;  
 XX  
 XX 29-JUL-2004 (first entry)  
 DT  
 XX Complementarity determining region from light chain clone 209-564.  
 DE  
 XX human; A34 protein; A33-like 3 protein; A33/JAM family; chromosome X;  
 KW chromosome 1; cancer; oesophageal cancer; ovarian cancer; stomach cancer;  
 KW Complementarity determining region; CDR; antibody.  
 XX  
 XX Mus musculus.  
 OS  
 XX WO2004037999-A2.  
 PN  
 XX 06-MAY-2004.  
 PD  
 XX 23-OCT-2003; 2003WO-US033707.  
 PF  
 XX 23-OCT-2002; 2002US-0420285P.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 XX Scanlan M, Ritter G, Old L, Jungbluth A;  
 PI WPI; 2004-365509/34.  
 DR  
 XX New pure immunoglobulin molecule that binds specifically to A34 antigen,  
 PT useful in preparing a composition for diagnosing or treating cancer.  
 PT  
 XX Claim 36; Fig 24; 99pp; English.  
 PS  
 XX ADO43560-ADO43577 represent the complementarity determining regions  
 CC (CDRs) from murine A34 variable light and heavy chains. The specification  
 CC describes A34 and A33-like 3 proteins, and immunoglobulin molecules that  
 CC bind specifically to their antigens. A34 and A33-like 3 proteins are  
 CC members of the A33/JAM family. The A34 gene is mapped to chromosome X,  
 CC and the A33-like 3 gene is mapped to chromosome 1. Immunoglobulin  
 CC molecules of the invention useful in preparing a composition for  
 CC diagnosing or treating cancer, especially oesophageal, ovarian and  
 CC stomach cancers.  
 CC  
 XX Sequence 9 AA;  
 SQ  
 Query Match 68.8%; Score 33; DB 8; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QLVEYPPT 9  
 Db | : |||||  
 2 QHLEYPPT 9  
 RESULT 8  
 ADO43562  
 ID ADO43562 standard; peptide; 9 AA.  
 XX  
 AC ADO43562;  
 XX  
 XX 29-JUL-2004 (first entry)  
 DT  
 XX Complementarity determining region from light chain clone 209-970.  
 DE  
 XX human; A34 protein; A33-like 3 protein; A33/JAM family; chromosome X;  
 KW chromosome 1; cancer; oesophageal cancer; ovarian cancer; stomach cancer;  
 KW Complementarity determining region; CDR; antibody.  
 XX  
 XX Mus musculus.  
 OS  
 XX WO2004037999-A2.  
 PN  
 XX 06-MAY-2004.  
 PD  
 XX 23-OCT-2003; 2003WO-US033707.  
 PF  
 XX 23-OCT-2002; 2002US-0420285P.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 XX Scanlan M, Ritter G, Old L, Jungbluth A;  
 PI WPI; 2004-365509/34.  
 DR  
 XX New pure immunoglobulin molecule that binds specifically to A34 antigen,  
 PT useful in preparing a composition for diagnosing or treating cancer.  
 PT  
 XX Claim 36; Fig 24; 99pp; English.  
 PS  
 XX ADO43560-ADO43577 represent the complementarity determining regions  
 CC (CDRs) from murine A34 variable light and heavy chains. The specification  
 CC describes A34 and A33-like 3 proteins, and immunoglobulin molecules that  
 CC bind specifically to their antigens. A34 and A33-like 3 proteins are  
 CC members of the A33/JAM family. The A34 gene is mapped to chromosome X,  
 CC and the A33-like 3 gene is mapped to chromosome 1. Immunoglobulin

PA (LUDW-) LUDWIG INST CANCER RES.  
 XX Scanlan M, Ritter G, Old L, Jungbluth A;  
 PI WPI; 2004-365509/34.  
 DR  
 XX New pure immunoglobulin molecule that binds specifically to A34 antigen,  
 PT useful in preparing a composition for diagnosing or treating cancer.  
 PT  
 XX Claim 36; Fig 24; 99pp; English.  
 PS  
 XX ADO43560-ADO43577 represent the complementarity determining regions  
 CC (CDRs) from murine A34 variable light and heavy chains. The specification  
 CC describes A34 and A33-like 3 proteins, and immunoglobulin molecules that  
 CC bind specifically to their antigens. A34 and A33-like 3 proteins are  
 CC members of the A33/JAM family. The A34 gene is mapped to chromosome X,  
 CC and the A33-like 3 gene is mapped to chromosome 1. Immunoglobulin  
 CC molecules of the invention useful in preparing a composition for  
 CC diagnosing or treating cancer, especially oesophageal, ovarian and  
 CC stomach cancers.  
 CC  
 XX Sequence 9 AA;  
 SQ  
 Query Match 68.8%; Score 33; DB 8; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QLVEYPPT 9  
 Db | : |||||  
 2 QHLEYPPT 9  
 RESULT 8  
 ADO43562  
 ID ADO43562 standard; peptide; 9 AA.  
 XX  
 AC ADO43562;  
 XX  
 XX 29-JUL-2004 (first entry)  
 DT  
 XX Complementarity determining region from light chain clone 209-970.  
 DE  
 XX human; A34 protein; A33-like 3 protein; A33/JAM family; chromosome X;  
 KW chromosome 1; cancer; oesophageal cancer; ovarian cancer; stomach cancer;  
 KW Complementarity determining region; CDR; antibody.  
 XX  
 XX Mus musculus.  
 OS  
 XX WO2004037999-A2.  
 PN  
 XX 06-MAY-2004.  
 PD  
 XX 23-OCT-2003; 2003WO-US033707.  
 PF  
 XX 23-OCT-2002; 2002US-0420285P.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 XX Scanlan M, Ritter G, Old L, Jungbluth A;  
 PI WPI; 2004-365509/34.  
 DR  
 XX New pure immunoglobulin molecule that binds specifically to A34 antigen,  
 PT useful in preparing a composition for diagnosing or treating cancer.  
 PT  
 XX Claim 36; Fig 24; 99pp; English.  
 PS  
 XX ADO43560-ADO43577 represent the complementarity determining regions  
 CC (CDRs) from murine A34 variable light and heavy chains. The specification  
 CC describes A34 and A33-like 3 proteins, and immunoglobulin molecules that  
 CC bind specifically to their antigens. A34 and A33-like 3 proteins are  
 CC members of the A33/JAM family. The A34 gene is mapped to chromosome X,  
 CC and the A33-like 3 gene is mapped to chromosome 1. Immunoglobulin



CC molecules of the invention useful in preparing a composition for  
 CC diagnosing or treating cancer, especially oesophageal, ovarian and  
 CC stomach cancers.

XX Sequence 9 AA;

Query Match 58.8%; Score 33; DB 8; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPPT 9

DB 2 QHLEYPT 9

RESULT 9

AAAY97234

ID AAY97234 standard; protein; 9 AA.

AC AAY97234;

XX 19-DEC-2000 (first entry)

DT Complementary determining region (CDRL3) of anti-SI (KDR) antibody.

DE Immunoglobulin; antibody; complementary determining region; CDR; VEGF;  
 XX vascular endothelial growth factor; KDR;  
 KW kinase insert domain containing receptor; multivalent; monovalent;  
 KW humanised antibody; chimeric antibody; tumour; diabody; triabody;  
 KW glioblastoma multiforme; hemangioblastoma; AIDS;  
 KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;  
 KW acquired immune deficiency syndrome; AIDS; human.

XX Homo sapiens.

OS Synthetic.

OS WO200044777-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US002180.

XX 29-JAN-1999; 99US-00240736.

XX 29-JAN-1999; 99US-0117726P.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Zhu Z, Witte L;

XX WPI; 2000-505966/45.

XX N-PSDB; AAAS3766.

XX Novel immunoglobulin molecules binding kinase insert domain-containing

XX receptor with the same affinity as vascular endothelial growth factor,

XX used to reduce tumor growth.

XX Claim 3; Page 50; 55pp; English.

XX New immunoglobulin molecules are described that bind kinase insert domain

XX -containing receptor (KDR) with a comparable affinity to human vascular

XX endothelial growth factor (VEGF). The antibodies neutralise KDR

XX activation. The immunoglobulin may be a multivalent single chain

XX antibody, a monovalent single chain antibody, a diabody, a triabody, a

XX humanised antibody or a chimerised antibody. The immunoglobulin molecules

XX bind specifically to an extracellular domain of the KDR receptor with the

XX same affinity as VEGF. Overexpression of VEGF has been implicated in a

XX number of human tumour cell lines including glioblastoma multiforme,

XX hemangioblastoma, central nervous system neoplasms and AIDS associated

XX Kaposi's sarcoma. The antibodies therefore have applications in treating

XX these conditions. This sequence encodes a preferred heavy chain

XX complementary determining region of the immunoglobulins of the invention

XX Sequence 9 AA;

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QY 1 QQLVEYPPT 9

DB 1 QQRSSYPPT 9

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Query Match 64.6%; Score 31; DB 3; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9

DB 1 QQRSSYPPT 9

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Query Match 64.6%; Score 31; DB 3; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9

DB 1 QQRSSYPPT 9

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CC central nervous system tumour, neuroblastoma, glioblastoma multiforme or  
 CC melanoma (all claimed). (Updated on 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 9 AA; 64.6%; Score 31; DB 4; Length 9;  
 Query Match 66.7%; Pred. No. 1.8e+06;  
 Best Local Similarity 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
 |||||  
 DB 1 QQRSSYPFT 9

RESULT 11  
 AAEL13142  
 ID AAEL13142 standard; peptide; 9 AA.  
 XX  
 AC AAEL13142;  
 XX  
 DT 28-JAN-2002 (first entry)  
 XX  
 DE Humanised antibody murine light chain hypervariable region (VL) CDR3.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;  
 KW cystostatic; light chain hypervariable region; VL; myelocytic leukaemia;  
 KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;  
 KW Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200174296-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PP 30-MAR-2001; 2001WO-US010504.  
 XX  
 PR 31-MAR-2000; 2000US-00540770.  
 XX  
 XX (IMCL-) IMCLONE SYSTEMS INC.  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Witte L, Rafil S;  
 XX  
 DR WPI; 2001-662942/76.  
 DR N-PSDB; AAD21668.  
 XX  
 PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow  
 PT tumors such as leukemias or multiple myeloma comprises treatment with an  
 PT antagonist of a vascular endothelial growth factor receptor.  
 XX  
 PS Claim 8; Page 15; 68pp; English.  
 XX  
 CC The invention relates to a method for inhibiting the growth of non-solid  
 CC tumour cells that are stimulated by a ligand of vascular endothelial  
 CC growth factor receptor (VEGFR) in mammals particularly humans. The method  
 CC involves treating the mammals with humanised VEGFR monoclonal antibodies  
 CC (antagonists). Humanised monoclonal antibody comprises humanised mouse  
 CC variable region joined to human constant region, where the humanised  
 CC mouse variable region contains mouse complementarity determining region  
 CC (CDR) grafted into human variable region. The method is useful for  
 CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute  
 CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,  
 CC multiple myelomas and lymphoid cells, particularly those related to non-  
 CC Hodgkin's and Hodgkin's disease. The present sequence is humanised  
 CC antibody murine light chain hypervariable region (VL) CDR-3 used in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 9 AA;  
 Query Match 64.6%; Score 31; DB 4; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
 |||||  
 DB 1 QQRSSYPFT 9

RESULT 12  
 AAB82896  
 ID AAB82896 standard; peptide; 9 AA.  
 XX  
 AC AAB82896;  
 XX  
 DT 26-NOV-2001 (first entry)  
 XX  
 DE Anti-human CD154 antibody ABI793 light chain variable region CDR3.  
 XX  
 KW CD154; gp39; CD40-L; antibody; ABI793; transplant rejection;  
 KW autoimmune disease; inflammation; atherosclerosis; Alzheimer's disease;  
 KW antiinflammatory; antiarteriosclerotic; immunosuppressive; therapy;  
 KW complementarity determining region; CDR3.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200168860-A1.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 14-MAR-2001; 2001WO-EP002875.  
 XX  
 PR 16-MAR-2000; 2000GB-00006398.  
 XX  
 XX (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Di Padova FE, Schuler W;  
 XX  
 DR WPI; 2001-590062/66.  
 XX  
 PT CD154 binding molecule, in particular antibody to human CD154 for use in  
 PT treatment, prevention of autoimmune, inflammatory diseases,  
 PT atherosclerosis, Alzheimer's disease and prevention of transplant  
 PT rejection.  
 XX  
 PS Claim 2; Page 23; 37pp; English.  
 XX  
 CC The present sequence is that of complementarity determining region 3  
 CC (CDR3) of the light chain variable region (VL; see also AAB82890) of  
 CC mouse anti-human CD154 monoclonal antibody ABI793. The invention provides  
 CC a CD154 binding molecule, in particular an antibody to human CD154, in  
 CC which the VH region has the CDR1, CDR2 and CDR3 of ABI793 VH and the VL  
 CC region has the CDR1, CDR2 and CDR3 of ABI793 VL. The CD154 binding  
 CC molecule is especially a human antibody in which the VH and VL domains  
 CC are essentially those of ABI793, with constant regions from human heavy  
 CC and light chains. The antibodies are used to inhibit an immune response  
 CC mediated by CD154-positive cell interactions with CD40-positive cells, in  
 CC the treatment and/or prevention of diseases, disorders or conditions  
 CC where CD154 modulation and/or interference with or inhibition of the  
 CC CD154:CD40 interactions is therapeutically beneficial, prevention of  
 CC macrophage-associated inflammatory processes and in the treatment of  
 CC diseases where suppression of antibody responses to antigens is desirable  
 CC (claimed). The CD154 binding molecules are useful for prevention of cell,  
 CC tissue or organ graft rejection, in the prevention and treatment of  
 CC autoimmune or inflammatory diseases, atherosclerosis or Alzheimer's  
 CC disease, and also for inhibiting B cell proliferation and  
 CC differentiation, T cell responses, induction or modulation of T or B cell  
 CC tolerance or inhibition of the growth of tumour cells expressing CD154  
 CC antigen. Such conditions include autoimmune and non-autoimmune disorders,  
 CC in particular, Addison's disease, Celiac sprue, glomerulonephritis,  
 CC Grave's disease, Hashimoto's thyroiditis, haemolytic disease of the  
 CC newborn, keratitis, multiple sclerosis, polymyositis, psoriasis,  
 CC rheumatic fever, rheumatoid arthritis, sarcoidosis, syphilis,  
 CC tuberculosis, ulcerative colitis, HIV infection, leukaemia or lymphoma  
 XX

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SQ Sequence 9 AA;
Query Match 64.6%; Score 31; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 1 QQYNSYPPT 9

RESULT 13
AAG63993
ID AAG63993 standard; peptide; 9 AA.
XX
AC AAG63993;
XX
DT 26-NOV-2001 (first entry)
XX
DE Complementarity determining region of light chain of antibody 2C4.
XX
KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
KW leukemia; eosinophil.
XX
OS Mus sp.
XX
PN WO200166126-A1.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US007193.
XX
PR 07-MAR-2000; 2000US-0187595P.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX
PI Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
PI Schleimer R;
XX
XX WPI; 2001-570749/64.
XX
XX
PT Novel monoclonal antibody specific for human sialoadhesin factor-2 for
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal.
XX
PS Claim 10; Page 34; 35pp; English.
XX
XX AAG63991-93 represent the complementarity determining regions (CDRs) of
XX the light chain variable region of murine monoclonal antibody 2C4. This
XX antibody binds to human sialoadhesin factor-2 (SAF-2). The antibody is
XX useful for treating or preventing allergic rhinitis, allergies, asthma,
XX anemia, eczema or diseases such as lymphoma, leukemia or systemic
XX mastocytosis in a mammal. It is also useful for detecting the presence of
XX a cell, especially eosinophil in a sample, by detecting binding of the
XX antibody to SAF-2. The antibody can be coupled to toxins,
XX antiproliferative drugs or radionuclides to kill cells in areas of
XX excessive SAF-2 expression
XX
SQ Sequence 9 AA;
Query Match 64.6%; Score 31; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 1 QQRSSYPPT 9

RESULT 14
AAG63993
ID AAG63993 standard; peptide; 9 AA.
XX
AC AAG63993;
XX
DT 26-NOV-2001 (first entry)
XX
DE Complementarity determining region of light chain of antibody 2C4.
XX
KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
KW leukemia; eosinophil.
XX
OS Mus sp.
XX
PN WO200166126-A1.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US007193.
XX
PR 07-MAR-2000; 2000US-0187595P.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX
PI Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
PI Schleimer R;
XX
XX WPI; 2001-570749/64.
XX
XX
PT Novel monoclonal antibody specific for human sialoadhesin factor-2 for
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal.
XX
PS Claim 10; Page 34; 35pp; English.
XX
XX AAG63991-93 represent the complementarity determining regions (CDRs) of
XX the light chain variable region of murine monoclonal antibody 2C4. This
XX antibody binds to human sialoadhesin factor-2 (SAF-2). The antibody is
XX useful for treating or preventing allergic rhinitis, allergies, asthma,
XX anemia, eczema or diseases such as lymphoma, leukemia or systemic
XX mastocytosis in a mammal. It is also useful for detecting the presence of
XX a cell, especially eosinophil in a sample, by detecting binding of the
XX antibody to SAF-2. The antibody can be coupled to toxins,
XX antiproliferative drugs or radionuclides to kill cells in areas of
XX excessive SAF-2 expression
XX
SQ Sequence 9 AA;
Query Match 64.6%; Score 31; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 1 QQRSSYPPT 9

RESULT 15
AAU74411
ID AAU74411 standard; peptide; 9 AA.
XX
AC AAU74411;
XX
DT 26-MAR-2002 (first entry)
XX
DE Light chain complementarity determining region L3 (CDRL3).
XX
KW Complementarity determining region; CDR; CDRL3; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
XX antibody light chain variable domain.
XX

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AAE25954
ID AAE25954 standard; peptide; 9 AA.
XX
AC AAE25954;
XX
DT 15-NOV-2002 (first entry)
XX
XX Mouse anti-KDR p1C11 scFv antibody CDRL3 peptide.
XX
XX Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;
XX foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;
XX VEGF; tumour growth; light chain complementarity determining region 3;
XX CDRL3; angiogenesis; p1C11; scFv antibody.
XX
XX Mus musculus.
XX
XX US2002064528-A1.
XX
XX 30-MAY-2002.
XX
XX 12-OCT-2001; 2001US-00976787.
XX
XX 28-JAN-2000; 2000US-00493539.
XX
XX (ZHUZ/) ZHU Z.
XX (WITT/) WITTE L.
XX
XX Zhu Z, Witte L;
XX
XX WPI; 2002-589175/63.
XX N-PSDB; AAD42819.
XX
XX Novel immunoglobulin molecule for reducing tumor growth, binds to kinase
XX insert domain-containing receptor with an affinity comparable to human
XX vascular endothelial growth factor, and neutralizes activation of KDR.
XX
XX Claim 3; Page 11; 34pp; English.
XX
XX The present invention relates to novel immunoglobulin molecules that bind
XX to kinase insert domain-containing receptor (KDR) (a human homologue of
XX mouse foetal liver kinase (Flk)-1 receptor) with an affinity comparable
XX to human vascular endothelial growth factor (VEGF) and that neutralises
XX activation of KDR. Sequences of the invention are useful for neutralising
XX the activation of KDR, for reducing tumour growth and for inhibiting
XX angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody
XX light chain complementarity determining region 3 (CDRL3) protein
XX
XX Sequence 9 AA;
Query Match 64.6%; Score 31; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 1 QQRSSYPPT 9

RESULT 15
AAU74411
ID AAU74411 standard; peptide; 9 AA.
XX
AC AAU74411;
XX
DT 26-MAR-2002 (first entry)
XX
DE Light chain complementarity determining region L3 (CDRL3).
XX
KW Complementarity determining region; CDR; CDRL3; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
XX antibody light chain variable domain.
XX

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Mus sp.
XX WO200190192-A2.
XX
XX
XX PD
XX PF
XX PR
XX PR
XX PA
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX PI
XX
XX WPI; 2002-106189/14.
XX N-PSDB; AAS20282.
XX
XX New bispecific immunoglobulin-like antigen-binding protein for reducing
PT tumor growth and for inhibiting angiogenesis, comprises a complex of two
PT polypeptides and two second polypeptides.
XX
XX Claim 55; Page 57; 64pp; English.
XX
XX The invention describes an antigen-binding protein (I) comprising a
CC complex of two polypeptides (P1) and two second polypeptides (P2) which
CC are stably associated in an immunoglobulin like complex. P1 has an
CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
CC light chain constant domain (CL domain), and P2 has an antigen-binding
CC site located to the N terminus of the CH1 domain. (I) is useful for:
CC neutralising the activation of a vascular endothelial growth factor
CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
CC reducing endothelial cell proliferation; blocking interaction of a protein and
CC migration of human leukaemia cells; blocking interaction of a protein and
CC its ligand; promoting interactions between immune cells and target cells;
CC and in vivo and in vitro for investigative, diagnostic or treatment
CC methods. The design of (I) provides for efficient production so that
CC substantially all of the antigen-binding proteins produced are assembled
CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
CC and in tetrameric form. The heavy chain constant domains which constitute
CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
CC antibody and which provide other antibody functions can be present. There
CC is no requirement for processing in vitro to obtain the complete product.
CC This peptide sequence represents the light chain variable domain
CC complementarity determining region L3 (CDRL3) incorporated into an
CC antigen-binding protein described in the method of the invention
XX
XX Sequence 9 AA;

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Query Match          64.6%; Score 31; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 QQLVEVPFT 9
   |||||
Db 1 QQRSSYPFT 9

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Job time : 175 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370583 residues

Total number of hits satisfying chosen parameters: 138632

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	36	75.0	9	10	US-09-940-727B-21
3	36	75.0	9	16	US-10-632-706-134
4	33	68.8	9	16	US-10-823-253-20
5	31	64.6	9	9	US-09-976-787-6
6	31	64.6	9	9	US-09-865-198-6
7	31	64.6	9	10	US-09-798-689-6
8	31	64.6	9	14	US-10-232-187-10
9	31	64.6	9	15	US-10-221-529-10
10	30	62.5	9	9	US-09-828-708-51
11	30	62.5	9	10	US-09-940-727B-24
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13	30	62.5	9	16	US-10-632-706-133

14	29	60.4	9	17	US-10-842-011-20	Sequence 20, Appl
15	29	60.4	9	17	US-10-842-011-37	Sequence 37, Appl
16	28	58.3	9	10	US-09-795-798-15	Sequence 15, Appl
17	28	58.3	9	14	US-10-195-752-110	Sequence 110, Appl
18	28	58.3	9	16	US-10-703-714-30	Sequence 30, Appl
19	28	58.3	9	16	US-10-703-714-36	Sequence 36, Appl
20	28	58.3	9	16	US-10-703-711-48	Sequence 48, Appl
21	28	58.3	9	17	US-10-783-311-138	Sequence 138, Appl
22	27	56.2	9	10	US-09-155-106-6	Sequence 6, Appl
23	27	56.2	9	10	US-09-940-727B-81	Sequence 81, Appl
24	27	56.2	9	13	US-10-091-236-16	Sequence 16, Appl
25	27	56.2	9	13	US-10-032-482-14	Sequence 14, Appl
26	27	56.2	9	14	US-10-091-313-6	Sequence 6, Appl
27	27	56.2	9	14	US-10-091-268-6	Sequence 6, Appl
28	27	56.2	9	14	US-10-268-501-12	Sequence 12, Appl
29	27	56.2	9	15	US-10-372-715-13	Sequence 13, Appl
30	27	56.2	9	15	US-10-608-626-12	Sequence 12, Appl
31	27	56.2	9	17	US-10-808-538-6	Sequence 6, Appl
32	26	54.2	7	14	US-10-128-581-7	Sequence 7, Appl
33	26	54.2	7	15	US-10-463-699-7	Sequence 7, Appl
34	26	54.2	7	16	US-10-776-172-7	Sequence 7, Appl
35	26	54.2	7	17	US-10-897-005-7	Sequence 7, Appl
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42	26	54.2	9	9	US-09-293-854-7	Sequence 7, Appl
43	26	54.2	9	9	US-09-996-288-16	Sequence 16, Appl
44	26	54.2	9	10	US-09-977-797A-62	Sequence 62, Appl
45	26	54.2	9	10	US-09-977-797A-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1  
US-09-940-727B-27  
; Sequence 27, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940, 727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-27

Query Match 91.7%; Score 44; DB 10; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.3e+06;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEVPFT 9  
|||  
Db 1 QQFVEVPFT 9

RESULT 2  
US-09-940-727B-21  
; Sequence 21, Application US/09940727B

; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-21

Query Match 75.0%; Score 36; DB 10; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
| | | | |  
Db 1 QHFDVYPFT 9

RESULT 3  
US-10-632-706-134  
; Sequence 134, Application US/10632706  
; Publication No. US20040175385A1  
; GENERAL INFORMATION:  
; APPLICANT: AMERSDORFER, PETER  
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
; FILE REFERENCE: 407T-8951200S  
; CURRENT APPLICATION NUMBER: US/10/632,706  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US 60/400,721  
; PRIOR FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 09/144,806  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 134  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-134

Query Match 75.0%; Score 36; DB 16; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
| | | | |  
Db 1 QQLISYPLT 9

RESULT 4  
US-10-823-253-20  
; Sequence 20, Application US/10823253  
; Publication No. US2005002934A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Jennifer  
; TITLE OF INVENTION: RECOMBINANT IL-9 ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 10271-112-999

; CURRENT APPLICATION NUMBER: US/10/823,253  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: 60/462,259  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/477,797  
; PRIOR FILING DATE: 2003-06-10  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-823-253-20

Query Match 68.8%; Score 33; DB 16; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
| | | | |  
Db 1 QQFVEYPLT 9

RESULT 5  
US-09-976-787-6  
; Sequence 6, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-976-787-6

Query Match 64.6%; Score 31; DB 9; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
| | | | |  
Db 1 QQRSSYPFT 9

RESULT 6  
US-09-865-198-6  
; Sequence 6, Application US/09865198  
; Patent No. US20020103345A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods  
; FILE REFERENCE: 11245/47102  
; CURRENT APPLICATION NUMBER: US/09/865,198  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: US 60/206,749  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT

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; ORGANISM: Mouse
US-09-865-198-6

Query Match          64.6%; Score 31; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
   |||
Db 1 QQRSSYPFT 9

RESULT 7
US-09-798-689-6
; Sequence 6, Application US/09798689
; Publication No. US20030103973A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; TITLE OF INVENTION: Combined with Radiation and Chemotherapy
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-6

Query Match          64.6%; Score 31; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
   |||
Db 1 QQRSSYPFT 9

RESULT 8
US-10-232-187-10
; Sequence 10, Application US/10232187
; Publication No. US20030092091A1
; GENERAL INFORMATION:
; APPLICANT: Abrahamson, Julie A.
; APPLICANT: Bochner, Bruce
; APPLICANT: Erickson-Miller, Connie L.
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Schleimer, Robert
; APPLICANT: Nulku, Turkan E.
; TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
; FILE REFERENCE: GH50042-1
; CURRENT APPLICATION NUMBER: US/10/232,187
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/187,595
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: PCT/US01/07193
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/315,943
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; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/349,830
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/394,741
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-187-10

Query Match          64.6%; Score 31; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
   |||
Db 1 QQRSSYPFT 9

RESULT 9
US-10-221-529-10
; Sequence 10, Application US/10221529
; Publication No. US20040038293A1
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS AG
; TITLE OF INVENTION: ANTIBODIES TO HUMAN CD154
; FILE REFERENCE: 4-31266A
; CURRENT APPLICATION NUMBER: US/10/221,529
; CURRENT FILING DATE: 2003-05-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-221-529-10

Query Match          64.6%; Score 31; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
   |||
Db 1 QQVNSYPFT 9

RESULT 10
US-09-828-708-51
; Sequence 51, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Burton, D.
; APPLICANT: Ditzel, H.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-51

Query Match          62.5%; Score 30; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 QQLVEYPFT 9  
||| |||  
DB 1 QQLNSYPLT 9

## RESULT 11

US-09-940-727B-24  
; Sequence 24, Application US/09940727B  
; Publication No. US2003007793A1

## GENERAL INFORMATION:

; APPLICANT: Landry, Donald W

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 0575/51400-B

; CURRENT APPLICATION NUMBER: US/09/940,727B

; CURRENT FILING DATE: 2002-09-04

; PRIOR APPLICATION NUMBER: 09/214,095

; PRIOR FILING DATE: 1998-12-28

; PRIOR APPLICATION NUMBER: PCT/US97/10965

; PRIOR FILING DATE: 1997-06-25

; PRIOR APPLICATION NUMBER: 08/672,345

; PRIOR FILING DATE: 1996-06-25

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 24

; LENGTH: 9

; TYPE: PRT

; ORGANISM: mouse

US-09-940-727B-24

Query Match 62.5%; Score 30; DB 10; Length 9;  
Best Local Similarity 55.6%; Pred. No. 1.3e+06;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
| : |||  
DB 1 QHFEDYPFT 9

## RESULT 12

US-09-940-727B-30

; Sequence 30, Application US/09940727B

; Publication No. US2003007793A1

## GENERAL INFORMATION:

; APPLICANT: Landry, Donald W

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 0575/51400-B

; CURRENT APPLICATION NUMBER: US/09/940,727B

; CURRENT FILING DATE: 2002-09-04

; PRIOR APPLICATION NUMBER: 09/214,095

; PRIOR FILING DATE: 1998-12-28

; PRIOR APPLICATION NUMBER: PCT/US97/10965

; PRIOR FILING DATE: 1997-06-25

; PRIOR APPLICATION NUMBER: 08/672,345

; PRIOR FILING DATE: 1996-06-25

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 30

; LENGTH: 9

; TYPE: PRT

; ORGANISM: mouse

US-09-940-727B-30

Query Match 62.5%; Score 30; DB 10; Length 9;  
Best Local Similarity 55.6%; Pred. No. 1.3e+06;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
| : |||  
DB 1 QHFEDYPFT 9

## RESULT 13

US-10-632-706-133

; Sequence 133, Application US/10632706

; Publication No. US20040175385A1

## GENERAL INFORMATION:

; APPLICANT: MARKS, JAMES D.

; APPLICANT: AMERSDORFER, PETER

; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM

; TITLE OF INVENTION: NEUROTOXINS

; FILE REFERENCE: 407T-895120US

; CURRENT APPLICATION NUMBER: US/10/632,706

; CURRENT FILING DATE: 2003-08-01

; PRIOR APPLICATION NUMBER: US 60/400,721

; PRIOR FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: US 09/144,806

; PRIOR FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 278

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 133

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: single chain antibody fragment

US-10-632-706-133

Query Match 62.5%; Score 30; DB 16; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
||| |||  
DB 1 QQLNSYPLT 9

## RESULT 14

US-10-842-011-20

; Sequence 20, Application US/10842011

; Publication No. US20050025763A1

## GENERAL INFORMATION:

; APPLICANT: Protein Design Labs

; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES

; FILE REFERENCE: 05882.0110.NPUS04

; CURRENT APPLICATION NUMBER: US/10/842,011

; CURRENT FILING DATE: 2004-05-07

; NUMBER OF SEQ ID NOS: 93

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 20

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-842-011-20

Query Match 60.4%; Score 29; DB 17; Length 9;  
Best Local Similarity 55.6%; Pred. No. 1.3e+06;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
||| |||  
DB 1 QQYSSYPPT 9

## RESULT 15

US-10-842-011-37

; Sequence 37, Application US/10842011

; Publication No. US20050025763A1

## GENERAL INFORMATION:

; APPLICANT: Protein Design Labs

; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES

; FILE REFERENCE: 05882.0110.NPUS04

; CURRENT APPLICATION NUMBER: US/10/842,011

; CURRENT FILING DATE: 2004-05-07

; NUMBER OF SEQ ID NOS: 93

; SOFTWARE: PatentIn version 3.2



; SEQ ID NO 37  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-842-011-37

Query Match 60.4%; Score 29; DB 17; Length 9;  
Best Local Similarity 55.6%; Pred. No. 1.3e+06;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYDPT 9  
|||  
Db 1 QQYSSVEYT 9

Search completed: April 18, 2005, 15:31:28  
Job time : 130 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:10:42 ; Search time 44 Seconds  
(without alignments)  
15.269 Million cell updates/sec

Title: US-09-674-716B-7  
Perfect score: 48  
Sequence: 1 QQLVEYFPFT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 99282

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: +  
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4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
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6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	91.7	9	2	US-08-672-345C-27
2	44	91.7	9	3	US-09-214-095D-27
3	36	75.0	9	2	US-08-672-345C-21
4	36	75.0	9	3	US-09-214-095D-21
5	34	70.8	9	3	US-09-406-532-20
6	33	68.8	9	1	US-08-438-123-3
7	32	66.7	9	1	US-08-264-093-26
8	31	64.6	9	4	US-09-798-689-6
9	30	62.5	9	2	US-08-672-345C-24
10	30	62.5	9	2	US-08-672-345C-30
11	30	62.5	9	3	US-09-214-095D-24
12	30	62.5	9	3	US-09-214-095D-30
13	28	58.3	9	2	US-08-116-778E-11
14	28	58.3	9	2	US-08-438-562-11
15	28	58.3	9	2	US-08-483-528B-99
16	28	58.3	9	3	US-08-974-899-15
17	28	58.3	9	3	US-09-042-353-368
18	28	58.3	9	3	US-08-758-417A-216
19	28	58.3	9	4	US-09-393-385B-110
20	28	58.3	9	4	US-09-795-798-15
21	27	56.2	8	3	US-08-444-818-362
22	27	56.2	8	3	US-08-444-818-363
23	27	56.2	8	3	US-08-444-818-364
24	27	56.2	9	2	US-08-672-345C-81
25	27	56.2	9	3	US-09-214-095D-81
26	27	56.2	9	4	US-09-170-769A-24
27	27	56.2	9	4	US-09-155-106-6

28	27	56.2	9	4	US-09-830-748B-3	Sequence 3, Appli
29	26	54.2	7	2	US-08-627-173-7	Sequence 7, Appli
30	26	54.2	7	2	US-08-535-882A-7	Sequence 7, Appli
31	26	54.2	7	3	US-08-981-384-1	Sequence 1, Appli
32	26	54.2	7	3	US-09-005-546-7	Sequence 7, Appli
33	26	54.2	7	4	US-10-128-581-7	Sequence 7, Appli
34	26	54.2	7	4	US-08-832-443C-7	Sequence 6, Appli
35	26	54.2	8	2	US-08-627-173-6	Sequence 6, Appli
36	26	54.2	8	2	US-08-535-882A-6	Sequence 6, Appli
37	26	54.2	8	3	US-09-005-546-6	Sequence 6, Appli
38	26	54.2	8	4	US-10-128-581-6	Sequence 6, Appli
39	26	54.2	8	4	US-08-832-443C-6	Sequence 6, Appli
40	26	54.2	9	2	US-08-627-173-5	Sequence 5, Appli
41	26	54.2	9	2	US-08-535-882A-5	Sequence 5, Appli
42	26	54.2	9	2	US-08-814-806-7	Sequence 7, Appli
43	26	54.2	9	3	US-09-005-546-5	Sequence 5, Appli
44	26	54.2	9	3	US-08-918-148-24	Sequence 24, Appli
45	26	54.2	9	4	US-09-293-854-7	Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
US-08-672-345C-27  
; Sequence 27, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-27

Query Match 91.7%; Score 44; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.1e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QQLVEYFPFT 9  
DB 1 QQFVEYFPFT 9

RESULT 2

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US-09-214-095D-27
; Sequence 27, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-27

Query Match          91.7%; Score 44; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 1 QQFVEYPFT 9

RESULT 3
US-08-672-345C-21
; Sequence 21, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-21

Query Match          75.0%; Score 36; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 1 QHFDVYPFT 9

US-09-214-095D-21
; Sequence 21, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen.sp.
US-09-214-095D-21

Query Match          75.0%; Score 36; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 1 QHFDVYPFT 9

RESULT 5
US-09-406-532-20
; Sequence 20, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(9)
; OTHER INFORMATION: light chain CDR 3
US-09-406-532-20

Query Match          70.8%; Score 34; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QLVVEYPFT 9
Db 2 QRLVEYPFT 9

RESULT 6
US-08-438-123-3
; Sequence 3, Application US/08438123
; Patent No. 5552293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Lowe, Price, LeBlanc & Becker  
STREET: Suite 300, 99 Canal Center Plaza  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: DOS Text File  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,123  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/906,350  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: J.G. Mullins  
REGISTRATION NUMBER: 33073  
REFERENCE/DOCKET NUMBER: 149-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703 684 1111  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Polypeptide  
US-08-438-123-3

Query Match 68.8%; Score 33; DB 1; Length 9;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVYEPFT 9  
|:|||||  
DB 2 QHLEYPFT 9

RESULT 7  
US-08-264-093-26  
Sequence 26, Application US/08264093  
Patent No. 5639863  
GENERAL INFORMATION:  
APPLICANT: Michael D. Dan  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO  
CELL CYCLE-INDEPENDENT GLIOMA SURFACE  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ridout & Maybee  
STREET: 2300 Richmond-Adelaide Centre  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 2J7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS 6.00  
SOFTWARE: ASCII Editor  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/264,093  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA: No. 5639863 applicable  
ATTORNEY/AGENT INFORMATION:  
NAME: Lake, James R.  
REGISTRATION NUMBER: 31081

REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 868-1482  
TELEFAX: (416) 362-0823  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: not applicable  
TOPOLOGY: linear  
US-08-264-093-26

Query Match 66.7%; Score 32; DB 1; Length 9;  
Best Local Similarity 62.5%; Pred. No. 4.1e+05;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVYEPFT 9  
|:|||||  
DB 2 QRIEFPFT 9

RESULT 8  
US-09-798-689-6  
Sequence 6, Application US/09798689  
Patent No. 6811779  
GENERAL INFORMATION:  
APPLICANT: Rockwell, Patricia  
APPLICANT: Goldstein, Neil I.  
TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
TITLE OF INVENTION: Combined With Radiation and Chemotherapy  
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
Patent No. 6811779  
CURRENT APPLICATION NUMBER: US/09/798,689  
CURRENT FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 09/401,163  
PRIOR FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: 08/967,113  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 08/706,804  
PRIOR FILING DATE: 1996-09-03  
PRIOR APPLICATION NUMBER: 08/476,533  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/326,552  
PRIOR FILING DATE: 1994-10-20  
PRIOR APPLICATION NUMBER: 08/196,041  
PRIOR FILING DATE: 1994-02-10  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 6  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Mouse  
US-09-798-689-6

Query Match 64.6%; Score 31; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9  
|:|||||  
DB 1 QQRSSYPFT 9

RESULT 9  
US-08-672-345C-24  
Sequence 24, Application US/08672345C  
Patent No. 5948658  
GENERAL INFORMATION:  
APPLICANT: Landry Donald, W.  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper and Dunham LLP

```
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-24

Query Match          62.5%; Score 30; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 QQLVEYPPT 9
Db      1 QHFEDYPT 9

RESULT 10
US-08-672-345C-30
; Sequence 30, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
```

```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-30

Query Match          62.5%; Score 30; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 QQLVEYPPT 9
Db      1 QHFEDYPT 9

RESULT 11
US-09-214-095D-24
; Sequence 24, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-24

Query Match          62.5%; Score 30; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 QQLVEYPPT 9
Db      1 QHFEDYPT 9

RESULT 12
US-09-214-095D-30
; Sequence 30, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-30

Query Match          62.5%; Score 30; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 QQLVEYPPT 9
Db      1 QHFEDYPT 9

RESULT 13
US-08-116-778E-11
; Sequence 11, Application US/08116778E
; Patent No. 5830470
```

GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUWANA, YOSHIIISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/116,778E  
FILING DATE: 07-SEP-93  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 249-59  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-116-778E-11

Query Match 58.3%; Score 28; DB 2; Length 9;  
Best Local Similarity 55.6%; Pred. No. 4.1e+05;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9  
|||  
Db 1 QQRSSYPPT 9

RESULT 14  
US-08-438-562-11  
Sequence 11, Application US/08438562  
Patent No. 5874255  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUWANA, YOSHIIISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,562  
FILING DATE: 10-MAY-95  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/116,778  
FILING DATE: 07-SEP-93  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 249-76  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-438-562-11

Query Match 58.3%; Score 28; DB 2; Length 9;  
Best Local Similarity 55.6%; Pred. No. 4.1e+05;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9  
|||  
Db 1 QQRSSYPPT 9

RESULT 15  
US-08-483-528B-99  
Sequence 99, Application US/08483528B  
Patent No. 5939532  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUWANA, YOSHIIISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,528B  
FILING DATE: 07-JUN-95  
CLASSIFICATION: 536  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-483-528B-99

Query Match 58.3%; Score 28; DB 2; Length 9;  
Best Local Similarity 55.6%; Pred. No. 4.1e+05;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9  
Db 1 QQRSSYPYT 9

Search completed: April 18, 2005, 15:20:15  
Job time : 45 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 13:59:59 ; Search time 9.88372 Seconds  
(without alignments)  
48.674 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	67	2 A84376	hypothetical prote
2	33	100.0	117	1 G2MSU1	Ig heavy chain V r
3	33	100.0	444	2 S09681	citrate transport
4	33	100.0	1043	2 E97302	hypothetical prote
5	30	90.9	86	2 T42185	conserved hypotet
6	30	90.9	298	2 AE1752	hypothetical prote
7	30	90.9	298	2 AH1728	AbiD phage protein
8	30	90.9	315	2 H86836	carbamate kinase (
9	30	90.9	348	2 G69142	GDP-D-mannose dehy
10	30	90.9	358	2 H83554	hypothetical prote
11	30	90.9	375	2 E83163	hypothetical prote
12	30	90.9	417	2 T08724	hypothetical prote
13	30	90.9	448	2 B95249	PTS system, IIC co
14	30	90.9	448	2 G98113	conserved hypotet
15	30	90.9	452	2 T00113	undecaprenyl-phosp
16	30	90.9	464	2 T28818	hypothetical prote
17	30	90.9	475	2 T46745	arginine/ornithine
18	30	90.9	476	2 D84505	probable membrane
19	30	90.9	480	2 D90038	PTS system, sucros
20	30	90.9	480	2 S39878	scra protein - Sta
21	30	90.9	490	2 C86879	arginine/ornithine
22	30	90.9	518	1 G69804	multidrug-efflux t
23	30	90.9	535	2 S78598	D-ribulokinase (EC
24	30	90.9	583	2 C72544	probable glycytl-tr
25	30	90.9	592	1 IKEBCA	colicin A - Citrob
26	30	90.9	592	2 T15600	hypothetical prote
27	30	90.9	608	2 JQ1462	phosphoenolpyruvat
28	30	90.9	667	1 VCLJGL	env polyprotein pr
29	30	90.9	847	2 JC4836	alpha-glucuronidas

#### ALIGNMENTS

##### RESULT 1

A84376

hypothetical protein Vng2253h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C;Accession: A84376

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,

; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84376

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <STO>

A;Cross-references: UNIPROT:Q9HN48; GB:AE004437; NID:g10581666; PIDN:AAG20373.1; GSPDB:

C;Genetics:

A;Gene: VNG2253H

Query Match 100.0%; Score 33; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5

Db 59 GYWMS 63

##### RESULT 2

G2MSU1

Ig heavy chain V region (UPC10) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004

C;Accession: A02081

R;Auffray, C.; Slikav, J.L.; Ollo, R.; Rougeon, F.

Ann. Immunol. (Paris) 132D, 77-88, 1981

A;Title: Correlation between D region structure and antigen-binding specificity: evidence

A;Reference number: A02081; MUID:83021113; PMID:6181731

A;Accession: A02081

A;Molecule type: mRNA

A;Residues: 1-117 <AUF>

A;Cross-references: UNIPROT:P01811

C;Comment: This chain was isolated from an Ig gamma-2a myeloma protein binding 2,6-leva

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

F;22-96/Disulfide bonds: #status predicted

Query Match 100.0%; Score 33; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||||

Db 31 GYWS 35

RESULT 3

S09681

citrate transport protein - klebsiella pneumoniae plasmid pES1

N;Alternate names: citrate carrier

C;Species: Klebsiella pneumoniae

C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004

C;Accession: S09681

R;van der Rest, M.E.; Schwarz, E.; Oesterheld, D.; Konings, W.N.

Eur. J. Biochem. 189, 401-407, 1990

A;Title: DNA sequence of a citrate carrier of Klebsiella pneumoniae.

A;Reference number: S09681; MUID:90249385; PMID:2186908

A;Accession: S09681

A;Molecule type: DNA

A;Residues: 1-444 <RES>

A;Cross-references: UNIPROT:P16482; EMBL:X51479; NID:G43800; PIDN:CAA35844.1; PID:G43801

C;Genetics:

A;Genome: plasmid pES1

C;Superfamily: citrate utilization determinant

C;Keywords: membrane protein

Query Match 100.0%; Score 33; DB 2; Length 444;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||||

Db 415 GYWS 419

RESULT 4

F97302

hypothetical protein CAC3275 [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C;Accession: F97302

R;Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: F97302

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1043 <KUR>

A;Cross-references: UNIPROT:Q97E41; GB:AB001437; PIDN:AAK81209.1; PID:G15026351; GSPDB:G15026351

C;Genetics:

A;Gene: CAC3275

Query Match 100.0%; Score 33; DB 2; Length 1043;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||||

Db 580 GYWS 584

RESULT 5

T42185

conserved hypothetical protein L7085 - Escherichia coli plasmid pO157

C;Species: Escherichia coli

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T42185

R;Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.

Nucleic Acids Res. 26, 4196-4204, 1998

A;Title: The complete DNA sequence and analysis of the large virulence plasmid of Escherichia coli O157:H7

A;Reference number: 222068; MUID:98391744; PMID:9722640

A;Accession: T42185

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-86 <BUR>

A;Cross-references: UNIPROT:Q9ZGR9; EMBL:AF074613; PIDN:AAC70153.1

A;Experimental source: strain EDL933; serotype O157:H7

C;Genetics:

A;Genome: plasmid pO157

A;Note: L7085

Query Match 90.9%; Score 30; DB 2; Length 86;

Best Local Similarity 80.0%; Pred. No. 71;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||||

Db 72 GYWS 76

RESULT 6

AB1752

hypothetical protein homolog lin2562 [imported] - Listeria innocua (strain Clp11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C;Accession: AB1752

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of Listeria species

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AB1752

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-298 <GLA>

A;Cross-references: UNIPROT:Q925X5; GB:AL592022; PIDN:CAC97789.1; PID:G16415084; GSPDB:G16415084

A;Experimental source: strain Clp11262

C;Genetics:

A;Gene: lin2562

Query Match 90.9%; Score 30; DB 2; Length 298;

Best Local Similarity 80.0%; Pred. No. 2.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||||

Db 45 GYWS 49

RESULT 7

AB1728

AB1D phage protein homolog lin2373 [imported] - Listeria innocua (strain Clp11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C;Accession: AB1728

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of Listeria species

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AB1728

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-298 <GLA>

A;Cross-references: UNIPROT:Q925X5; GB:AL592022; PIDN:CAC97600.1; PID:G16414896; GSPDB:G16414896

A;Experimental source: strain Clp11262

C;Genetics:  
A;Gene: lin2373

Query Match 90.9%; Score 30; DB 2; Length 298;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 45 GYWLS 49

#### RESULT 8

H86836  
carbamate kinase (EC 2.7.2.2) [imported] - Lactococcus lactis subsp. lactis (strain IL14)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: H86836  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: H86836  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-315 <STO>  
A;Cross-references: UNIPROT:Q9CEY7; GB:AE005176; PID:g12724712; PIDN:AAK05794.1; GSPDB:G  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: arcC3  
C;Superfamily: carbamate kinase  
C;Keywords: phosphotransferase

Query Match 90.9%; Score 30; DB 2; Length 315;  
Best Local Similarity 80.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 88 GYWNA 92

#### RESULT 9

G69142  
GDP-D-mannose dehydratase - Methanobacterium thermoautotrophicum (strain Delta H)  
C;Species: Methanobacterium thermoautotrophicum  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 12-Jul-2004  
C;Accession: G69142  
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct  
A;Reference number: A69000; MUID:98037514; PMID:9371463  
A;Accession: G69142  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-348 <MTH>  
A;Cross-references: UNIPROT:O26433; GB:AE000818; GB:AE000666; NID:g2621384; PIDN:AAE8483  
A;Experimental source: strain Delta H  
C;Genetics:  
A;Gene: MTH333  
C;Superfamily: GDP-D-mannose 4,6 dehydratase

Query Match 90.9%; Score 30; DB 2; Length 348;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 156 GYWT 160

#### RESULT 10

H83554  
hypothetical protein PA0736 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: H83554  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: H83554  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-358 <STO>  
A;Cross-references: UNIPROT:Q9I5J3; GB:AE004508; GB:AE004091; NID:g9946611; PIDN:AAG041  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA0736

Query Match 90.9%; Score 30; DB 2; Length 358;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 203 GYWLS 207

#### RESULT 11

E83163  
hypothetical protein PA3863 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 16-Aug-2004  
C;Accession: E83163  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: E83163  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-375 <STO>  
A;Cross-references: UNIPROT:Q9HXE3; GB:AE004803; GB:AE004091; NID:g9950035; PIDN:AAG072  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA3863  
C;Superfamily: Sarcosine oxidase

Query Match 90.9%; Score 30; DB 2; Length 375;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 19 GYWLS 23

#### RESULT 12

T08724  
hypothetical protein DKFZp566D213.1 - human  
C;Species: Homo sapiens (man)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T08724  
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, May 1999  
A;Reference number: Z16468  
A;Accession: T08724  
A;Molecule type: mRNA  
A;Residues: 1-417 <KOE>

Tue Apr 19 06:15:13 2005

us-09-674-716b-9.open.rpr

A;Cross-references: UNIPROT:Q9Y409; EMBL:AL050275  
A;Experimental source: fetal kidney; clone DKFZp566D213  
C;Genetics:  
A;Note: DKFZp566D213.1

Query Match 90.9%; Score 30; DB 2; Length 417;  
Best Local Similarity 80.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 402 GYWLS 406

## RESULT 13

B95249  
FTS system, IIC component, probable [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: B95249  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: B95249  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-448 <KUR>  
A;Cross-references: UNIPROT:Q97NC2; GB:AE005672; PIDN:AAK76187.1; PID:G14973641; GSPDB:C  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP2129

Query Match 90.9%; Score 30; DB 2; Length 448;  
Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 186 GYWLS 190

## RESULT 14

G98113  
conserved hypothetical protein spr1938 [imported] - Streptococcus pneumoniae (strain R6)  
C;Species: Streptococcus pneumoniae  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C;Accession: G98113  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
e, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A;Reference number: A97872; MUID:21429245; PMID:11544234  
A;Accession: G98113  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-448 <KUR>  
A;Cross-references: UNIPROT:Q8DN40; GB:AE007317; PIDN:AAL00740.1; PID:G15459636; GSPDB:C  
C;Genetics:  
A;Gene: spr1938

Query Match 90.9%; Score 30; DB 2; Length 448;  
Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 186 GYWLS 190

## RESULT 15

T00113  
undecaprenyl-phosphate galactosephosphotransferase homolog - Actinobacillus actinomycet-  
C;Species: Actinobacillus actinomycetemcomitans  
C;Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 09-Jul-2004  
C;Accession: T00113  
R;Nakano, Y.; Yoshida, Y.; Yamashita, Y.; Koga, T.  
Biochim. Biophys. Acta 1442, 409-414, 1998  
A;Title: A gene cluster for 6-deoxy-L-talan synthesis in Actinobacillus actinomycetemcom  
A;Reference number: Z14111; MUID:99023768; PMID:9805002  
A;Accession: T00113  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-452 <NAK>  
A;Cross-references: UNIPROT:O6G260; EMBL:AB010415; NID:G3132248; PIDN:BA28142.1; PID:G  
A;Experimental source: strain NCTC 9710  
C;Superfamily: xps2A protein

Query Match 90.9%; Score 30; DB 2; Length 452;  
Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||:  
Db 11 GYWLS 15

Search completed: April 18, 2005, 14:23:30  
Job time : 14.8837 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:57:43 ; Search time 45.4651 Seconds  
(without alignments)  
56.316 Million cell updates/sec

Title: US-09-674-716B-9  
Perfect score: 33  
Sequence: 1 GYWS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	67	Q9HN48	Q9HN48 halobacteri
2	33	100.0	73	Q8PR71	Q8PR71 xanthomonas
3	33	100.0	85	Q8PBA4	Q8PBA4 xanthomonas
4	33	100.0	117	HV41 MOUSE	P01811 mus musculu
5	33	100.0	285	Q8W52	Q8W52 lactobacill
6	33	100.0	377	Q8AWR8	Q8AWR8 pollimyrus
7	33	100.0	377	Q91B67	Q91B67 campyloform
8	33	100.0	377	Q91AD5	Q91AD5 stomatorhin
9	33	100.0	377	Q91AD6	Q91AD6 stomatorhin
10	33	100.0	377	Q91AD7	Q91AD7 stomatorhin
11	33	100.0	377	Q91AD8	Q91AD8 stomatorhin
12	33	100.0	377	Q91AD9	Q91AD9 pollimyrus
13	33	100.0	377	Q91AE0	Q91AE0 pollimyrus
14	33	100.0	377	Q91AE1	Q91AE1 pollimyrus
15	33	100.0	377	Q91AE6	Q91AE6 paramomyro
16	33	100.0	377	Q91AE9	Q91AE9 mormyrus ru
17	33	100.0	377	Q91AF0	Q91AF0 mormyrus ov
18	33	100.0	377	Q91AF4	Q91AF4 marcusenius
19	33	100.0	377	Q91AF5	Q91AF5 marcusenius
20	33	100.0	377	Q91AF6	Q91AF6 marcusenius
21	33	100.0	377	Q91AF7	Q91AF7 marcusenius
22	33	100.0	377	Q91AF8	Q91AF8 marcusenius
23	33	100.0	377	Q91AF9	Q91AF9 ivindomyrus
24	33	100.0	377	Q91AG1	Q91AG1 hyperopsis
25	33	100.0	377	Q91AG2	Q91AG2 hippopotamy
26	33	100.0	377	Q91AG3	Q91AG3 hippopotamy
27	33	100.0	377	Q91AG4	Q91AG4 hippopotamy
28	33	100.0	377	Q91AG6	Q91AG6 gnathomus
29	33	100.0	377	Q91AG7	Q91AG7 genomyrus
30	33	100.0	377	Q91AG9	Q91AG9 campyloform
31	33	100.0	377	Q91AH0	Q91AH0 campyloform

32	33	100.0	377	2	Q9IAH1	Q9IAH1 brienyomys
33	33	100.0	377	2	Q9IAH2	Q9IAH2 brienyomys
34	33	100.0	377	2	Q9IAH3	Q9IAH3 brienyomys
35	33	100.0	377	2	Q9IAH4	Q9IAH4 brienyomys
36	33	100.0	377	2	Q9IAH6	Q9IAH6 boulengerom
37	33	100.0	396	2	Q7SY78	Q7SY78 xenopus lae
38	33	100.0	399	2	Q6BRL7	Q6BRL7 debaryomyce
39	33	100.0	444	1	CITI_KLEPN	P16482 klebsiella
40	33	100.0	721	2	Q7XBS0	Q7XBS0 oryza sativ
41	33	100.0	721	2	Q9FRN4	Q9FRN4 oryza sativ
42	33	100.0	1028	2	Q8SXA6	Q8SXA6 drosophila
43	33	100.0	1043	2	Q97EA1	Q97EA1 clostridium
44	33	100.0	1254	2	Q86NS1	Q86NS1 drosophila
45	33	100.0	1254	2	Q9VFS1	Q9VFS1 drosophila

ALIGNMENTS

RESULT 1

Q9HN48	PRELIMINARY;	PRT;	67 AA.
ID Q9HN48			
AC Q9HN48			
DT 01-MAR-2001	(TREMBLrel. 16, Created)		
DT 01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT 01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE Vng2253h.			
GN OrderedLocusNames=VNG2253H;			
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).			
OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;			
OC Halobacteriaceae; Halobacterium.			
OX NCBI_TaxID=64091;			
RP [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE-20504483; PubMed-11016950; DOI=10.1073/pnas.190337797;			
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Fan M.,			
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,			
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,			
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,			
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,			
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,			
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,			
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;			
RL "Genome sequence of Halobacterium species NRC-1.";			
DR EMBL; A3005110; AAG20373.1; -;			
DR PIR; A84376; A84376.			
KW Complete proteome.			
SQ SEQUENCE 67 AA; 6601 MW; AGBAF23FCBE8B648 CRC64;			

Query Match 100.0%; Score 33; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GYWS 5
DB	59	GYWS 63

RESULT 2

Q8PR71	PRELIMINARY;	PRT;	73 AA.
ID Q8PR71			
AC Q8PR71			
DT 01-OCT-2002	(TREMBLrel. 22, Created)		
DT 01-OCT-2002	(TREMBLrel. 22, Last sequence update)		
DT 01-OCT-2002	(TREMBLrel. 22, Last annotation update)		
DE Hypothetical protein XAC0095.			
GN OrderedLocusNames=XAC0095;			
OS Xanthomonas axonopodis (pv. citri).			
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;			
OC Xanthomonadaceae; Xanthomonas.			
OX NCBI_TaxID=92829;			
RP [1]			

Qy		1 GYMS 5       
Dd		31 GYMS 35
RESULT 5		
Q88W52		PRELIMINARY;
ID	Q88W52	PRT;    285 AA.
AC	Q88W52;	
DT	01-JUN-2003	(TReMBLrel. 24; Created)
DT	01-JUN-2003	(TReMBLrel. 24; Last sequence update)
DT	01-OCT-2003	(TReMBLrel. 25; Last annotation update)
DE		Integral membrane protein.
GN		OrderedLocusNames=lp_1809;
OS		Lactobacillus plantarum.

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=1590;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCIMB 8826 / WCFS1;  
 RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;  
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,  
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,  
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,  
 RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,  
 RA De Vos W.M., Siezen R.J.;  
 RT "Complete genome sequence of *Lactobacillus plantarum* WCFS1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).  
 DR EMBL; AL935257; CAD64219.1; -;  
 DR InterPro; IPR007163; DUF368.  
 DR Pfam; PF04018; DUF368; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 285 AA; 30888 MW; D93DB9353EA9D881 CRC64;  
 Query Match 100.0%; Score 33; DB 2; Length 285;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYWS 5  
 Db |||||  
 274 GYWS 278  
 RESULT 6  
 Q8AWR8 PRELIMINARY; PRT; 377 AA.  
 ID Q8AWR8  
 AC Q8AWR8;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Recombination-activating protein 2 (Fragment).  
 OS *Pollimyrus adspersus*.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
 OC Osteoglossiformes; Mormyridae; Pollimyrus.  
 OX NCBI\_TaxID=203438;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Lavoue S., Sullivan J.P., Hopkins C.D.;  
 RX "Phylogenetic utility of the first two introns of the S7 ribosomal  
 RT protein gene in African electric fishes (Mormyridae: Teleostei) and  
 RT congruence with other molecular markers.";  
 RL Biol. J. Linn. Soc. Lond. 78:273-292(2003).  
 DR EMBL; AY124315; AAM92557.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA recombination; IEA.  
 DR InterPro; IPR011043; Gal oxid\_central.  
 DR InterPro; IPR004321; RAG2.  
 DR Pfam; PF03089; RAG2; 1.  
 DR NON\_TER 1  
 FT NON\_TER 377 377  
 SQ SEQUENCE 377 AA; 41472 MW; 1D90B1F4CCT7ADAFE CRC64;  
 Query Match 100.0%; Score 33; DB 2; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYWS 5  
 Db |||||  
 368 GYWS 372  
 RESULT 7  
 Q9I867 PRELIMINARY; PRT; 377 AA.  
 ID Q9I867  
 AC Q9I867;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Recombination-activating protein 2 (Fragment).  
 OS *Campylomormyrus tamandua*.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
 OC Osteoglossiformes; Mormyridae; Campylomormyrus.  
 OX NCBI\_TaxID=91719;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20115608; PubMed=10648209;  
 RX Sullivan J.P., Lavoue S., Hopkins C.D.;  
 RT "Molecular systematics of the african electric fishes (Mormyridae:  
 RT teleostei) and a model for the evolution of their electric organs.";  
 RL J. Exp. Biol. 203:665-683(2000).  
 DR EMBL; AF201625; AAF43336.1; -;  
 DR EMBL; AF201624; AAF43335.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR011043; Gal oxid\_central.  
 DR InterPro; IPR004321; RAG2.  
 DR Pfam; PF03089; RAG2; 1.  
 DR NON\_TER 1  
 FT NON\_TER 377 377  
 SQ SEQUENCE 377 AA; 41387 MW; D52A9E361A56AB43 CRC64;  
 Query Match 100.0%; Score 33; DB 2; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYWS 5  
 Db |||||  
 368 GYWS 372  
 RESULT 8  
 Q9IAD5 PRELIMINARY; PRT; 377 AA.  
 ID Q9IAD5  
 AC Q9IAD5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Recombination-activating protein 2 (Fragment).  
 OS *Stomatohinus sp. AMNH228158*.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
 OC Osteoglossiformes; Mormyridae; Stomatohinus.  
 OX NCBI\_TaxID=112282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20115608; PubMed=10648209;  
 RX Sullivan J.P., Lavoue S., Hopkins C.D.;  
 RT "Molecular systematics of the african electric fishes (Mormyridae:  
 RT teleostei) and a model for the evolution of their electric organs.";  
 RL J. Exp. Biol. 203:665-683(2000).  
 DR EMBL; AF201659; AAF43370.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR011043; Gal oxid\_central.  
 DR InterPro; IPR004321; RAG2.  
 DR Pfam; PF03089; RAG2; 1.  
 DR NON\_TER 1  
 FT NON\_TER 377 377  
 SQ SEQUENCE 377 AA; 41485 MW; 4AA141FC3B092825 CRC64;  
 Query Match 100.0%; Score 33; DB 2; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYWS 5

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Db          368 GYWS 372
|||||
RESULT 9
Q9IAD6      PRELIMINARY;      PRT;      377 AA.
ID Q9IAD6;
AC Q9IAD6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Stomatohinus sp. CU79703.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Stomatohinus.
OX NCBI_TaxID=112284;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the african electric fishes (Mormyroidea:
RT teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201658; AAF43369.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR011043; Gal_oxid_central.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
DR NON_TER 1
FT NON_TER 377
FT NON_TER 377
SQ SEQUENCE 377 AA; 41457 MW; AAA04081C908E8FF CRC64;

Query Match          100.0%; Score 33; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db          368 GYWS 372
|||||
RESULT 10
Q9IAD7      PRELIMINARY;      PRT;      377 AA.
ID Q9IAD7;
AC Q9IAD7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Stomatohinus sp. AMNH228162.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Stomatohinus.
OX NCBI_TaxID=112283;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the african electric fishes (Mormyroidea:
RT teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201657; AAF43368.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR011043; Gal_oxid_central.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
DR NON_TER 1
FT NON_TER 377
FT NON_TER 377
SQ SEQUENCE 377 AA; 41457 MW; AAA04081C908E8FF CRC64;

Query Match          100.0%; Score 33; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db          368 GYWS 372
|||||
RESULT 11
Q9IAD8      PRELIMINARY;      PRT;      377 AA.
ID Q9IAD8;
AC Q9IAD8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Stomatohinus walkeri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Stomatohinus.
OX NCBI_TaxID=112160;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the african electric fishes (Mormyroidea:
RT teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201656; AAF43367.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR011043; Gal_oxid_central.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
DR NON_TER 1
FT NON_TER 377
FT NON_TER 377
SQ SEQUENCE 377 AA; 41529 MW; 4FD1CC06990F0E2F CRC64;

Query Match          100.0%; Score 33; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db          368 GYWS 372
|||||
RESULT 12
Q9IAD9      PRELIMINARY;      PRT;      377 AA.
ID Q9IAD9;
AC Q9IAD9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Pollimyrus sp. AMNH228155.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Pollimyrus.
OX NCBI_TaxID=112281;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the african electric fishes (Mormyroidea:
RT teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201655; AAF43366.1; -.
DR GO; GO:0005634; C:nucleus; IEA.

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DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0006310; P:DNA recombination; IEA.  
 DR InterPro; IPR011043; Gal\_oxid\_central.  
 DR InterPro; IPR004321; RAG2.  
 DR Pfam; PF03089; RAG2; 1.  
 FT NON\_TER 1 377  
 FT NON\_TER 377 377  
 SQ SEQUENCE 377 AA; 41424 MW; 1B84D6E64659A1C7 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 DB 368 GYWS 372

## RESULT 13

Q9IAE0 PRELIMINARY; PRT; 377 AA.  
 ID Q9IAE0  
 AC Q9IAE0  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Recombination-activating protein 2 (Fragment).  
 OS Pollimyrus isidori.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
 OC Osteoglossiformes; Mormyridae; Pollimyrus.  
 OX NCBI\_TaxID=91713;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20115608; PubMed=10648209;  
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;  
 RT "Molecular systematics of the african electric fishes (Mormyroidea:  
 RT teleostei) and a model for the evolution of their electric organs.";  
 RL J. Exp. Biol. 203:665-683(2000).  
 DR EMBL; AF201654; AAF43365.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0006310; P:DNA recombination; IEA.  
 DR InterPro; IPR011043; Gal\_oxid\_central.  
 DR InterPro; IPR004321; RAG2.  
 DR Pfam; PF03089; RAG2; 1.  
 FT NON\_TER 1 377  
 FT NON\_TER 377 377  
 SQ SEQUENCE 377 AA; 41457 MW; 393E1B1FA838E9C8 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 DB 368 GYWS 372

## RESULT 14

Q9IAE1 PRELIMINARY; PRT; 377 AA.  
 ID Q9IAE1  
 AC Q9IAE1  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Recombination-activating protein 2 (Fragment).  
 OS Pollimyrus petricolus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
 OC Osteoglossiformes; Mormyridae; Pollimyrus.  
 OX NCBI\_TaxID=91715;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=20115608; PubMed=10648209;  
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;  
 RT "Molecular systematics of the african electric fishes (Mormyroidea:  
 RT teleostei) and a model for the evolution of their electric organs.";  
 RL J. Exp. Biol. 203:665-683(2000).  
 DR EMBL; AF201653; AAF43364.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0006310; P:DNA recombination; IEA.  
 DR InterPro; IPR011043; Gal\_oxid\_central.  
 DR InterPro; IPR004321; RAG2.  
 DR Pfam; PF03089; RAG2; 1.  
 FT NON\_TER 1 377  
 FT NON\_TER 377 377  
 SQ SEQUENCE 377 AA; 41473 MW; E7970A9EC67D6193 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 DB 368 GYWS 372

## RESULT 15

Q9IAE6 PRELIMINARY; PRT; 377 AA.  
 ID Q9IAE6  
 AC Q9IAE6  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Recombination-activating protein 2 (Fragment).  
 OS Paramormyrops gabonensis.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;  
 OC Osteoglossiformes; Mormyridae; Paramormyrops.  
 OX NCBI\_TaxID=91733;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20115608; PubMed=10648209;  
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;  
 RT "Molecular systematics of the african electric fishes (Mormyroidea:  
 RT teleostei) and a model for the evolution of their electric organs.";  
 RL J. Exp. Biol. 203:665-683(2000).  
 DR EMBL; AF201648; AAF43359.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0006310; P:DNA recombination; IEA.  
 DR InterPro; IPR011043; Gal\_oxid\_central.  
 DR InterPro; IPR004321; RAG2.  
 DR Pfam; PF03089; RAG2; 1.  
 FT NON\_TER 1 377  
 FT NON\_TER 377 377  
 SQ SEQUENCE 377 AA; 41403 MW; 0A4599C604C8123 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
 DB 368 GYWS 372

Search completed: April 18, 2005, 14:21:55  
 Job time : 46.4651 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:32:07 ; Search time 52.6744 Seconds  
(without alignments)  
36.712 Million cell updates/sec

Title: US-09-674-716B-9  
Perfect score: 33  
Sequence: 1 GYMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	5	3 AAY32257	Aay32257 Light cha
2	33	100.0	10	7 ADM07744	Adm07744 Canine im
3	33	100.0	73	7 ADG30700	Adg30700 Xanthomon
4	33	100.0	137	3 AAY32260	Aay32260 Mouse ant
5	33	100.0	163	7 ABM73967	Abm73967 DNA clone
6	33	100.0	345	7 ABM73656	Abm73656 DNA clone
7	33	100.0	444	3 AAY32263	Aay32263 Humanised
8	33	100.0	466	7 ABO67808	Abob67808 Klebsiell
9	33	100.0	1096	8 ADP99004	Adp99004 C. albica
10	33	100.0	1254	4 ABB62006	Abb62006 Drosophil
11	30	90.9	40	4 ABG07533	Abg07533 Novel hum
12	30	90.9	43	2 AAR95472	Aar95472 V39, mono
13	30	90.9	63	6 ABR48102	Abr48102 Human sec
14	30	90.9	63	6 ABR00271	Abr00271 Human gen
15	30	90.9	63	7 ADB91793	Adb91793 Human sec
16	30	90.9	63	7 ADC74531	Adc74531 Human sec
17	30	90.9	64	2 AAY07813	Aay07813 Human sec
18	30	90.9	175	8 ADN74285	Adn74285 Thale cre
19	30	90.9	181	2 AAY35482	Aay35482 Chlamydia
20	30	90.9	210	4 AAU17327	Aau17327 Novel sig
21	30	90.9	210	7 ADB94035	Adb94035 Human nov
22	30	90.9	242	3 AAY76114	Aay76114 Rat HT gl
23	30	90.9	242	4 AAB56053	Aab56053 Skin cell
24	30	90.9	242	5 ABB72253	Abb72253 Rat prote
25	30	90.9	242	5 ABB72301	Abb72301 Rat prote

ALIGNMENTS

RESULT 1

AAY32257  
ID AAY32257 standard; peptide; 5 AA.

XX AAY32257;

XX 15-FEB-2000 (first entry)

XX Light chain CDR H1 of mouse anti-CD23 Mab C11.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
therapy.

XX Mus musculus.

XX WO9558679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX ) GLAXO GROUP LTD.

XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX N-PSDB; AA234742.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
diabetes, multiple sclerosis and psoriasis.

XX Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 1 (CDR H1)  
of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11  
(see also AAY32263). The invention provides altered antibodies, such as  
chimeric or humanised antibodies, which comprise sufficient of the amino  
acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

Abb72290 Rat prote  
Abp39269 Staphyloc  
Abm72990 Staphyloc  
Ade05885 Staphyloc  
Aau35317 Enterococ  
Aab19867 GALV retr  
Abu29423 Protein e  
Abb5045 Lactococc  
Adh29444 Bacterial  
Adh88144 Enterococ  
Adn18477 Bacterial  
Aag1982 Arabidops  
Aab19870 Activatin  
Aag1981 Arabidops  
Abo80711 Pseudomon  
Aab38394 Human sec  
Aad41195 Human sec  
Abr48101 Human sec  
Abr00270 Human gen  
Adb91792 Human sec

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents  
 XX  
 XX Sequence 5 AA;

Query Match 100.0%; Score 33; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
 |||||  
 Db 1 GYWMS 5

RESULT 2  
 ADM07744 standard; peptide; 10 AA.

AC ADM07744;  
 DT 20-MAY-2004 (first entry)

XX Canine immunoglobulin heavy chain variable domain CDR1 peptide 12.  
 DE canine; dog; heavy; immunoglobulin; antibody light chain variable domain;  
 KW antiallergic; allergy; IGE; gene therapy;  
 KW complementarity determining region; CDR1.  
 XX

OS Canis familiaris.

XX WO2003060080-A2.  
 XX 24-JUL-2003.

XX 20-DEC-2002; 2002WO-US041362.

XX 21-DEC-2001; 2001US-0344874P.

XX (IDEX-) IDEXX LAB INC.

XX Krah ER, Guo H, Aiyappa A, Lawton R;

XX WPI; 2003-598521/56.

XX New canine heavy and light chain variable domain polypeptides, useful for  
 XX treating canine allergy.

XX Claim 15; Page 95; 130pp; English.

XX The invention relates to a novel canine heavy or light chain variable  
 CC domain polypeptide. The protein of the invention demonstrates  
 CC antiallergic activity and may be useful for treating canine allergy,  
 CC possibly via gene therapy. The current sequence is that of a canine  
 CC immunoglobulin heavy chain variable domain complementarity determining  
 CC region (CDR) peptide of the invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 33; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. NO. 11;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db |||||  
 6 GYWMS 10

RESULT 3  
 ADG30700 standard; protein; 73 AA.

XX ADG30700;

XX 26-FEB-2004 (first entry)

XX Xanthomonas axonopodis pv citri plant pathology-related XAC0095 protein.

XX Xanthomonas microorganism; plant; pathology; bacterial pest; Xac; Xcc;  
 KW XAC.

XX Xanthomonas axonopodis pv. citri.

XX WO2003089647-A1.

XX 30-OCT-2003.

XX 22-APR-2003; 2003WO-BR000060.

XX 22-APR-2002; 2002US-0374620P.

XX (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.

XX Da Silva ACR, Farah SC, Quaggio RB, Reinach FDC, Ferro JA;

XX De Oliveira JCF, De Laia ML, Setubal JC, Furlan LR;

XX WPI; 2003-865444/80.

XX N-PSDB; ADG30699.

XX New nucleic acid molecule from a Xanthomonas microorganism, useful in  
 PT determining the presence of Xanthomonas bacteria in a sample.

XX Claim 8; SEQ ID NO 57; 145pp; English.

XX The invention relates to a novel isolated nucleic acid molecule from a  
 CC Xanthomonas microorganism where the nucleic acid molecule is associated  
 CC with pathogenicity caused by the Xanthomonas microorganism, or its  
 CC variant, that causes reduced or enhanced pathogenicity. The nucleic acid  
 CC of the invention may be useful in detecting the presence of Xanthomonas  
 CC bacteria in a sample, as well as in plant pathology, for example, for  
 CC identifying nucleic acid molecules and proteins involved in pathology  
 CC caused by bacterial pests. The current sequence is that of the  
 CC Xanthomonas axonopodis pv. citri (Xac) plant pathology-related XAC  
 XX protein of the invention.

XX Sequence 73 AA;

Query Match 100.0%; Score 33; DB 7; Length 73;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
 |||||  
 Db 6 GYWMS 10

RESULT 4  
 AAY32260 standard; protein; 137 AA.

XX AAY32260;

XX 15-FEB-2000 (first entry)

XX Mouse anti-CD23 MAb C11 heavy chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;

QY



XX 17-JUL-2003.  
XX 16-DEC-2002; 2002WO-IB005403.  
XX 20-DEC-2001; 2001JP-00387059.  
XX 20-DEC-2001; 2001JP-00387131.  
XX 20-DEC-2001; 2001JP-00403299.  
XX 20-DEC-2001; 2001JP-00403300.  
XX 27-SEP-2002; 2002JP-00327515.  
XX (UYN1-) UNIV JAPAN OKAYAMA.  
XX Sato K, Takeda K, Kohara Y;  
XX WPI; 2003-587127/55.  
XX Single nucleotide polymorphism sites in barley varieties and DNA  
XX sequences containing them for analysis and identification of barley  
XX varieties and production of barley transformants with desired  
XX characteristics.  
XX Disclosure; SEQ ID XX; 284bp; Japanese.  
XX The present invention relates to oligonucleotide clones originating in  
XX barley (Hordeum vulgare) which contain single nucleotide polymorphisms  
XX (SNP). The oligonucleotides may be used for analysis of SNPs among barley  
XX varieties, identification of particular varieties and genotype-phenotype  
XX analysis, isolation of specific genes and creation of new varieties by  
XX transformation of barley varieties with them and production of new barley  
XX varieties with desired properties. The present sequence represents an  
XX oligonucleotide clone sequence featured in the specification. The  
XX sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published-pct-sequences  
XX  
XX Sequence 345 AA;  
Query Match 100.0%; Score 33; DB 7; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYWMS 5  
Db 266 GYWMS 270  
RESULT 7  
ID AAY32263 standard; protein; 444 AA.  
XX AAY32263;  
XX  
XX 15-FEB-2000 (first entry)  
XX Humanised anti-CD23 MAB C11 heavy chain.  
XX  
XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;  
XX monoclonal antibody; chimeric antibody; humanised antibody;  
XX complementarity determining region; CDR; autoimmune disease;  
XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
XX urticaria; nephrotic syndrome; glomerulonephritis;  
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
XX therapy.  
XX Homo sapiens.  
XX Synthetic.  
XX Key Location/Qualifiers  
XX Region 1. .30

FT Region /note= "framework region 1"  
FT 31. .35  
FT /note= "CDR 1"  
FT 36. .49  
FT /note= "framework region 2"  
FT 50. .68  
FT /note= "CDR 2"  
FT 69. .100  
FT /note= "framework region 3"  
FT 101. .103  
FT /note= "CDR 3"  
FT 104. .111  
FT /note= "framework region 4"  
FT 112. .444  
FT /note= "constant region"  
XX  
XX WO9958679-A1.  
XX  
XX 18-NOV-1999.  
XX  
XX 07-MAY-1999; 99WO-GB001434.  
XX  
XX 09-MAY-1998; 98GB-00009839.  
XX (GLAX ) GLAXO GROUP LTD.  
XX  
XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
XX WPI; 2000-053101/04.  
XX N-PSDB; AA234748.  
XX  
XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
XX diabetes, multiple sclerosis and psoriasis.  
XX  
XX Claim 9; Fig 4; 81pp; English.  
XX  
XX This amino acid sequence represents the heavy chain of humanised anti-  
XX CD23 (FCERII) monoclonal antibody C11, composed of a human framework  
XX (HSIGKVII) and the heavy chain complementarity determining regions (see  
XX AAY32257-59) of murine antibody C11. The DNA was constructed by splice  
XX overlap PCR. The invention provides altered antibodies, such as chimeric  
XX or humanised antibodies, which comprise sufficient of the amino acid  
XX sequences of the C11 light and heavy chain complementarity determining  
XX regions to render them capable of binding to the CD23 type II molecule  
XX expressed on haematopoietic cells. The antibodies are used to block  
XX soluble CD23 formation in human therapy, for the treatment of arthritis,  
XX lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,  
XX diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,  
XX glomerulonephritis, inflammatory bowel disease, ulcerative colitis,  
XX Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
XX intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
XX versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
XX bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
XX malignancies (claimed). They are also useful for studying interactions  
XX between CD23 and various ligands and determining the binding agents  
XX  
XX Sequence 444 AA;  
Query Match 100.0%; Score 33; DB 3; Length 444;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYWMS 5  
Db 31 GYWMS 35  
RESULT 8  
ID ABO67808 standard; protein; 466 AA.  
XX ABO67808;  
XX  
XX ABO67808;  
XX

DT 29-JUL-2004 (first entry)  
 XX Klebsiella pneumoniae polypeptide seqid 14325.  
 DE Recombinant expression vector; transcription regulatory element;  
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.  
 KW Klebsiella pneumoniae.  
 OS US6610836-B1.  
 XX 26-AUG-2003.  
 XX 27-JAN-2000; 2000US-00489039.  
 XX 29-JAN-1999; 99US-0117747P.  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 XX Breton GL, Osborne M;  
 XX WPI; 2003-895346/82.  
 DR N-PSDB; ABD01379.  
 XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
 PT preparing a vaccine composition against Klebsiella pneumoniae.  
 XX Disclosure; SEQ ID NO 14325; 932pp; English.  
 XX The invention describes a new isolated nucleic acid encoding a Klebsiella  
 CC pneumoniae polypeptide. Also described are: a recombinant expression  
 CC vector comprising the nucleic acid, operably linked to a transcription  
 CC regulatory element; and a cell comprising the recombinant expression  
 CC vector. The nucleic acid is useful for preparing a vaccine composition  
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
 CC Klebsiella pneumoniae polypeptide of the invention  
 XX  
 SQ Sequence 466 AA;  
 Query Match 100.0%; Score 33; DB 7; Length 466;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GYWS 5  
 Db |||||  
 437 GYWS 441  
 RESULT 9  
 ADP99004  
 ID ADP99004 standard; protein; 1096 AA.  
 XX ADP99004;  
 AC ADP99004;  
 XX 23-SEP-2004 (first entry)  
 XX C. albicans specific gene, CayMR047C, protein sequence.  
 XX Diploid fungal cell; allele; gene disruption cassette;  
 KW promoter replacement fragment; antifungal; fungicide; gene therapy;  
 KW infection; Candida albicans.  
 XX Candida albicans.  
 OS WO2004056965-A2.  
 XX 08-JUL-2004.  
 XX 19-DEC-2003; 2003WO-US040618.  
 XX 19-DEC-2002; 2002US-0434832P.  
 XX (ELIT-) ELITRA PHARM INC.  
 PA

PA (ELIT-) ELITRA CANADA LTD.  
 XX Roemer T, Jiang B, Boone C, Busey H;  
 PI WPI; 2004-500296/47.  
 DR N-PSDB; ADP98694.  
 DR  
 XX Constructing a strain of diploid fungal cells in which both alleles of a  
 PT gene are modified comprises modifying the alleles of a gene in the fungal  
 PT cells by recombination using a gene disruption cassette and a promoter  
 PT replacement fragment.  
 XX  
 PS Claim 44; SEQ ID NO 7179; 163pp; English.  
 XX  
 CC The invention relates to a novel method for constructing a strain of  
 CC diploid fungal cells in which both alleles of a gene are modified. The  
 CC method comprises modifying the alleles of a gene in diploid fungal cells  
 CC by recombination using a gene disruption cassette and a promoter  
 CC replacement fragment. The invention further comprises: assembling a  
 CC collection of diploid fungal cells each of which comprises modified  
 CC alleles of a different gene; a strain of diploid fungal cells comprising  
 CC modified alleles of a gene, where the first allele of the gene is  
 CC inactivated by a gene disruption cassette comprising a nucleotide  
 CC sequence encoding an expressible selectable marker; and the expression of  
 CC the second allele of the gene is regulated by a heterologous promoter  
 CC that is operably linked to the coding region of the second allele of the  
 CC gene, and where the gene encodes the polypeptide mentioned above; a  
 CC collection of diploid fungal strains comprising the diploid strains cited  
 CC above, where substantially all the different genes that encode the above  
 CC amino acid sequences are modified and are present in different diploid  
 CC strains in the collection; a nucleic acid molecule microarray comprising  
 CC nucleic acid molecules, where each nucleic acid molecule comprises a  
 CC nucleotide sequence that is hybridizable to a target nucleotide sequence  
 CC comprising any of the 310 nucleotide sequences listed in the  
 CC specification (ADP98516-ADP98825); identifying a gene that is essential  
 CC to the survival or growth of a fungus, that contributes to the virulence  
 CC and/or pathogenicity of a fungus, or that contributes to the resistance  
 CC of a diploid fungus to an antifungal agent; identifying an antifungal  
 CC agent that inhibits the growth of a diploid fungus, or a therapeutic  
 CC agent for treatment of a mammalian disease; correlating changes in the  
 CC levels of proteins or gene transcripts with the inhibition of growth or  
 CC proliferation of a diploid fungal cell; a purified or isolated nucleic  
 CC acid molecule comprising a nucleotide sequence encoding a gene product  
 CC required for proliferation of Candida albicans, where the gene product  
 CC consists of any of the above-mentioned amino acid sequences; a vector  
 CC comprising a promoter operably linked to the nucleic acid molecule cited  
 CC above; a host cell containing the vector; a purified or isolated  
 CC polypeptide comprising any of the 61 amino acid sequences given in the  
 CC specification (ADP96718-ADP96778); a fusion protein comprising a fragment  
 CC of a first polypeptide fused to a second polypeptide, the fragment  
 CC consisting of at least 6 consecutive residues of any of ADP98826-ADP99135  
 CC; producing a polypeptide; identifying a compound which modulates the  
 CC activity of a gene product encoded by a nucleic acid comprising any of  
 CC ADP98516-ADP98825; eliciting an immune response in an animal; a strain of  
 CC Candida albicans, where a first allele of a gene comprising any of  
 CC ADP98516-ADP98825 is inactive and a second allele of the gene is under  
 CC the control of a heterologous promoter; identifying a compound or binding  
 CC partner that binds to the polypeptide comprising any of ADP98826-  
 CC ADP99135, or its fragment; identifying a compound having the ability to  
 CC inhibit growth or proliferation of Candida albicans; inhibiting growth or  
 CC proliferation of Candida albicans cells; manufacturing an antimycotic  
 CC compound; treating an infection of a subject by Candida albicans;  
 CC preventing or containing contamination of an object by Candida albicans,  
 CC or for preventing or inhibiting formation on a surface of a biofilm  
 CC comprising Candida albicans; a pharmaceutical composition comprising a  
 CC therapeutic amount of an agent which reduces the activity or level of a  
 CC gene product encoded by a nucleic acid comprising any of ADP98516-  
 CC ADP98825 in a pharmaceutical carrier; an antibody preparation which binds  
 CC the polypeptide; methods for evaluating a compound against a target gene  
 CC product encoded by any of ADP98516-ADP98825; identifying an antimycotic  
 CC compound; a computer or a computer readable medium that comprises at  
 CC least one of the nucleotide sequences mentioned in the specification or  
 CC at least one amino acid sequence selected from ADP98826-ADP99135; a

CC method assisted by a computer for identifying a putatively essential gene  
 CC of a fungus; and a protein array comprising proteins, where at least one  
 CC protein comprises an amino acid sequence or a portion of an amino acid  
 CC sequence selected from ADP98516-ADP98825. The novel methods and  
 CC compositions have fungicide activity. The compositions may be used in  
 CC gene therapy. The composition and methods are useful for drug screening  
 CC purposes or for diagnosing, preventing or treating infections associated  
 CC with Candida albicans. These may also be used for constructing strains  
 CC useful for identification and validation of gene products as effective  
 CC targets for therapeutic intervention, for identifying and validating gene  
 CC products as effective targets for therapeutic intervention, and for  
 CC collecting identified essential genes. This sequence represents the  
 CC protein of a Candida albicans fungal specific gene of the invention.  
 CC NOTE: This sequence was downloaded from an electronic sequence listing  
 CC provided on the WIPO website.

XX SQ Sequence 1096 AA;  
 Query Match 100.0%; Score 33; DB 8; Length 1096;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVMS 5  
 |||||  
 Db 955 GYVMS 959

RESULT 10  
 ABB62006  
 ID ABB62006 standard; protein; 1254 AA.

AC ABB62006;

XX 26-MAR-2002 (first entry)

DT Drosophila melanogaster polypeptide SEQ ID NO 12810.

XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI: 2001-656860/75.

XX N-PSDB; ABL06109.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.

XX Disclosure; SEQ ID NO 12810; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS77737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 1254 AA;

Query Match 100.0%; Score 33; DB 4; Length 1254;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVMS 5  
 |||||

Db 1139 GYVMS 1143

RESULT 11

ABG07533

ID ABG07533 standard; protein; 40 AA.

XX AC ABG07533;

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #7524.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX N-PSDB; AAS71720.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX Claim 20; SEQ ID NO 37892; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX



SQ Sequence 40 AA;

Query Match 90.9%; Score 30; DB 4; Length 40;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
 |||:|  
 33 GYWLS 37

Db

RESULT 12  
 AAR95472  
 ID AAR95472 standard; peptide; 43 AA.  
 XX AC  
 XX AC  
 XX AAR95472;  
 XX 05-NOV-1996 (first entry)  
 XX V39, monoclonal antibody SM-3 derived antigen binding peptide.  
 DE V39, monoclonal antibody SM-3 derived antigen binding peptide.  
 XX Abtide; prostate specific mucin antigen; human prostate cancer; LNCaP;  
 KW diagnostic; detection; imaging; tumour; phage; peptide library; breast;  
 KW polymorphic; epithelial.  
 XX Synthetic.  
 OS  
 XX WO9609411-A1.  
 XX 28-MAR-1996.  
 XX 20-SEP-1995; 95WO-US011934.  
 XX 21-SEP-1994; 94US-00310192.  
 XX 07-JUN-1995; 95US-00488161.  
 XX (CYTO-) CYTOGEN CORP.  
 XX Alvarez VL;  
 XX WPI; 1996-188471/19.  
 XX New isolated peptide(s) with specific binding activities - obtd. by  
 PT screening random peptide libraries, for use in diagnostic and therapeutic  
 PT compans.  
 XX Claim 38; Page 75; 106pp; English.  
 XX AAR95459-R95509 are antigen binding peptides ("abtides") derived from the  
 CC monoclonal antibody SM-3 which recognises a specific polymorphic  
 CC epithelial mucin tumour antigen found on human breast cancer cells. The  
 CC abtides are identified from random peptide libraries using specific  
 CC ligand binding. Abtides mimic the binding specificity of large molecules  
 CC such as antibodies and receptors but have a much smaller size allowing  
 CC their production at a lower cost and reducing the extent of their  
 CC immunogenicity aiding in vivo delivery. The abtides are useful for the  
 CC diagnosis, detection, imaging and treatment of disease, e.g. tumours,  
 CC prostate cancer and breast cancer  
 XX

SQ Sequence 43 AA;

Query Match 90.9%; Score 30; DB 2; Length 43;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
 |||:|  
 6 GYWLS 10

Db

RESULT 13  
 ABR48102  
 ID ABR48102 standard; protein; 63 AA.

XX ABR48102;  
 XX 12-JUN-2003 (first entry)  
 XX Human secreted protein, SEQ ID 993.  
 DE  
 XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;  
 KW vulnery; antiinflammatory; nootropic; neuroprotective;  
 KW antiparkinsonian; gene therapy; human; cardiovascular disorder.  
 XX  
 XX Homo sapiens.  
 XX WO200295010-A2.  
 XX 28-NOV-2002.  
 XX 19-MAR-2002; 2002WO-US009785.  
 XX 21-MAR-2001; 2001US-0277340P.  
 PR 19-JUL-2001; 2001US-0306171P.  
 PR 13-NOV-2001; 2001US-0331287P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Rosen CA, Ruben SM;  
 XX WPI; 2003-129429/12.  
 XX Novel human secreted proteins, useful for detecting, preventing,  
 PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular  
 PT disorders such as arrhythmia.  
 XX Claim 13; SEQ ID NO 993; 1881pp; English.  
 XX The present invention relates to novel human secreted proteins (ABR47633-  
 CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins  
 CC and their coding sequences are useful for the preparation of a diagnostic  
 CC or pharmaceutical composition for diagnosing or treating a cardiovascular  
 CC disorder (e.g. arrhythmia, tachycardia, cardiac arrest, coronary  
 CC arteriosclerosis and myocardial ischaemia), neural disorders, immune  
 CC system disorders, muscular disorders, reproductive disorders,  
 CC gastrointestinal disorders, pulmonary disorders, renal disorders,  
 CC proliferative disorders and/or cancerous diseases and conditions, for  
 CC wound healing and epithelial cell proliferation, to treat inflammation or  
 CC infection, for treating thrombosis and arteriosclerosis, for treating or  
 CC preventing neural damage which occurs in neuronal disorders or  
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's  
 CC disease, to enhance bone and periodontal regeneration and aid in tissue  
 CC transplants or bone grafts, to prevent skin aging or hair loss, to  
 CC stimulate growth and differentiation of haematopoietic cells and bone  
 CC marrow cells when used in combination with other cytokines, to maintain  
 CC organs before transplantation or for supporting cell culture of primary  
 CC tissues, to increase or decrease differentiation or proliferation of  
 CC embryonic stem cells, or to modulate mammalian characteristics or  
 CC metabolism. Note: The sequence data for this patent was published in  
 CC electronic format and is available from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 63 AA;

Query Match 90.9%; Score 30; DB 6; Length 63;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
 |||:|  
 45 GYWLS 49

Db

RESULT 14  
 ABR00271  
 ID ABR00271 standard; protein; 63 AA.

```
XX ABR00271;
XX AC
XX DT
XX DE
XX DE 03-APR-2003 (first entry)
XX DE Human gene 139 encoded secreted protein HPRAL78, SEQ ID NO:560.
XX KW Human; secreted protein; digestive disorder; gastrointestinal disorder;
XX KW mouth; oesophagus; stomach; small intestine; large intestine; liver;
XX KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
XX KW immune disorder; inflammation; infection; wound healing; drug screening;
XX KW chromosome identification; chromosome mapping; cytostatic; gene therapy;
XX KW antiinflammatory; immunosuppressive; vulnery; chromosome 3p25.2.
XX OS
XX OS Homo sapiens.
XX PN WO200276488-A1.
XX PF 03-OCT-2002.
XX PF 19-MAR-2002; 2002WO-US008276.
XX PR 21-MAR-2001; 2001US-0277340P.
XX PR 19-JUL-2001; 2001US-0306171P.
XX PR 13-NOV-2001; 2001US-0331287P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Ruben SM;
XX PI WPI; 2003-029900/02.
XX DR N-PSDB; ABZ71450.
XX PS Claim 13; Page 1107; 1216pp; English.
XX CC ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted
XX CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.
XX CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The
XX CC invention also encompasses antibodies specific for the secreted proteins,
XX CC the use of the secreted proteins in drug screening, and recombinant
XX CC vectors and host cells comprising a nucleic acid of the invention. The
XX CC secreted proteins, nucleic acids encoding them, antibodies or antibody
XX CC fragments specific for the secreted proteins, and modulators of protein
XX CC activity are useful for diagnosing, treating, ameliorating or preventing
XX CC digestive disorders. Such conditions include disorders of the mouth,
XX CC oesophagus, stomach, small intestine, large intestine, liver, biliary
XX CC tract and pancreas, and include cancers of these organs and tissues. The
XX CC secreted proteins and their nucleic acids may also be used in the
XX CC treatment of immune disorders, inflammation, infection,
XX CC hyperproliferative disorders, and to promote wound healing. Nucleic acids
XX CC of the invention may be used for chromosome identification, chromosome
XX CC mapping, in gene therapy, for identifying individuals from minute
XX CC biological samples, as hybridisation probes, and as molecular weight
XX CC markers. The present sequence represents a human secreted protein of the
XX CC invention
XX SQ Sequence 63 AA;
XX Query Match 90.9%; Score 30; DB 6; Length 63;
XX Best Local Similarity 80.0%; Pred. No. 2.6e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 GYWMS 5
XX Db |||:|
XX 45 GYWLS 49
XX RESULT 15
XX ADB91793
```

```
XX ID
XX AC
XX DT
XX DE
XX DE 04-DEC-2003 (first entry)
XX DE Human secreted protein #SEQ ID 739.
XX KW Secreted protein; gene therapy; antidiabetic; diabetes; human.
XX OS
XX OS Homo sapiens.
XX PN WO2003004622-A2.
XX PF 16-JAN-2003.
XX PF 19-MAR-2002; 2002WO-US008124.
XX PR 21-MAR-2001; 2001US-0277340P.
XX PR 19-JUL-2001; 2001US-0306171P.
XX PR 13-NOV-2001; 2001US-0331287P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Ruben SM;
XX PI WPI; 2003-229407/22.
XX PT Nucleic acid encoding a human secreted protein is useful in diagnosing or
XX PT treating diabetes or conditions related to diabetes.
XX PS Claim 3; SEQ ID NO 739; 1537pp; English.
XX CC The invention relates to isolated nucleic acid molecules ADB91065-
XX CC ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-
XX CC ADB91834. Also disclosed is a recombinant vector comprising a
XX CC polynucleotide of the invention, and a recombinant host cell comprising
XX CC the recombinant vector. The polypeptide of the invention is useful in
XX CC identifying a binding partner by contacting the polypeptide with a
XX CC binding partner, and determining whether the binding partner increases or
XX CC decreases activity of the polypeptide. The polypeptide, polynucleotide,
XX CC antibody or its fragment, agonist or antagonist are useful for preparing
XX CC a pharmaceutical composition for diagnosing or treating diabetes or
XX CC conditions related to diabetes. The present sequence is that of the human
XX CC immunoglobulin Fc portion used to generate fusion proteins, increasing
XX CC the stability of the fused protein as compared to the secreted protein
XX CC only. Note: The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 63 AA;
XX Query Match 90.9%; Score 30; DB 7; Length 63;
XX Best Local Similarity 80.0%; Pred. No. 2.6e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 GYWMS 5
XX Db |||:|
XX 45 GYWLS 49
XX Search completed: April 18, 2005, 14:15:19
XX Job time : 55.6744 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:22:17 ; Search time 37.7907 Seconds  
(without alignments)  
43.975 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubppaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubppaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubppaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubppaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubppaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubppaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubppaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubppaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	5	17 US-10-783-311-283	Sequence 283, App
2	33	100.0	5	17 US-10-783-311-315	Sequence 315, App
3	33	100.0	10	16 US-10-327-598-450	Sequence 450, App
4	33	100.0	73	15 US-10-418-861B-57	Sequence 57, Appl
5	33	100.0	103	16 US-10-437-963-178878	Sequence 178878, App
6	33	100.0	132	17 US-10-783-311-279	Sequence 279, App
7	33	100.0	132	17 US-10-783-311-311	Sequence 311, App
8	33	100.0	504	16 US-10-437-963-128079	Sequence 128079, App
9	33	100.0	721	16 US-10-437-963-144813	Sequence 144813, App
10	33	100.0	1096	17 US-10-741-849-7179	Sequence 7179, App
11	30	90.9	64	14 US-10-144-929-162	Sequence 162, App
12	30	90.9	64	15 US-10-144-929-162	Sequence 162, App
13	30	90.9	77	15 US-10-424-599-231107	Sequence 231107, App

14	30	90.9	88	16	US-10-767-701-41902	Sequence 41902, A
15	30	90.9	95	16	US-10-767-701-53836	Sequence 53836, A
16	30	90.9	167	15	US-10-424-599-178190	Sequence 178190, App
17	30	90.9	181	15	US-10-289-762-900	Sequence 900, App
18	30	90.9	210	9	US-09-764-868-892	Sequence 892, App
19	30	90.9	229	15	US-10-424-599-210785	Sequence 210785, App
20	30	90.9	242	10	US-09-866-050A-393	Sequence 393, App
21	30	90.9	242	10	US-09-866-050A-502	Sequence 502, App
22	30	90.9	242	10	US-09-866-050A-625	Sequence 625, App
23	30	90.9	310	9	US-09-815-242-10910	Sequence 10910, A
24	30	90.9	310	15	US-10-282-122A-57347	Sequence 57347, A
25	30	90.9	315	15	US-10-369-493-18477	Sequence 18477, A
26	30	90.9	348	15	US-10-369-493-1130	Sequence 1130, App
27	30	90.9	381	16	US-10-437-963-149574	Sequence 149574, App
28	30	90.9	392	14	US-10-050-704-180	Sequence 180, App
29	30	90.9	392	14	US-10-144-929-156	Sequence 156, App
30	30	90.9	392	15	US-10-144-929-156	Sequence 156, App
31	30	90.9	392	16	US-10-798-512-180	Sequence 180, App
32	30	90.9	414	13	US-10-087-192-828	Sequence 828, App
33	30	90.9	419	16	US-10-437-963-141970	Sequence 141970, App
34	30	90.9	420	9	US-09-909-320-109	Sequence 109, App
35	30	90.9	420	9	US-09-909-088B-109	Sequence 109, App
36	30	90.9	420	9	US-09-305-291A-109	Sequence 109, App
37	30	90.9	420	9	US-09-907-824-109	Sequence 109, App
38	30	90.9	420	9	US-09-907-824-109	Sequence 109, App
39	30	90.9	420	9	US-09-907-841-109	Sequence 109, App
40	30	90.9	420	10	US-09-904-011-109	Sequence 109, App
41	30	90.9	420	10	US-09-903-640-109	Sequence 109, App
42	30	90.9	420	10	US-09-908-093-109	Sequence 109, App
43	30	90.9	420	10	US-09-906-742-109	Sequence 109, App
44	30	90.9	420	10	US-09-906-838-109	Sequence 109, App
45	30	90.9	420	10	US-09-907-613-109	Sequence 109, App

#### ALIGNMENTS

RESULT 1  
US-10-783-311-283  
; Sequence 283, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 283  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-283

Query Match 100.0%; Score 33; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||  
Db 1 GYWS 5

RESULT 2  
US-10-783-311-315  
; Sequence 315, Application US/10783311  
; Publication No. US20050009136A1

; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; APPLICANT: Hogan, Shannon  
; TITLE OF INVENTION: PAP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 315  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-315

Query Match 100.0%; Score 33; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

\*QY 1 GYWS 5  
Db 1 GYWS 5

RESULT 3  
US-10-327-598-450  
; Sequence 450, Application US/10327598  
; Publication No. US20040101039A1  
; GENERAL INFORMATION:  
; APPLICANT: Krah, Eugene  
; APPLICANT: Guo, Hongliang  
; APPLICANT: Aiyappa, Ashok  
; APPLICANT: Lawton, Robert  
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and  
; TITLE OF INVENTION: for Making and Using Them  
; FILE REFERENCE: 01-799-A  
; CURRENT APPLICATION NUMBER: US/10/327,598  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US 60/344,874  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 1139  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 450  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: canis familiaris;  
US-10-327-598-450

Query Match 100.0%; Score 33; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
Db 6 GYWS 10

RESULT 4  
US-10-418-861B-57  
; Sequence 57, Application US/1041861B  
; Publication No. US20040010131A1  
; GENERAL INFORMATION:  
; APPLICANT: da Silva, Ana Claudia Rasera  
; APPLICANT: Farah, Shaker Chuck  
; APPLICANT: Quaggio, Ronaldo Bento  
; APPLICANT: Reinach, Fernando de Castro  
; APPLICANT: Ferro, Jesus Aparecido  
; APPLICANT: De Oliveira, Julio Cesar Franco  
; APPLICANT: De Laia, Marcelo Luiz

; APPLICANT: Setubal Joao C.  
; APPLICANT: Furlan, Luiz Roberto  
; TITLE OF INVENTION: Isolated Xanthomonas nucleic acid molecules, proteins encoded th  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: FAPESP 205.1 US  
; CURRENT APPLICATION NUMBER: US/10/418,861B  
; CURRENT FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: US 60/374,620  
; PRIOR FILING DATE: 2002-04-22  
; NUMBER OF SEQ ID NOS: 85  
; SEQ ID NO 57  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Xanthomonas  
; FEATURE:  
US-10-418-861B-57

Query Match 100.0%; Score 33; DB 15; Length 73;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
Db 6 GYWS 10

RESULT 5  
US-10-437-963-178878  
; Sequence 178878, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 178878  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(103)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_76394C.1.pgp  
US-10-437-963-178878

Query Match 100.0%; Score 33; DB 16; Length 103;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
Db 15 GYWS 19

RESULT 6  
US-10-783-311-279  
; Sequence 279, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; APPLICANT: Hogan, Shannon

; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 279  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-279

Query Match 100.0%; Score 33; DB 17; Length 132;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||||  
Db 31 GYWMS 35

RESULT 7  
US-10-783-311-311  
; Sequence 311, Application US/10783311  
; Publication No. US2005009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; APPLICANT: Hogan, Shannon  
; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 311  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-311

Query Match 100.0%; Score 33; DB 17; Length 132;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||||  
Db 31 GYWMS 35

RESULT 8  
US-10-437-963-128079  
; Sequence 128079, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 128079  
; LENGTH: 504  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(504)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_30468C.1.pep  
US-10-437-963-128079

Query Match 100.0%; Score 33; DB 16; Length 504;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||||  
Db 4 GYWMS 8

RESULT 9  
US-10-437-963-144813  
; Sequence 144813, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 144813  
; LENGTH: 721  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_45593C.1.pep  
US-10-437-963-144813

Query Match 100.0%; Score 33; DB 16; Length 721;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||||  
Db 319 GYWMS 323

RESULT 10  
US-10-741-849-71179  
; Sequence 7179, Application US/10741849  
; Publication No. US20050019931A1  
; GENERAL INFORMATION:  
; APPLICANT: Roemer, Terry  
; APPLICANT: Jiang, Bo  
; APPLICANT: Boone, Charles  
; APPLICANT: Bussey, Howard  
; APPLICANT: Use  
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of  
; TITLE OF INVENTION: Use  
; FILE REFERENCE: 10182-023-999  
; CURRENT APPLICATION NUMBER: US/10/741,849

/ CURRENT FILING DATE: 2003-12-19  
/ PRIOR APPLICATION NUMBER: US 60/434,832  
/ PRIOR FILING DATE: 2002-12-19  
/ NUMBER OF SEQ ID NOS: 8000  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 7179  
/ LENGTH: 1096  
/ TYPE: PRT  
/ ORGANISM: Candida albicans  
US-10-741-849-7179

Query Match 100.0%; Score 33; DB 17; Length 1096;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
Db 955 GYWS 959

RESULT 11  
US-10-144-929-162  
/ Sequence 162, Application US/10144929  
/ Publication No. US20030069405A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ruben et al.  
/ TITLE OF INVENTION: 70 Human Secreted Proteins  
/ FILE REFERENCE: P2014P1  
/ CURRENT APPLICATION NUMBER: US/10/144,929  
/ CURRENT FILING DATE: 2002-05-15  
/ PRIOR APPLICATION NUMBER: US/09/251,329  
/ PRIOR FILING DATE: 1999-02-17  
/ PRIOR APPLICATION NUMBER: PCT/US98/17044  
/ PRIOR FILING DATE: 1998-08-18  
/ NUMBER OF SEQ ID NOS: 257  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 162  
/ LENGTH: 64  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: SITE  
/ LOCATION: (64)  
/ OTHER INFORMATION: Xaa equals stop translation  
US-10-144-929-162

Query Match 90.9%; Score 30; DB 14; Length 64;  
Best Local Similarity 80.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
Db 45 GYWS 49

RESULT 12  
US-10-144-929-162  
/ Sequence 162, Application US/10144929  
/ Publication No. US20040014954A9  
/ GENERAL INFORMATION:  
/ APPLICANT: Ruben et al.  
/ TITLE OF INVENTION: 70 Human Secreted Proteins  
/ FILE REFERENCE: P2014P1  
/ CURRENT APPLICATION NUMBER: US/10/144,929  
/ CURRENT FILING DATE: 2002-05-15  
/ PRIOR APPLICATION NUMBER: US/09/251,329  
/ PRIOR FILING DATE: 1999-02-17  
/ PRIOR APPLICATION NUMBER: PCT/US98/17044  
/ PRIOR FILING DATE: 1998-08-18  
/ NUMBER OF SEQ ID NOS: 257  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 162  
/ LENGTH: 64

/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: SITE  
/ LOCATION: (64)  
/ OTHER INFORMATION: Xaa equals stop translation  
US-10-144-929-162

Query Match 90.9%; Score 30; DB 15; Length 64;  
Best Local Similarity 80.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
Db 45 GYWS 49

RESULT 13  
US-10-424-599-231107  
/ Sequence 231107, Application US/10424599  
/ Publication No. US20040031072A1  
/ GENERAL INFORMATION:  
/ APPLICANT: La Rosa Thomas J  
/ APPLICANT: Kovalic David K  
/ APPLICANT: Zhou Yihua  
/ APPLICANT: Cao Yongwei  
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
/ FILE REFERENCE: 38-21(53223)B  
/ CURRENT APPLICATION NUMBER: US/10/424,599  
/ CURRENT FILING DATE: 2003-04-28  
/ NUMBER OF SEQ ID NOS: 285684  
/ SEQ ID NO 231107  
/ LENGTH: 77  
/ TYPE: PRT  
/ ORGANISM: Glycine max  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: PAT\_MRT3847\_50710C.1.pap  
US-10-424-599-231107

Query Match 90.9%; Score 30; DB 15; Length 77;  
Best Local Similarity 80.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
Db 36 GYWS 40

RESULT 14  
US-10-767-701-41902  
/ Sequence 41902, Application US/10767701  
/ Publication No. US20040172684A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Kovalic, David K.  
/ APPLICANT: Zhou, Yihua  
/ APPLICANT: Cao, Yongwei  
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
/ TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
/ FILE REFERENCE: 38-21(53535)B  
/ CURRENT APPLICATION NUMBER: US/10/767,701  
/ CURRENT FILING DATE: 2004-01-29  
/ NUMBER OF SEQ ID NOS: 63128  
/ SEQ ID NO 41902  
/ LENGTH: 88  
/ TYPE: PRT  
/ ORGANISM: Sorghum bicolor  
/ FEATURE:  
/ NAME/KEY: unsure  
/ LOCATION: (1)...(88)  
/ OTHER INFORMATION: unsure at all Xaa locations  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: LIB3478-024-P1-K1-F2.pap

US-10-767-701-41902

Query Match 90.9%; Score 30; DB 16; Length 88;  
Best Local Similarity 80.0%; Pred. No. 6.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5  
| | | | |  
Db 70 GYWLS 74

RESULT 15

US-10-767-701-53836  
; Sequence 53836, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 53836  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 13586731.pap  
US-10-767-701-53836

Query Match 90.9%; Score 30; DB 16; Length 95;  
Best Local Similarity 80.0%; Pred. No. 7.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5  
| | | | |  
Db 16 GYWLS 20

Search completed: April 18, 2005, 14:54:42  
Job time : 38.7907 secs

***This Page Blank (uspto)***



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:01:43 ; Search time 13.6047 Seconds  
(without alignments)  
27.435 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	466	4	US-09-489-039A-14325
2	33	100.0	637	4	US-09-248-796A-19134
3	30	90.9	43	2	US-08-488-161-39
4	30	90.9	43	3	US-09-273-685-39
5	30	90.9	43	5	PCT-US95-11934-39
6	30	90.9	181	4	US-09-198-452A-900
7	30	90.9	181	4	US-09-902-540-9914
8	30	90.9	238	4	US-09-902-540-13083
9	30	90.9	242	4	US-09-312-283C-393
10	30	90.9	243	3	US-09-134-001C-4114
11	30	90.9	334	4	US-09-134-000C-6029
12	30	90.9	383	4	US-09-252-991A-29457
13	30	90.9	396	4	US-09-252-991A-20263
14	30	90.9	408	4	US-09-107-532A-6992
15	30	90.9	414	4	US-09-949-016-6862
16	30	90.9	420	4	US-09-907-794A-109
17	30	90.9	420	4	US-09-905-125A-109
18	30	90.9	420	4	US-09-902-775A-109
19	30	90.9	420	4	US-09-906-700-109
20	30	90.9	420	4	US-09-903-603A-109
21	30	90.9	420	4	US-09-904-520A-109
22	30	90.9	420	4	US-09-909-064-109
23	30	90.9	420	4	US-09-905-381A-109
24	30	90.9	420	4	US-09-906-618-109
25	30	90.9	448	4	US-09-583-110-4257
26	30	90.9	452	4	US-09-107-433-4995
27	30	90.9	478	4	US-09-107-532A-6868

28	30	90.9	484	4	US-09-634-238-216	Sequence 216, Appl
29	30	90.9	534	4	US-09-107-532A-6549	Sequence 5549, Ap
30	30	90.9	538	4	US-09-489-039A-8363	Sequence 8363, Ap
31	30	90.9	667	4	US-09-315-127-5	Sequence 5, Appli
32	30	90.9	667	4	US-09-315-127-6	Sequence 6, Appli
33	30	90.9	667	4	US-09-070-630-13	Sequence 13, Appl
34	30	90.9	685	4	US-09-489-039A-12981	Sequence 12981, A
35	30	90.9	911	4	US-09-902-540-14901	Sequence 14901, A
36	30	90.9	1218	4	US-09-438-185A-837	Sequence 837, Appl
37	30	90.9	1498	4	US-09-792-616-9	Sequence 9, Appli
38	30	90.9	1503	4	US-09-792-616-3	Sequence 3, Appli
39	30	90.9	1503	4	US-09-647-140B-8	Sequence 8, Appli
40	29	87.9	5	2	US-08-480-434-22	Sequence 22, Appl
41	29	87.9	5	2	US-08-480-434-31	Sequence 31, Appl
42	29	87.9	5	2	US-08-053-451B-22	Sequence 22, Appl
43	29	87.9	5	2	US-08-053-451B-31	Sequence 31, Appl
44	29	87.9	14	1	US-08-204-656B-11	Sequence 11, Appl
45	29	87.9	14	1	US-08-470-702-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-09-489-039A-14325  
; Sequence 14325, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 14325  
; LENGTH: 466  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-14325

Query Match 100.0%; Score 33; DB 4; Length 466;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
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Db 437 GYWS 441

RESULT 2  
US-09-248-796A-19134  
; Sequence 19134, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 19134  
; LENGTH: 637  
; TYPE: PRT  
; ORGANISM: Candida albicans  
; FEATURE:

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; NAME/KEY: UNSURE
; LOCATION: (338)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-19134

Query Match          100.0%; Score 33; DB 4; Length 637;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      496 GYWS 500

RESULT 3
US-08-488-161-39
; Sequence 39, Application US/08488161
; Patent No. 5885577
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,161
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,161
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-161-39

Query Match          90.9%; Score 30; DB 2; Length 43;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      6 GYWS 10

US-09-273-685-39
; Sequence 39, Application US/09273685
; Patent No. 6015561
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
```

```
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/273,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,161
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-273-685-39

Query Match          90.9%; Score 30; DB 3; Length 43;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      6 GYWS 10

RESULT 5
PCT-US95-11934-39
; Sequence 39, Application PC/TUS9511934
; GENERAL INFORMATION:
; APPLICANT: Cytogen Corporation
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11934
; FILING DATE: 20-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
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; PRIOR FILLING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9914
; LENGTH: 181
;
; BEST LOCAL SIMILARITY 80.0%; Pred. NO. 4.8e+02; Gaps 0;
; Matches 4; Conservative 1; Mismatches 0; Indels
QY      1 GYWS 5

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Db      224 GYWS 228
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; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29457
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-29457

Query Match      90.9%; Score 30; DB 4; Length 383;
Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYWS 5
||||:|
Db      228 GYWS 232

RESULT 13
US-09-252-991A-20263
; Sequence 20263, Application US/09252991A
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20263
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20263

Query Match      90.9%; Score 30; DB 4; Length 396;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYWS 5
||||:|
Db      40 GYWS 44

RESULT 14
US-09-107-532A-6992
; Sequence 6992, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC

Db      111 GYWS 115

RESULT 12
US-09-252-991A-29457
; Sequence 29457, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
```

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Db      224 GYWS 228
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; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29457
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-29457

Query Match      90.9%; Score 30; DB 4; Length 383;
Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYWS 5
||||:|
Db      228 GYWS 232

RESULT 13
US-09-252-991A-20263
; Sequence 20263, Application US/09252991A
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20263
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20263

Query Match      90.9%; Score 30; DB 4; Length 396;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYWS 5
||||:|
Db      40 GYWS 44

RESULT 14
US-09-107-532A-6992
; Sequence 6992, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC

Db      111 GYWS 115

RESULT 12
US-09-252-991A-29457
; Sequence 29457, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
```

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;; OPERATING SYSTEM: <Unknown>
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;;   APPLICATION NUMBER: US/09/107,532A
;;   FILING DATE: 30-Jun-1998
;; PRIOR APPLICATION DATA:
;;   APPLICATION NUMBER: 60/085,598
;;   FILING DATE: 14 May 1998
;;   APPLICATION NUMBER: 60/051571
;;   FILING DATE: July 2, 1997
;; ATTORNEY/AGENT INFORMATION:
;;   NAME: Ariniello, Pamela Deneke
;;   REGISTRATION NUMBER: 40,489
;;   REFERENCE/DOCKET NUMBER: GTC-012
;; TELECOMMUNICATION INFORMATION:
;;   TELEPHONE: (781)893-5007
;;   TELEFAX: (781)893-8277
;; INFORMATION FOR SEQ ID NO: 6992:
;;   SEQUENCE CHARACTERISTICS:
;;     LENGTH: 408 amino acids
;;     TYPE: amino acid
;;     TOPOLOGY: linear
;;     MOLECULE TYPE: protein
;;     HYPOTHETICAL: YES
;;     ORIGINAL SOURCE:
;;       ORGANISM: Enterococcus faecium
;;     FEATURE:
;;       NAME/KEY: misc feature
;;       LOCATION: (B) LOCATION 1...408
;;   SEQUENCE DESCRIPTION: SEQ ID NO: 6992:
US-09-107-532A-6992

Query Match          90.9%; Score 30; DB 4; Length 408;
Best Local Similarity 80.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 263 GYWMT 267

RESULT 15
US-09-949-016-6862
; Sequence 6862, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6862
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6862

Query Match          90.9%; Score 30; DB 4; Length 414;
Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 11 GYWLS 15
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Search completed: April 18, 2005, 14:25:31  
Job time : 18.6047 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 15:29:25 ; Search time 43 Seconds  
(without alignments)  
11.188 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: p1r1.\*

2: p1r2.\*

3: p1r3.\*

4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	60.6	5	2 JH0253	gut pentapeptide -
2	16	48.5	5	2 A32516	cholecystokinin-5
3	13	39.4	4	2 S09478	globulin IV alpha
4	13	39.4	5	2 PT0308	Ig heavy chain CRD
5	11	33.3	3	3 F37196	bradykinin-potenti
6	11	33.3	4	2 A34626	RPCH-related neuro
7	11	33.3	4	2 B53284	T-cell receptor be
8	11	33.3	4	2 PT0661	T-cell receptor be
9	11	33.3	5	2 A60803	neuropeptide - sea
10	11	33.3	5	2 PT0281	Ig heavy chain CRD
11	11	33.3	5	2 PT0729	T-cell receptor be
12	11	33.3	5	2 PT0580	T-cell receptor be
13	11	33.3	5	2 G37196	bradykinin-potenti
14	9	27.3	3	3 I50412	gene p20K protein
15	9	27.3	4	2 A32480	achatin-1 - Giant
16	9	27.3	5	2 S70154	URF2 protein - Xan
17	9	27.3	5	2 B37325	pap fibrial regul
18	9	27.3	5	2 A37114	hypoxanthine phosph
19	9	27.3	5	2 B61445	Leu-enkephalin - b
20	9	27.3	5	2 A61445	Met-enkephalin - b
21	9	27.3	5	2 B61168	cocoonase (EC 3.4.
22	9	27.3	5	2 I40469	dnazx-like protein
23	8	24.2	3	3 GKHU	growth-modulating
24	8	24.2	4	2 I38888	COI intron 16 prot
25	8	24.2	4	2 PL0140	carbon-monoxide de
26	8	24.2	5	2 PT0278	Ig heavy chain CRD
27	8	24.2	5	2 S69237	surface protein te
28	7	21.2	3	3 A22565	R-phycoerythrin al
29	7	21.2	3	3 A43391	TRH-like tripeptid

30 7 21.2 3 3 S68328 blood cell protein  
31 7 21.2 4 2 A37832 phenol 2-monooxyge  
32 7 21.2 4 2 I61883 protamine P1 - ora  
33 7 21.2 4 2 PT0240 Ig heavy chain CRD  
34 7 21.2 4 2 S43959 Ig mu chain V regi  
35 7 21.2 4 2 I37013 protamine P1 - Cer  
36 7 21.2 4 2 I84439 tyrosine-melanocyt  
37 7 21.2 4 2 A32039 protamine P1 - sav  
38 7 21.2 5 1 HOROHA proctolin - Americ  
39 7 21.2 5 2 I39964 ribosomal protein  
40 7 21.2 5 2 I39966 ribosomal protein  
41 7 21.2 5 2 E60274 major protein anti  
42 7 21.2 5 2 F22565 R-phycoerythrin ga  
43 7 21.2 5 2 PQ0009 angiotensin-conver  
44 7 21.2 5 2 PQ0009 photosystem I 10.4  
45 7 21.2 5 2 PQ0689

#### ALIGNMENTS

##### RESULT 1

JH0253

gut pentapeptide - Japanese eel

C;Species: Anguilla japonica (Japanese eel)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995

C;Accession: JH0253

R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.

Biochem. Biophys. Res. Commun. 180, 828-832, 1991

A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.

A;Reference number: JH0253; MUID:92062113; PMID:1953755

A;Accession: JH0253

A;Molecule type: protein

A;Residues: 1-5 <UES>

A;Experimental source: gut

C;Comment: This peptide increased basal tone of the circular muscle of the esophagost

, and of the circular muscle of the gastro-intestinal junction.

Query Match 60.6%; Score 20; DB 2; Length 5;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3

Db 1 GFW 3

##### RESULT 2

A32516

cholecystokinin-5 - dog

N;Alternate names: CCK-5

C;Species: Canis lupus familiaris (dog)

C;Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000

C;Accession: A32516

R;Shively, J.; Reeve Jr., J.R.; Byssesein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H

Am. J. Physiol. 252, G272-G275, 1987

A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and inte

A;Reference number: A32516; MUID:87153871; PMID:3826354

A;Accession: A32516

A;Molecule type: protein

A;Residues: 1-5 <SHI>

C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecyst.

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; neuropeptide

F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 48.5%; Score 16; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WM 4

Db 2 WM 3

## RESULT 3

S09478  
 globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)  
 N;Alternate names: IIS globulin alpha subunit gamma chain  
 C;Species: Cucurbita sp. (cucurbit)  
 C;Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 08-Nov-1996  
 C;Accession: S09478  
 R;Ohmura, M.; Hara, I.; Matsubara, H.  
 Plant Cell Physiol. 21, 157-167, 1980  
 A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and  
 A;Reference number: S09066  
 A;Accession: S09478  
 A;Molecule type: protein  
 A;Residues: 1-4 <OHM>

Query Match 39.4%; Score 13; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
 ||  
 3 GY 4

Db

## RESULT 4

PT0308  
 Ig heavy chain CRD3 region (clone 6-88) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C;Accession: PT0308  
 R;Ramada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A;Reference number: PT0222; MUID:91108337; PMID:1899102  
 A;Accession: PT0308  
 A;Molecule type: DNA  
 A;Residues: 1-5 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 39.4%; Score 13; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WMS 5  
 ||  
 2 WES 4

Db

## RESULT 5

F37196  
 bradykinin-potentiating peptide 6 - island jararaca  
 C;Species: Bothrops insularis (island jararaca)  
 C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C;Accession: F37196  
 R;Cintrá, A.C.O.; Vieira, C.A.; Giglio, J.R.  
 J. Protein Chem. 9, 221-227, 1990  
 A;Title: Primary structure and biological activity of bradykinin potentiating peptides

A;Reference number: A37196; MUID:90351557; PMID:2386615  
 A;Accession: F37196

A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-3 <CIN>  
 C;Keywords: pyroglutamic acid  
 P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 11; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3

Db 3 W 3

## RESULT 6

A34626  
 RPCH-related neuroptide - ferruginous spindle  
 C;Species: Fuscus ferrugineus (ferruginous spindle)  
 C;Date: 06-Jul-1990 #sequence\_revision 06-Jul-1990 #text\_change 31-Dec-1993  
 C;Accession: A34626  
 R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;  
 Blochem. Biophys. Res. Commun. 167, 273-279, 1990  
 A;Title: A molluscan neuroptide related to the crustacean hormone, RPCH.  
 A;Reference number: A34626; MUID:90179762; PMID:2310394  
 A;Accession: A34626

A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-4 <KUR>  
 C;Keywords: neuroptide

Query Match 33.3%; Score 11; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
 ||  
 4 W 4

Db

## RESULT 7

B53284  
 T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 02-May-1992 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C;Accession: B53284  
 R;Harindranath, N.; Alexander, C.B.; Mage, R.G.  
 Mol. Immunol. 28, 881-888, 1991  
 A;Title: Evolutionarily conserved organization and sequences of germline diversity and  
 A;Reference number: A53284; MUID:91342695; PMID:1678859  
 A;Accession: B53284  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-4 <HAR>  
 A;Cross-references: GB:S60737; NID:q233916; PIDN:AAB19518.1; PID:q233918  
 A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)  
 C;Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
 ||  
 2 W 2

Db

## RESULT 8

PT0661  
 T-cell receptor beta chain V-D-J region (121-18V) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
 C;Accession: PT0661  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0661  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-4 <FE>

A;Cross-references: UNIPROT:Q8BZQ7; UNIPROT:Q8CCN5  
 A;Experimental source: day 4 postnatal thymus, strain BALB/c  
 C;Keywords: T-cell receptor



Query Match 33.3%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
DB 3 W 3

RESULT 9  
A60803  
neuropeptide - sea anemone (Anthopleura elegantissima)  
C;Species: Anthopleura elegantissima  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: A60803  
R;Graff, D.; Grimmelikhuijzen, C.J.P.  
Brain Res. 442, 354-358, 1988  
A;Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemones.  
A;Reference number: A60803; MUID:88222764; PMID:2897223  
A;Accession: A60803  
A;Molecule type: protein  
A;Residues: 1-5 <GRA>  
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
DB 5 W 5

RESULT 10  
PT0281  
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0281  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0281  
A;Molecule type: DNA  
A;Residues: 1-5 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
DB 4 W 4

RESULT 11  
PT0729  
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0640; PT0685; PT0729  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0640  
A;Status: translation not shown

A;Molecule type: mRNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1J  
A;Accession: PT0685  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <FE2>  
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C  
A;Accession: PT0729  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <FE3>  
A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG  
C;Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
DB 5 W 5

RESULT 12  
PT0580  
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0580  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0580  
A;Molecule type: mRNA  
A;Status: translation not shown  
A;Residues: 1-5 <FEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
DB 4 W 4

RESULT 13  
G37196  
bradykinin-potentiating peptide 7 - island jararaca  
C;Species: Bothrops insularis (island jararaca)  
C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C;Accession: G37196  
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A;Title: Primary structure and biological activity of bradykinin potentiating peptides  
A;Reference number: A37196; MUID:90351557; PMID:2386615  
A;Accession: G37196  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <CIN>  
A;Cross-references: UNIPROT:P30425  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
DB 4 W 4

Db 3 W 3

## RESULT 14

IS0412  
 gene p20K protein - chicken (fragment)  
 C;Species: Gallus gallus (chicken)  
 C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C;Accession: IS0412  
 R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.  
 J. Biol. Chem. 268, 8131-8139, 1993  
 A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken  
 A;Reference number: A46643; MUID:93216790; PMID:8463325  
 A;Accession: IS0412  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-3 <MAO>  
 A;Cross-references: GB:L02537; NID:G212616; PID:G212617  
 C;Genetics:  
 A;Gene: p20K

Query Match 27.3%; Score 9; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MS 5  
 ||  
 Db 1 MS 2

## RESULT 15

A32480  
 achatin-I - giant African snail  
 N;Contains: achatin-II  
 C;Species: Achatina fulica (giant African snail)  
 C;Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 09-Jul-2004  
 C;Accession: A32480  
 R;Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun  
 Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989  
 A;Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru  
 A;Reference number: A32480; MUID:89273551; PMID:2597281  
 A;Accession: A32480  
 A;Molecule type: protein  
 A;Residues: 1-4 <KAM>  
 A;Cross-references: UNIPROT:P35904  
 A;Note: stereochemistry of the active form confirmed by chemical synthesis  
 R;Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto  
 FEBS Lett. 307, 253-256, 1992  
 A;Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro  
 (H-Gly-Phe-Ala-Asp-OH).  
 A;Reference number: A46691; MUID:92354723; PMID:1644179  
 A;Contents: annotation; X-ray crystallography, 0.85 angstroms  
 A;Note: achatin-II has L-phenylalanine  
 C;Keywords: D-amino acid  
 F;2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 27.3%; Score 9; DB 2; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
 ||  
 Db 1 GF 2

Search completed: April 18, 2005, 15:39:08  
 Job time : 50 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:21:19 ; Search time 178 Seconds  
(without alignments)  
14.384 Million cell updates/sec

Title: US-09-674-716B-9  
Perfect score: 33  
Sequence: 1 GYMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 53

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	45.5	4	1 OCP3 OCTMI	P58649 octopus min
2	15	45.5	5	1 UF01 MOUSE	P38639 mus musculus
3	11	33.3	2	1 GWA SEPOF	P83570 sepiia offic
4	11	33.3	5	1 BPP7 BOTIN	P30425 bothrops in
5	10	30.3	5	1 PAP2 PARMA	P81864 pardachirus
6	10	30.3	5	1 RE32 LITRU	P82073 litoria rub
7	9	27.3	4	1 ACHI ACHFU	P35904 achatina fu
8	9	27.3	4	1 OCP1 OCTMI	P58648 octopus min
9	8	24.2	3	1 GRWM HUMAN	P01157 homo sapien
10	8	24.2	4	1 DCML PSECH	P19316 pseudomonas
11	7	21.2	4	1 FAR3 HIRME	P42562 hirudo medi
12	7	21.2	4	1 FAR3 HIRME	P42563 hirudo medi
13	7	21.2	4	1 FYRI ANTEL	P58706 anthopleura
14	7	21.2	4	2 Q96AT0	O96at0 homo sapien
15	7	21.2	5	1 AL14 CARMA	P81817 carcinus ma
16	7	21.2	5	1 FARP ARTTR	P41853 artiposthi
17	7	21.2	5	1 PRCT CARMA	P67857 carcinus ma
18	7	21.2	5	1 PRCT LIMPO	P67858 limulus pol
19	7	21.2	5	1 PRCT PERAM	P67859 periplaneta
20	7	21.2	5	1 PSK DAUCA	P58261 daucus caro
21	6	18.2	4	1 DCMS PSECH	P19318 pseudomonas
22	6	18.2	4	1 EOS1 HUMAN	P02731 homo sapien
23	6	18.2	4	1 FMRF MACNI	P01162 macrocallis
24	6	18.2	5	1 AP21 BISFO	P84182 eisenia foe
25	6	18.2	5	1 BIOA CITFR	P13071 citrobacter
26	6	18.2	5	1 BIOB CITFR	P12997 citrobacter
27	6	18.2	5	1 TPIS CANFA	P54714 canis famli
28	6	18.2	5	1 UX4A CHLTR	P38005 chlamydia t
29	6	18.2	5	2 Q99007	Q99007 hordeum vul
30	5	15.2	4	1 ILME SEPOF	P83568 sepiia offic
31	5	15.2	5	1 EI03 LITRU	P82099 litoria rub

32	5	15.2	5	2	P83073	P83073 bacillus ce
33	4	12.1	4	1	FFKA ANTEL	P58705 anthopleura
34	4	12.1	4	1	YLM1 YEAST	P36515 saccharomyc
35	4	12.1	5	1	MPA4 JUNVI	P81826 juniperus v
36	4	12.1	5	1	RE11 LITRU	P82070 litoria rub
37	4	12.1	5	1	RE21 LITRU	P82071 litoria rub
38	4	12.1	5	1	RE31 LITRU	P82072 litoria rub
39	4	12.1	5	1	UC22 MAIZE	P80628 zea mays (m
40	3	9.1	4	1	FLRF HIRME	P42561 hirudo medi
41	3	9.1	4	1	FLRN ANTEL	P58707 anthopleura
42	3	9.1	4	2	Q16047	Q16047 homo sapien
43	3	9.1	5	1	EI04 LITRU	P82100 litoria rub
44	3	9.1	5	1	FARP CHICK	P83308 gallus gall
45	3	9.1	5	1	SUGA_ACHDO	P19991 acheta dome

ALIGNMENTS

RESULT 1  
OCP3 OCTMI STANDARD; PRT; 4 AA.  
AC P58649;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cardioactive peptides Ocp-3/Ocp-4.  
OS Octopus minor (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=89766;  
RN [1]  
RP SEQUENCE SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
RC TISSUE=Brain;  
RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;  
RA Iwakoshi E., Hisada M., Minakata H.;  
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
RT Octopus minor";  
RL Peptides 21:623-630(2000).  
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and  
CC inotropic effects on the heart. Ocp-4 is a 1000 time less active  
CC than Ocp-3.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.  
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI; RANGE=1-4; NOTE=Ref.1.  
KW D-amino acid; Direct protein sequencing; Hormone.  
FM MOD RES 2 2 D-serine (in form Ocp-4).  
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 45.5%; Score 15; DB 1; Length 4;  
Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GYW 3  
Db 1 GSW 3

RESULT 2  
UF01 MOUSE STANDARD; PRT; 5 AA.  
ID UF01 MOUSE  
AC P38639;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;

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RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 19 kDa.
KW Direct protein sequencing.
FT NON_TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 45.5%; Score 15; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GW 3
DB 3 GRW 5

RESULT 3
ID GWA SEPOF STANDARD; PRT; 2 AA.
AC P83570;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neuropeptide GWA.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidae; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN (1)
SQ SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Optic lobe;
RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related
RT peptide inhibiting the motility of the mature oviduct in the
RT cuttlefish, Sepia officinalis.";
RL Peptides 18:1469-1474(1997).
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity
CC targeting the distal oviduct. Inhibits the motility of the oviduct
CC by decreasing tonus, frequency and amplitude of contractions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=WALDI; RANGE=1-2; NOTE=Ref.1.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 2 2 Tryptophan amide.
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 2 W 2

RESULT 4
ID BPP7 BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;

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RN SEQUENCE.
RP TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it. It acts
CC as an indirect hypotensive agent.
DR PIR; G37196; G37196.
KW Direct protein sequencing; Hypotensive agent;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 3 W 3

RESULT 5
ID PAP2 PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleioidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN (1)
SQ SEQUENCE.
RP TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels in
CC membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pardaxin family.
KW Direct protein sequencing; Toxin.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GW 3
DB 1 GFF 3

RESULT 6
ID RE32 LITRU STANDARD; PRT; 5 AA.
AC P82073;

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DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Rubellidin 3.2.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria rubella. Comparison with the skin peptides from Litoria  
 RT rubella".  
 RT Aust. J. Chem. 52:639-645(1999).  
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 KW Amphibian defense peptide; Direct protein sequencing.  
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;  
 Query Match 30.3%; Score 10; DB 1; Length 5;  
 Best Local Similarity 33.3%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYW 3  
 DB 2 GFF 4

RESULT 7  
 ACHI\_ACHFU  
 ID ACHI\_ACHFU STANDARD; PRT; 4 AA.  
 AC P35904;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Achatin-I.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
 RC STRAIN=ferussac; TISSUE=ganglion;  
 RX MEDLINE=89273551; PubMed=2597281;  
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,  
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
 RT fulica Ferussac containing a D-amino acid residue".  
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
 RN [2]  
 RP CHARACTERIZATION.  
 RC STRAIN=Perussac; TISSUE=Heart atrium;  
 RX MEDLINE=91264856; PubMed=1675568;  
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 RT Achatina fulica, and its possible function".  
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
 RN [3]  
 RP CRYSTALLIZATION.  
 RX MEDLINE=93014529; PubMed=1399265;  
 RA Ihida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
 RA Iwashita T., Nomoto K.;  
 RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-  
 RT Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid  
 RT residue".  
 RL Int. J. Pept. Protein Res. 39:258-264(1992).

CC -1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency  
 CC and produces a spike broadening of the identified heart excitatory  
 CC neuron (PON); also enhances the amplitude and frequency of the  
 CC heart beat. Has also an effect on several other muscles.  
 DR PIR; A32480; A32480.  
 KW D-amino acid; Direct protein sequencing; Hormone.  
 FT MOD\_RES 2 2 D-phenylalanine.  
 SQ SEQUENCE 4 AA; 408 MW; 6AAD9C810000000 CRC64;  
 Query Match 27.3%; Score 9; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GY 2  
 DB 1 GF 2

RESULT 8  
 OCP1\_OCTMI  
 ID OCP1\_OCTMI STANDARD; PRT; 4 AA.  
 AC P58678;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cardioactive peptides Ocp-1/Ocp-2.  
 OS Octopus minor (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=89766;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RC TISSUE=Brain;  
 RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;  
 RA Iwakoshi E., Hisada M., Minakata H.;  
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 RT Octopus minor".  
 RL Peptides 21:623-630(2000).  
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and  
 CC inotropic effects on the heart. Ocp-2 is a 1000 time less active  
 CC than Ocp-1.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.  
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.  
 KW D-amino acid; Direct protein sequencing; Hormone.  
 FT MOD\_RES 2 2 D-phenylalanine (in form Ocp-1).  
 SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;  
 Query Match 27.3%; Score 9; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GY 2  
 DB 1 GF 2

RESULT 9  
 GRWM\_HUMAN  
 ID GRWM\_HUMAN STANDARD; PRT; 3 AA.  
 AC P01157;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Growth-modulating peptide.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77162369; PubMed=858356;  
 RA Schlesinger D.H., Pickart L., Thaler M.M.;

RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";  
RL Experientia 33:324-325(1977).  
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate  
CC growth of some cell types and to inhibit other types in vitro.  
CC GO: GO:0001558; P:regulation of cell growth; NAS.  
KW Direct protein sequencing.  
SQ SEQUENCE 3 AA; 340 MW; 6331E810000000000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 3;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
|:  
1 GH 2

Db

RESULT 10  
DCML\_PSECH STANDARD; PRT; 4 AA.  
AC P19916;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
DE dehydrogenase subunit L) (CO-DH L) (Fragment).  
GN Name-cuFl;  
OS Pseudomonas carboxydohydrogena.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae.  
ON NCBI\_TaxID=290;  
RN [1]  
RP SEQUENCE

RX MEDLINE=90055678; PubMed=2818128;  
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
RT "Homology and distribution of CO dehydrogenase structural genes in  
RT carboxydohydrophic bacteria.";  
RL Arch. Microbiol. 152:335-341(1989).  
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
CC dioxide.  
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).  
CC -!- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1  
CC molybdopterin cytosine dinucleotide (MCD) per subunit.  
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small  
CC subunit.  
DR PIR; P10140.  
KW Direct protein sequencing; Molybdenum; Oxidoreductase.  
FT NON\_TER 4 4  
SQ SEQUENCE 4 AA; 441 MW; 7761E876F00000000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
|:  
2 GH 3

Db

RESULT 11  
FAR3\_HIRME STANDARD; PRT; 4 AA.  
AC P42562;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE FMRFamide-like neuropeptide YLRP-amide.  
OS Hirudo medicinalis (Medicinal leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.  
ON NCBI\_TaxID=6421;  
RN [1]  
RP SEQUENCE.

RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";  
RL Experientia 33:324-325(1977).  
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate  
CC growth of some cell types and to inhibit other types in vitro.  
CC GO: GO:0001558; P:regulation of cell growth; NAS.  
KW Direct protein sequencing.  
SQ SEQUENCE 3 AA; 340 MW; 6331E810000000000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 3;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
|:  
1 GH 2

Db

RESULT 12  
FAR4\_HIRME STANDARD; PRT; 4 AA.  
AC P42563;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE FMRFamide-like neuropeptide YMRP-amide.  
OS Hirudo medicinalis (Medicinal leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.  
ON NCBI\_TaxID=6421;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of Rfamde neuropeptides in the medicinal leech.";  
RL Peptides 12:897-908(1991).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 4 4 Phenylalanine amide.  
SQ SEQUENCE 4 AA; 598 MW; 69D4073B300000000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2  
|:  
1 Y 1

Db

RESULT 13  
FYRI ANTEL STANDARD; PRT; 4 AA.  
AC P58706;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Antho-Riamide I [Contains: Antho-Riamide II].  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
ON NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-Z;  
RA Nother H.-P., Rinehart K.L. Jr., McFarlane I.D.,  
RA Grimmelikhuijzen C.J.P.;  
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,  
RT biologically active L-3-phenylacetyl-Tyr-Arg-Ile-NH2 and its des-

```

RT phenyllactyl fragment Tyr-Arg-Ile-NH2." ;
RL Peptides 12:1165-1173(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Notherker H.-P., Gimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Ramide and Antho-Ramide." ;
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron specific.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT CHAIN 1 4 Antho-Ramide I.
FT CHAIN 2 4 Antho-Ramide II.
FT MOD_RES 1 1 3-phenyllactic acid.
FT MOD_RES 4 4 Isoleucine amide.
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
DB 2 Y 2

RESULT 14
Q96ATO PRELIMINARY; PRT; 4 AA.
AC Q96ATO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FLJ30656 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fhney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016791; AAI16791.2;
SQ SEQUENCE 4 AA; 512 MW; 633DCB56F0000000 CRC64;

```

```

Query Match 21.2%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
DB 2 Y 2

RESULT 15
AL14_CARMA STANDARD; PRT; 5 AA.
ID AL14_CARMA
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas." ;
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT MOD_RES 5 5 Leucine amide (Potential).
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
DB 1 Y 1

Search completed: April 18, 2005, 15:38:14
Job time : 180 secs

```

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: April 18, 2005, 15:20:24 ; Search time 167 Seconds  
(without alignments)  
11.580 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYVMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 45841

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1980s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	5	3	AAY32257
2	29	87.9	5	2	AAR62882
3	27	81.8	5	2	AAR97316
4	27	81.8	5	2	AAY05038
5	27	81.8	5	4	AAB61293
6	27	81.8	5	5	AAU75739
7	27	81.8	5	5	AAU75739
8	27	81.8	5	6	ABU11259
9	27	81.8	5	7	ADC82794
10	27	81.8	5	8	ADL27482
11	27	81.8	5	8	ADM95105
12	27	81.8	5	8	ADM98314
13	27	81.8	5	8	ADO36523
14	27	81.8	5	8	ADO36535
15	27	81.8	5	8	ADR15171
16	27	81.8	5	8	ADR15143
17	25	75.8	5	2	AAR76079
18	24	72.7	4	5	AAE22200
19	24	72.7	4	8	ADJ38912
20	24	72.7	5	2	AAR85499
21	24	72.7	5	2	AAW23429
22	24	72.7	5	2	AAW93474
23	24	72.7	5	4	AAB62861
24	24	72.7	5	5	ABB07357
25	24	72.7	5	8	ADM10172

26	24	72.7	5	8	ADM10201	Adm10201 Human pro
27	24	72.7	5	8	ADR19265	Adr19265 Glycosyla
28	24	72.7	5	8	ADR71367	Adr71367 Human pro
29	24	72.7	5	8	ADR71338	Adr71338 Human pro
30	23	69.7	5	2	AAR74931	Aar74931 H-CDR-1 o
31	23	69.7	5	2	AAR74929	Aar74929 H-CDR-1 o
32	23	69.7	5	2	AAW24546	Aaw24546 CDR #1 of
33	23	69.7	5	2	AAW83034	Aaw83034 Anti-Fas
34	23	69.7	5	2	AAW62192	Aaw62192 Mouse ant
35	23	69.7	5	2	AAW57588	Aaw57588 Chimeric
36	23	69.7	5	2	AAW44181	Aaw44181 Monoclonal
37	23	69.7	5	2	AAW02550	Aaw02550 Artificia
38	23	69.7	5	2	AAW89632	Aaw89632 Mouse hum
39	23	69.7	5	2	AAW05045	Aaw05045 Tumour an
40	23	69.7	5	3	AAW14741	Aab14741 Mouse ant
41	23	69.7	5	3	AAW90891	Aaw90891 Murine an
42	23	69.7	5	3	AAV77518	Aay77518 Antibody
43	23	69.7	5	3	AAW80139	Aay80139 Chimeric
44	23	69.7	5	3	AAW12174	Aab12174 Human CDR
45	23	69.7	5	3	AAW92158	Aay92158 Murine 15

## ALIGNMENTS.

### RESULT 1

AAV32257

ID AAY32257 standard; peptide; 5 AA.

XX

AC AAY32257;

XX

DT 15-FEB-2000 (first entry)

XX

DE Light chain CDR H1 of mouse anti-CD23 Mab C11.

XX

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;

KW monoclonal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; rhinitis; eczema; insulinitis;

KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX therapy.

XX

OS Mus musculus.

XX

PN WO9558679-A1.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-GB001434.

XX

PR 09-MAY-1998; 98GB-00009839.

XX

PA (GLAX ) GLAXO GROUP LTD.

XX

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX

DR WPI; 2000-053101/04.

XX

DR N-PSDB; AA234742.

XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,

XX diabetes, multiple sclerosis and psoriasis.

XX

PS Claim 1; Page 40; 81pp; English.

XX

CC This sequence represents complementarity determining region 1 (CDR H1)

CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11

CC (see also AAY32263). The invention provides altered antibodies, such as

CC chimeric or humanised antibodies, which comprise sufficient of the amino

CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC Sjogren's syndrome, allergic colitis, Crohn's disease,  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents  
 XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 33; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
 |||||  
 DB 1 GYWMS 5

## RESULT 2

AAR62882  
 ID AAR62882 standard; peptide; 5 AA.

XX AAR62882;

XX 25-MAR-2003 (revised)

DT 18-JUL-1995 (first entry)

XX Murine anti-human atherosclerotic plaque Mab Z2D3 VH CDR1.

DE Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;  
 KW murine monoclonal antibody; heavy chain variable region: CDR1;  
 KW complementarity determining region; imaging; plaque ablation.  
 XX

OS Mus musculus.

XX Key Location/Qualifiers  
 FH Region 1..5  
 FT /label= CDR1  
 FT

XX WO9425053-A1.

PN 10-NOV-1994.

XX 26-APR-1994; 94WO-US004641.

XX 26-APR-1993; 93US-00053451.

XX (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.

XX Ditlow CC, Chen FW, Calenoff B;

XX WPI; 1994-357904/44.

DR N-PSDB; AAQ78734.

XX New antigen comprising hydroxy:steroid and quat. ammonium salt - and  
 PT related antibodies, useful e.g. for imaging, ablating or treating  
 PT atherosclerotic plaque, and detecting plaque specific antibodies.  
 XX

PS Claim 199; Page 147; 288pp; English.

XX Mice were immunised with an extract of human atherosclerotic plaque, then  
 CC spleen cells were fused with SP2/01-Ag-14 myeloma cells. Hybridomas were  
 CC screened by ELISA for reactivity with the immunogen and clone Z2D3 was  
 CC isolated. The Z2D3 antibody reacts specifically with atherosclerotic  
 CC tissue; it recognises a non-protein antigen containing cholesterol (or  
 CC similar steroid that is a substrate for cholesterol oxidase) and a  
 CC quaternary ammonium salt (pref. a phosphatidylcholine or related compound

CC that is a substrate for phospholipase C). The CDR sequences for the heavy  
 CC and light chains of Z2D3 were determined; peptides comprising the CDRs  
 CC are claimed, including chimeric (CDR-grafted) murine-human antibodies.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 5 AA;

Query Match 87.9%; Score 29; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
 |||||  
 DB 1 GFWMS 5

## RESULT 3

AAR97316  
 ID AAR97316 standard; peptide; 5 AA.

XX AAR97316;

XX 15-OCT-1996 (first entry)

XX Humanised monoclonal antibody heavy chain CDR.

XX Monoclonal antibody; humanised; mouse; framework region; FR; CDR;  
 KW complementary determining region; anti-carcinoembryonic antigen; CEA;  
 KW diagnosis; imaging; therapy; immune response.  
 XX

OS Mus musculus.

XX WO9611013-A1.

XX 18-APR-1996.

XX 28-SEP-1995; 95WO-US011964.

XX 05-OCT-1994; 94US-00318157.

XX (IMMU-) IMMUNOMEDICS INC.

XX Hansen HJ, Armour KL;

XX WPI; 1996-209653/21.

XX New humanised anti-CEA monoclonal antibody - having engrafted murine  
 CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.

XX Claim 5; Page 38; 62pp; English.

XX New humanised monoclonal antibodies (Mabs) comprising the complementary  
 CC determining regions (CDRs) of a parental murine class III anti-  
 CC carcinoembryonic (CEA) Mab engrafted to the framework regions (FRs) of a  
 CC heterologous antibody which can be derived from any species including  
 CC human, retain the anti-CEA binding specificity of the parental murine Mab  
 CC but are less immunogenic in a human subject than the parental Mab. The  
 CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA  
 CC -producing cancers and patients receiving the humanised antibodies and  
 CC conjugates show improved therapeutic results, decreased immune responses  
 CC and decreased immune-mediated adverse effects compared to the parent  
 CC antibody. This sequence is a murine derived CDR region which corresponds  
 CC to CDR 1 in the heavy chain of the humanised Mab. See AAR97313-97333  
 XX

SQ Sequence 5 AA;

Query Match 81.8%; Score 27; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
 |||||  
 DB 2 YWMS 5

```

XX
KW Human; antibody; scFv; CDR; complementarity determining region;
KW TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder; stroke;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; liver
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX
XX WO200100810-A1.
XX
XX 04-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-US018152.
XX
XX 30-JUN-1999; 99US-00345468.
XX 06-DEC-1999; 99US-00454824.
XX 14-FEB-2000; 2000US-00503387.
XX
XX (WILL-) MILLENNIUM PHARM INC.
XX
XX Busfield SJ, Vilhelal J, Jandrot-Perrus M, Vainchencker W;
XX Gill DS, Qian MD, Kingsbury G;
XX WPI; 2001-080877/09.
XX
XX New genes encoding human platelet-expressed collagen receptor,
XX glycoprotein VI, and its modulators, useful for preventing, treating and
XX diagnosing hemorrhagic disorders, thrombotic diseases and immunological
XX disorders.
XX
XX Claim 31; Page 102; 227pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor
XX glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
XX and polypeptides and their modulators, e.g. antisense nucleic acids,
XX ribozymes and antibodies, are useful for preventing, treating and
XX diagnosing disorders associated with aberrant expression or activity of
XX GPVI. These disorders include bleeding disorders (e.g.
XX thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.
XX thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
XX coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
XX cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
XX immunological diseases (e.g. platelet disorder) and embryonic liver
XX disorders. Preferably they are used to prevent acute cardiac ischaemia
XX following angioplasty and metastatic cancers, especially of the colon and
XX liver
XX
XX Sequence 5 AA;
SQ
Query Match 81.8%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
DB 2 YWMS 5

RESULT 6
AAU75739
ID AAU75739 standard; peptide; 5 AA.
XX
XX AAU75739;
XX
XX 08-MAY-2002 (first entry)
XX
XX Anti-(MCP)-1 antibody heavy chain protein hypervariable region CDRL1.
XX Human; antibody; MCP; monocyte chemoattractant; antiasthmatic;
KW

```

KW anti-allergic; anti-inflammatory; idiopathic thrombocytopenia;  
 KW immunosuppressive; cytostatic; vasotropic; antiarteriosclerotic;  
 KW antirheumatic; antiarthritic; osteopathic; antigen-binding site;  
 KW immunoglobulin heavy chain; monocyte migration; T cell migration;  
 KW CC-type chemokine; eotaxin; allergy; allergic rhinitis; cancer;  
 KW hypersensitivity response; allergic contact dermatitis;  
 KW inflammatory disease; asthma; psoriasis; COPD; osteoporosis;  
 KW inflammatory bowel disease; multiple sclerosis; autoimmune disease;  
 KW rheumatoid arthritis; diabetes; systemic lupus erythematosus;  
 KW bone disease; osteoporosis; osteoarthritis; periodontal disease;  
 KW haematological disorder; haemolytic anaemia; graft rejection;  
 KW leucocyte infiltration; restenosis; arteriosclerosis; CDRI.  
 XX  
 OS Homo sapiens.  
 XX WO200202640-A2.  
 XX PD  
 XX PN  
 XX PF 10-JAN-2002.  
 XX PD  
 XX PF 29-JUN-2001; 2001WO-EP007468.  
 XX PF  
 XX PR 30-JUN-2000; 2000GB-00016138.  
 XX PR  
 XX (NOVS ) NOVARTIS AG.  
 XX PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX PA  
 XX PI Hiestand P, Hofstetter H, Payne TG, Urfer R, Di Padova FE;  
 XX PI  
 XX WPI; 2002-164525/21.  
 XX DR  
 XX XX  
 XX XX  
 XX PT New compound that binds human monocyte chemoattractant protein-1, useful  
 XX PT e.g. for treating inflammation, comprises immunoglobulin chains with  
 XX PT specific hypervariable regions.  
 XX PT  
 XX PS Claim 1; Page 35; 42pp; English.  
 XX PS  
 XX CC This invention relates to a molecule that binds MCP-1 (human monocyte  
 XX CC chemoattractant protein-1). The molecule has at least one antigen -  
 XX CC binding site comprising at least one immunoglobulin (Ig) heavy and/or  
 XX CC light chain variable domain (Vh, Vl). The antibody of the invention  
 XX CC inhibits binding of MCP-1 (and also eotaxin) to specific receptors, so  
 XX CC preventing migration of monocytes and T cells. These are human antibodies  
 XX CC with very high affinity for MCP-1, but no significant reaction with other  
 XX CC human CC-type chemokines or MCP-1 from other species. The MCP-1 binding  
 XX CC molecules, specifically antibodies that cross-react with eotaxin, are  
 XX CC used to prevent or treat MCP-1 or eotaxin-mediated disorders,  
 XX CC particularly those that involve migration or activation of monocytes and  
 XX CC T cells, e.g. allergies (allergic rhinitis, hypersensitivity responses,  
 XX CC allergic contact dermatitis), inflammatory diseases (asthma, psoriasis,  
 XX CC COPD, inflammatory bowel disease, multiple sclerosis) autoimmune diseases  
 XX CC (rheumatoid arthritis; diabetes, systemic lupus erythematosus), diseases  
 XX CC of bone and cartilage (osteoporosis, osteoarthritis, periodontal disease)  
 XX CC haematological disorders (haemolytic anaemia, idiopathic  
 XX CC thrombocytopenia) graft rejection, cancers that include leucocyte  
 XX CC infiltration, (re)stenosis, arteriosclerosis, osteoporosis and many other  
 XX CC diseases listed in the specification. The present sequence represents the  
 XX CC human anti-(MCP) antibody heavy chain sequence hypervariable domain  
 XX CC peptide CDRI of the invention  
 XX CC  
 XX SQ Sequence 5 AA;  
 Query Match 81.8%; Score 27; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YWMS 5  
 Db ||||  
 2 YWMS 5  
 RESULT 7  
 AAO17609  
 ID AAO17609 standard; peptide; 5 AA.

XX AAO17609;  
 XX AC  
 XX DT 08-AUG-2002 (first entry)  
 XX DE Human FAPalpha specific VL region from VH50 CDRI peptide.  
 XX KW Human; FAPalpha; fibroblast activating protein alpha; antibody; Ab;  
 KW gene therapy; cancer; wound healing; inflammation; cytostatic.  
 XX OS Homo sapiens.  
 XX PN WO200168708-A2.  
 XX PD 20-SEP-2001.  
 XX PF 16-MAR-2001; 2001WO-EP004716.  
 XX PF 17-MAR-2000; 2000DE-01013286.  
 XX PR 11-SEP-2000; 2000GB-00022216.  
 XX XX (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.  
 XX XX Park J, Garin-Chesa P, Pfizenmaier K, Moosmayer D, Mersmann M;  
 PI Schmidt A;  
 DR WPI; 2002-041180/05.  
 DR N-PSDB; AAL46554.  
 XX PT New human humanized antibody that specifically binds to fibroblasts  
 XX PT activating protein alpha, useful for treating cancer or tumor, and for  
 XX PT imaging tumors associated with activated stromal fibroblasts, e.g. lung  
 XX PT or breast cancer.  
 XX PS Disclosure; Fig 6C; 109pp; English.  
 XX CC The present invention relates to a human or humanised antibody (Ab) which  
 XX CC specifically binds to fibroblast activating protein alpha (FAPalpha). The  
 XX CC antibodies are useful for preparing a composition for the treatment of  
 XX CC cancer, and for imaging tumours associated with activated stromal  
 XX CC fibroblasts, such as colorectal cancer, non-small-cell lung cancer,  
 XX CC breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder  
 XX CC cancer, pancreatic cancer and metastatic brain cancer, and diseases  
 XX CC associated with the same, such as inflammation and wound healing. The  
 XX CC present sequence is a peptide described in the exemplification of the  
 XX CC invention  
 XX CC  
 XX SQ Sequence 5 AA;  
 Query Match 81.8%; Score 27; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YWMS 5  
 Db ||||  
 2 YWMS 5  
 RESULT 8  
 ABU11259  
 ID ABU11259 standard; peptide; 5 AA.  
 XX AC  
 XX AC ABU11259;  
 XX DT 06-FEB-2003 (first entry)  
 XX XX Human TANGO 268 VHCDRI Peptide #3.  
 XX XX Human; mouse; variable heavy; VH; antigen; cancer;  
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;  
 KW TANGO 268; extracellular matrix; collagen; platelet release;  
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;  
 KW degranulation; thrombocytopenia; antibody; thrombotic disorder;  
 KW

KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;  
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;  
 KW cardiovascular disease; angina pectoris; myocardial infarction;  
 KW coronary restenosis; atherosclerosis; immunological disorder;  
 KW developmental disorder; embryonic disorder; liver disorder;  
 KW cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

XX WO200280968-A1.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Valleval J, Jandrot-Perrus M, Vainchencker W;  
 PI Gill DS, Qian DM, Kingsbury G;

XX WPI; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to TANGO  
 PT 268 antigen, useful for treating bleeding disorders such as  
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.  
 XX Disclosure; Page 111; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable  
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;  
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically  
 CC binding to a TANGO 268 (also referred as glycoprotein VI (gpVI)) antigen.  
 CC The antibodies of the invention act to decrease or block TANGO 268  
 CC binding to extracellular matrix components, or as a collagen or platelet  
 CC release and aggregation blocker. The antibodies of the invention are  
 CC useful for modulating proliferation, migration, morphology,  
 CC differentiation and/or function of megakaryocytes and platelets,  
 CC including during development e.g. embryogenesis, modulating leukocyte-  
 CC platelet and platelet-endothelium interactions in inflammation and/or  
 CC thrombosis, and modulating platelet aggregation and degranulation. They  
 CC are also useful for modulating disorders associated with abnormal or  
 CC aberrant megakaryocyte and/or platelet proliferation, migration,  
 CC morphology, differentiation and/or function, e.g. bleeding disorders such  
 CC as thrombocytopenia. Other diseases which may be modulated by these  
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.  
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases  
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);  
 CC coronary diseases (e.g. cardiovascular diseases including angina  
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,  
 CC etc); immunological disorders, developmental disorders, embryonic  
 CC disorders, liver disorders, cerebral vascular diseases, venous  
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The  
 CC antibodies of the invention only causes a transient decrease in platelet  
 CC counts, platelet aggregation, and/or platelet activation and so have some  
 CC advantages over prior art methods. The present sequence represents a  
 CC peptide sequence used to generate the antibodies of the invention

XX Sequence 5 AA;

Query Match 81.8%; Score 27; DB 6; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YNWS 5

Db |||||

2 YNWS 5

RESULT 9

ID ADC82794

ADC82794 standard; peptide; 5 AA.

XX

AC

XX

DT

XX

DE

XX

KW

KW

KW

KW

XX

OS

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PN

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PR

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PR

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PA

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PI

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DR

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XX

ADC82794;

01-JAN-2004 (first entry)

CDR region #3 in heavy chain of human Fab fragment.

Binding molecule; selective affinity; ligand;

anti-immunoglobulin reagent; phage expressed antibody library;

tumour antigen; complementarity determining region; CDR; human disease;

cellular pathology; human; Fab; heavy chain.

Homo sapiens.

US2003044772-A1.

06-MAR-2003.

15-OCT-2001; 2001US-00977797.

04-AUG-1997; 97US-0113667P.

04-AUG-1998; 98US-00129026.

(MOLE-) APPLIED MOLECULAR EVOLUTION.

Watkins JD, Huse WD, Wu H;

WPI; 2003-625402/59.

N-PSDB; ADC82793.

Identifying binding molecules having selective affinity for ligands for  
 discovering reagents for treating diseases, by contacting solid support  
 coated with anti-immunoglobulin reagent, to a phage expressed antibody  
 library.

Example 5; Page 16; 26pp; English.

The present invention relates to a method for identifying a binding  
 molecule having selective affinity for a ligand. The method involves  
 providing a solid support coated with an anti-immunoglobulin reagent, and  
 a phage expressed antibody library, and contacting the solid support to  
 the phage expressed antibody library. The invention also discloses a  
 method for identifying an antibody having selective affinity for a  
 tumour, and a complementarity determining region (CDR) of an antibody  
 selective for a tumour antigen. The methods of the invention are useful  
 for identifying a binding molecule having selective affinity for a  
 ligand, for the discovery of specific reagents for diagnosis and  
 treatment of human diseases, for identifying binding molecules to, for  
 example tumour cells or other cellular pathologies for the selective  
 targeting of therapeutic agents, or for the identification of binding  
 molecules to normal or diseased tissues for the selective targeting of,  
 for example diagnostic agents such as imaging reagents. The methods are  
 rapid and efficient for the identification of binding molecules which  
 exhibit selective affinity for one or more ligands of interest. The  
 methods allow the simultaneous screening of multiple binding molecules  
 against multiple ligands of interest. Moreover, very little information  
 is required regarding the identity or function of either the binding  
 molecule or the ligand. For example diverse populations of binding  
 molecules can be simultaneously screened against diverse populations of  
 ligands to rapidly identify numerous molecules exhibiting a desired  
 binding specificity. The methods provide improved sensitivity and  
 specificity of detection through the selective immobilisation of the  
 binding molecule population on a solid support. The present sequence  
 represents a CDR region in the heavy chain of human Fab fragment.

Sequence 5 AA;

Query Match 81.8%; Score 27; DB 7; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YNWS 5

|||||

Db 2 YWMS 5

RESULT 10  
ADL27482  
ID ADL27482 standard; peptide; 5 AA.  
XX  
AC ADL27482;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE CDR from the heavy chain of antibody EGP16D8-1-2.  
XX  
KW glycoprotein; EGP6D8-1-1; EGP13F6-1-2; EGP13C6-1-1;  
KW Ebola virus infection; antibody; heavy chain;  
KW Complementarity determining region; CDR.  
XX  
OS Mus sp.  
XX  
PN WO2004018649-A2.  
XX  
PD 04-MAR-2004.  
XX  
PF 21-AUG-2003; 2003WO-US027450.  
XX  
PR 23-AUG-2002; 2002US-00226795.  
XX  
PA (USSA ) US ARMY MEDICAL RES INST INFECTIOUS DISE.  
XX  
PI Hart MK, Wilson JA;  
XX  
DR WPI; 2004-226835/21.  
XX  
PT New isolated monoclonal antibody that binds Ebola virus GP, which  
PT monoclonal antibody comprises a heavy chain variable region, useful for  
PT treating or ameliorating Ebola virus infection.  
XX  
PS Claim 31; Page 64; 68pp; English.  
XX  
CC The specification describes monoclonal antibodies that bind Ebola virus  
CC glycoprotein. The antibodies are EGP6D8-1-1, EGP13F6-1-2, and EGP13C6-1-  
CC 1. The monoclonal antibodies of the invention are useful for treating or  
CC ameliorating an Ebola virus infection. The antibodies were found to be  
CC effective when administered 2 days after challenge. After significant  
CC viral replication had occurred. ADL27482-ADL27484 represents  
CC complementarity determining regions (CDRs) from the heavy chain of a  
CC monoclonal antibody of the invention.  
XX  
SQ Sequence 5 AA;  
Query Match 81.8%; Score 27; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YWMS 5  
Db 2 YWMS 5  
RESULT 11  
ADM95105  
ID ADM95105 standard; peptide; 5 AA.  
XX  
AC ADM95105;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Murine MN-14 Mab heavy chain variable region CDR1.  
XX  
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;  
KW complementarity determining region; pancreatic cancer; breast cancer;  
KW ovarian cancer.  
XX

OS Mus sp.  
XX  
PN WO2004032962-A1.  
XX  
PD 22-APR-2004.  
XX  
PF 11-OCT-2002; 2002WO-US032307.  
XX  
PR 08-OCT-2002; 2002US-0416531P.  
XX  
PA (IMMU-) IMMUNOMEDICS INC.  
XX  
PI Goldenberg DM, Hansen HJ;  
XX  
DR WPI; 2004-364813/34.  
XX  
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma  
PT comprises administering, either concurrently or sequentially, Class III  
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and  
PT therapeutic agent(s).  
XX  
PS Claim 6; SEQ ID NO 23; 88pp; English.  
XX  
CC The invention relates to a method of treating a non-medullary thyroid  
CC carcinoma or treating medullary thyroid carcinoma involves administering  
CC to a subject, either concurrently or sequentially, a Class III anti-CEA  
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at  
CC least one therapeutic agent. The antibody or its fragment comprises the  
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal  
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-  
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,  
CC ovarian cancer, in a subject. This sequence corresponds to the CDR1 of  
CC the murine MN-14 antibody heavy chain variable region and used to  
CC generate the humanised/chimeric antibody of the invention.  
XX  
SQ Sequence 5 AA;  
Query Match 81.8%; Score 27; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YWMS 5  
Db 2 YWMS 5  
RESULT 12  
ADM98314  
ID ADM98314 standard; peptide; 5 AA.  
XX  
AC ADM98314;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Humanised murine MN-14 antibody heavy chain variable region CDR1 peptide.  
XX  
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; humanised;  
KW murine; mouse; antibody; MN-14; non-medullary thyroid carcinoma;  
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;  
KW hepatocellular carcinoma; breast cancer; lung cancer;  
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;  
KW apoptosis.  
XX  
OS Mus sp.  
XX  
PN Synthetic.  
XX  
PD WO2004032857-A2.  
XX  
PR 22-APR-2004.  
XX  
PF 08-OCT-2003; 2003WO-US031801.  
XX  
PR 08-OCT-2002; 2002US-0416531P.



XX (MEDA-) MEDAREX INC.  
 PA (CELL-) CELYTECH R & D.  
 XX Huang H, Holmes S, Mason S;  
 XX WPI; 2004-411694/38.  
 DR  
 XX  
 XX New human monoclonal antibody to heparanase, for use in treating or  
 PT preventing cancer, autoimmune disease, arthritis, asthma, lupus  
 PT erythematous, allograft rejection, atherosclerosis, and Alzheimer's  
 PT disease.  
 XX  
 XX Claim 14; SEQ ID NO 49; 108pp; English.  
 PS  
 XX The present invention describes an isolated human monoclonal antibody  
 CC which binds to and inhibits activity of human heparanase. Human anti-  
 CC heparanase antibodies of the present invention have cytostatic,  
 CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,  
 CC dermatological, antiarteriosclerotic, neuroprotective and neurotropic  
 CC activities, and can be used as heparanase antagonists. The antibody,  
 CC methods and compositions of the present invention are useful in treating  
 CC or preventing cancer or tumors, e.g. melanoma, lymphoma, prostate  
 CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,  
 CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a  
 CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus  
 CC erythematous, allograft rejection, vascular stenosis, atherosclerosis,  
 CC and Alzheimer's disease. The present sequence represents a human anti-  
 CC heparanase CDR amino acid sequence, which is used in the exemplification  
 CC of the present invention.  
 XX  
 XX Sequence 5 AA;  
 SQ

Query Match 81.8%; Score 27; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
 ||||  
 Db 2 YWMS 5

## RESULT 15

ADR15171  
 ID ADR15171 standard; peptide; 5 AA.  
 XX  
 AC ADR15171;  
 XX  
 XX 21-OCT-2004 (first entry)  
 XX  
 XX Anti-protein C inhibitor antibody heavy chain CDR1 peptide #2.  
 DE  
 XX anti-protein C inhibitor antibody; anti-PCI antibody;  
 KW activated protein C; aPC; sepsis; disseminated intravascular coagulation;  
 KW arterial thrombosis; protein C inhibitor; heavy chain; CDRI.  
 XX  
 OS Unidentified.  
 XX  
 XX WO2004065418-A1.  
 FN  
 XX  
 XX 05-AUG-2004.  
 XX  
 XX 20-JAN-2004; 2004WO-JP000429.  
 PF  
 XX  
 XX 20-JAN-2003; 2003JP-00011529.  
 PR  
 XX  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA  
 XX Koga T, Kimura N, Yoshino T, Ono K;  
 XX WPI; 2004-593430/57.  
 DR  
 XX New anti-protein C inhibitor (PCI) antibody, inhibiting PCI with respect

PT to activation protein C (apc) activity, and apc production by  
 PT thrombin/thrombomodulin composite, useful for treating sepsis, arterial  
 PT thrombosis.  
 XX  
 XX Claim 4; SEQ ID NO 52; 105pp; Japanese.  
 PS  
 XX The invention comprises anti-protein C inhibitor (PCI) antibody. The anti-  
 CC -PCI antibody of the invention is useful for treating or preventing a  
 CC disease which develops and/or progresses due to reduced activated protein  
 CC C (apc) activity. Such diseases include: sepsis, disseminated  
 CC intravascular coagulation, and arterial thrombosis. The present amino  
 CC acid sequence represents an anti-protein C inhibitor antibody peptide of  
 CC the invention.  
 XX  
 XX Sequence 5 AA;  
 SQ

Query Match 81.8%; Score 27; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
 ||||  
 Db 2 YWMS 5

Search completed: April 18, 2005, 15:35:15  
 Job time : 179 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:38:19 ; Search time 130 Seconds  
(without alignments)  
12.783 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370693 residues

Total number of hits satisfying chosen parameters: 22949

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	5	17 US-10-783-311-283	Sequence 283, App
2	33	100.0	5	17 US-10-783-311-315	Sequence 315, App
3	27	81.8	5	9 US-09-832-312-61	Sequence 61, Appl
4	27	81.8	5	9 US-09-253-794-23	Sequence 23, Appl
5	27	81.8	5	10 US-09-977-797A-76	Sequence 76, Appl
6	27	81.8	5	11 US-09-829-495-61	Sequence 61, Appl
7	27	81.8	5	15 US-10-226-795-23	Sequence 23, Appl
8	27	81.8	5	16 US-10-703-714-37	Sequence 37, Appl
9	27	81.8	5	16 US-10-703-714-49	Sequence 49, Appl
10	27	81.8	5	16 US-10-680-734-23	Sequence 23, Appl
11	27	81.8	5	17 US-10-842-011-15	Sequence 15, Appl
12	27	81.8	5	17 US-10-842-011-30	Sequence 30, Appl
13	24	72.7	4	10 US-09-948-004-32	Sequence 32, Appl

14	24	72.7	5	9 US-09-192-854-151	Sequence 151, App
15	24	72.7	5	9 US-09-968-561A-265	Sequence 265, App
16	24	72.7	5	10 US-09-155-106-1	Sequence 1, Appl
17	24	72.7	5	10 US-09-968-744A-265	Sequence 265, App
18	24	72.7	5	11 US-09-968-561A-265	Sequence 265, App
19	24	72.7	5	15 US-10-436-549-496	Sequence 496, App
20	24	72.7	5	15 US-10-436-549-525	Sequence 525, App
21	24	72.7	5	16 US-10-297-371A-4	Sequence 4, Appl
22	24	72.7	5	16 US-10-745-102-2	Sequence 2, Appl
23	24	72.7	5	16 US-10-712-425-496	Sequence 496, App
24	24	72.7	5	16 US-10-712-425-525	Sequence 525, App
25	24	72.7	5	17 US-10-783-311-91	Sequence 91, Appl
26	24	72.7	5	17 US-10-842-011-9	Sequence 9, Appl
27	24	72.7	5	17 US-10-879-994-70	Sequence 70, Appl
28	24	72.7	5	17 US-10-808-538-1	Sequence 1, Appl
29	24	72.7	5	17 US-10-773-032-496	Sequence 496, App
30	24	72.7	5	17 US-10-773-032-525	Sequence 525, App
31	24	72.7	5	17 US-10-903-858-19	Sequence 19, Appl
32	23	69.7	5	9 US-09-748-960-12	Sequence 12, Appl
33	23	69.7	5	9 US-09-832-312-49	Sequence 49, Appl
34	23	69.7	5	9 US-09-770-002-1	Sequence 1, Appl
35	23	69.7	5	9 US-09-423-800-62	Sequence 62, Appl
36	23	69.7	5	10 US-09-977-797A-90	Sequence 90, Appl
37	23	69.7	5	10 US-09-269-921-6	Sequence 6, Appl
38	23	69.7	5	10 US-09-509-098-8	Sequence 8, Appl
39	23	69.7	5	11 US-09-829-495-49	Sequence 49, Appl
40	23	69.7	5	14 US-10-182-018-62	Sequence 62, Appl
41	23	69.7	5	14 US-10-216-484-2	Sequence 2, Appl
42	23	69.7	5	14 US-10-169-003-62	Sequence 62, Appl
43	23	69.7	5	14 US-10-218-253-6	Sequence 6, Appl
44	23	69.7	5	14 US-10-337-981-62	Sequence 62, Appl
45	23	69.7	5	14 US-10-384-933-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-10-783-311-283  
; Sequence 283, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; PRIOR FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 283  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-283

Query Match 100.0%; Score 33; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5  
|||  
Db 1 GYWS 5

RESULT 2  
US-10-783-311-315  
; Sequence 315, Application US/10783311  
; Publication No. US20050009136A1

GENERAL INFORMATION:  
APPLICANT: Nixon, Andrew  
TITLE OF INVENTION: PAPP-A LIGANDS  
FILE REFERENCE: 10280-059001  
CURRENT APPLICATION NUMBER: US/10/783,311  
CURRENT FILING DATE: 2004-02-19  
PRIOR APPLICATION NUMBER: US 60/448,515  
PRIOR FILING DATE: 2003-02-19  
NUMBER OF SEQ ID NOS: 394  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 315  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-315

Query Match 100.0%; Score 33; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
|||||  
Db 1 GYWMS 5

RESULT 3  
US-09-832-312-61  
Sequence 61, Application US/09832312  
Patent No. US20010049829A1  
GENERAL INFORMATION:  
APPLICANT: Busfield et al.  
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF  
FILE REFERENCE: 7853-234  
CURRENT APPLICATION NUMBER: US/09/832,312  
CURRENT FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 09/610,118  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 09/503,387  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: 09/454,824  
PRIOR FILING DATE: 1999-12-06  
PRIOR APPLICATION NUMBER: 09/345,468  
PRIOR FILING DATE: 1999-06-30  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 61  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-832-312-61

Query Match 81.8%; Score 27; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||||  
Db 2 YWMS 5

RESULT 4  
US-09-253-794-23  
Sequence 23, Application US/09253794  
Patent No. US20020018750A1  
GENERAL INFORMATION:  
APPLICANT: HANSEN, Hans J.  
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CBA HUMANIZED  
MOUSE MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/253,794  
FILING DATE: 22-Feb-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,157  
FILING DATE: 05-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/464  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-253-794-23

Query Match 81.8%; Score 27; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||||  
Db 2 YWMS 5

RESULT 5  
US-09-977-797A-76  
Sequence 76, Application US/09977797A  
Publication No. US2003004772A1  
GENERAL INFORMATION:  
APPLICANT: Watkins, Jeffrey D.  
APPLICANT: Huse, William D.  
APPLICANT: Wu, Herren  
TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules  
FILE REFERENCE: AME-06805  
CURRENT APPLICATION NUMBER: US/09/977,797A  
CURRENT FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: 09/129,026  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 08/905,825  
PRIOR FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 136  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 76  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-977-797A-76

Query Match 81.8%; Score 27; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||  
Db 2 YWMS 5

## RESULT 6

US-09-829-495-61  
; Sequence 61, Application US/09829495  
; Publication No. US2004001826A1  
; GENERAL INFORMATION:  
; APPLICANT: Busfield SJ  
; APPLICANT: Villevall J  
; APPLICANT: Jandrot-Perrus M  
; APPLICANT: Vainchenker W  
; APPLICANT: Gill DS  
; APPLICANT: Qian MD  
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF  
; FILE REFERENCE: 7853-234  
; CURRENT APPLICATION NUMBER: US/09/829,495  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/610,118  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/503,387  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 09/454,824  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 09/345,468  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 61  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-829-495-61

Query Match 81.8%; Score 27; DB 11; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||  
Db 2 YWMS 5

## RESULT 7

US-10-226-795-23  
; Sequence 23, Application US/10226795  
; Publication No. US20040053865A1  
; GENERAL INFORMATION:  
; APPLICANT: HART, MARY KATE  
; APPLICANT: WILSON, JULIE  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING  
; FILE REFERENCE: ARMY 166  
; CURRENT APPLICATION NUMBER: US/10/226,795  
; CURRENT FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy  
; OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence  
US-10-226-795-23

Query Match 81.8%; Score 27; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||  
Db 2 YWMS 5

## RESULT 8

US-10-703-714-37  
; Sequence 37, Application US/10703714  
; Publication No. US20040170630A1  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Haichun  
; APPLICANT: Holmes, Steven  
; APPLICANT: Mason, Sean  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE  
; FILE REFERENCE: MXI-294  
; CURRENT APPLICATION NUMBER: US/10/703,714  
; CURRENT FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: 60/424803  
; PRIOR FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-703-714-37

Query Match 81.8%; Score 27; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||  
Db 2 YWMS 5

## RESULT 9

US-10-703-714-49  
; Sequence 49, Application US/10703714  
; Publication No. US20040170630A1  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Haichun  
; APPLICANT: Holmes, Steven  
; APPLICANT: Mason, Sean  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE  
; FILE REFERENCE: MXI-294  
; CURRENT APPLICATION NUMBER: US/10/703,714  
; CURRENT FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: 60/424803  
; PRIOR FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-703-714-49

Query Match 81.8%; Score 27; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||  
Db 2 YWMS 5

## RESULT 10

US-10-680-734-23  
; Sequence 23, Application US/10680734  
; Publication No. US20040191248A1  
; GENERAL INFORMATION:  
; APPLICANT: GOLDENBERG, DAVID M.

; APPLICANT: HANSEN, HANS J.  
; TITLE OF INVENTION: ANTIBODY THERAPY  
; FILE REFERENCE: 40923-0051US5  
; CURRENT APPLICATION NUMBER: US/10/680,734  
; CURRENT FILING DATE: 2003-10-08  
; PRIOR APPLICATION NUMBER: 60/467,161  
; PRIOR FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: PCT/US02/32307  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/416,531  
; PRIOR FILING DATE: 2002-10-08  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 23  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-680-734-23

Query Match 81.8%; Score 27; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||  
Db 2 YWMS 5

RESULT 11  
US-10-842-011-15  
; Sequence 15, Application US/10842011  
; Publication No. US20050025763A1  
; GENERAL INFORMATION:  
; APPLICANT: Protein Design Labs  
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES  
; FILE REFERENCE: 05882.0110.NPUS04  
; CURRENT APPLICATION NUMBER: US/10/842,011  
; CURRENT FILING DATE: 2004-05-07  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-842-011-15

Query Match 81.8%; Score 27; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||  
Db 2 YWMS 5

RESULT 12  
US-10-842-011-30  
; Sequence 30, Application US/10842011  
; Publication No. US20050025763A1  
; GENERAL INFORMATION:  
; APPLICANT: Protein Design Labs  
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES  
; FILE REFERENCE: 05882.0110.NPUS04  
; CURRENT APPLICATION NUMBER: US/10/842,011  
; CURRENT FILING DATE: 2004-05-07  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 30  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-842-011-30

Query Match 81.8%; Score 27; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||  
Db 2 YWMS 5

RESULT 13  
US-09-948-004-32  
; Sequence 32, Application US/09948004  
; Publication No. US20030017979A1  
; GENERAL INFORMATION:  
; APPLICANT: MACK, Matthias  
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in  
; FILE REFERENCE: E 2411 EP  
; CURRENT APPLICATION NUMBER: US/09/948,004  
; CURRENT FILING DATE: 2001-09-05  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
US-09-948-004-32

Query Match 72.7%; Score 24; DB 10; Length 4;  
Best Local Similarity 75.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
|||  
Db 1 YWMS 4

RESULT 14  
US-09-192-854-151  
; Sequence 151, Application US/09192854  
; Patent No. US20020068276A1  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Greg  
; APPLICANT: Tomlinson, Ian  
; TITLE OF INVENTION: Methods for Selecting Functional Peptides  
; FILE REFERENCE: 3789/72916  
; CURRENT APPLICATION NUMBER: US/09/192,854  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/066,729  
; EARLIER FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 151  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-192-854-151

Query Match 72.7%; Score 24; DB 9; Length 5;  
Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYMS 5  
|||  
Db 1 GYMS 5

RESULT 15  
US-09-968-561A-265  
; Sequence 265, Application US/09968561A  
; Patent No. US2002016462A1

GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands  
; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 265  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-265

Query Match 72.7%; Score 24; DB 9; Length 5;  
Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5  
Db 1 GYWS 5

Search completed: April 18, 2005, 15:50:47  
Job time : 131 secs

*This Page Blank (uspto)*

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 15:31:43 ; Search time 40 Seconds  
(without alignments)  
9.331 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 27945

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	87.9	5	2	US-08-480-434-22
2	29	87.9	5	2	US-08-480-434-31
3	29	87.9	5	2	US-08-053-451B-22
4	29	87.9	5	2	US-08-053-451B-31
5	27	81.8	5	1	US-08-244-626-12
6	27	81.8	5	2	US-08-480-434-32
7	27	81.8	5	2	US-08-318-157B-23
8	27	81.8	5	2	US-08-053-451B-32
9	27	81.8	5	4	US-09-253-794-23
10	25	75.8	5	1	US-08-353-400-27
11	24	72.7	4	4	US-09-948-004-32
12	24	72.7	5	4	US-08-753-750B-38
13	24	72.7	5	4	US-09-508-413A-22
14	24	72.7	5	4	US-09-152-854-151
15	24	72.7	5	4	US-09-155-106-1
16	24	72.7	5	6	5185431-15
17	24	72.7	5	6	5185431-15
18	23	69.7	5	1	US-08-318-970B-1
19	23	69.7	5	1	US-08-318-370B-3
20	23	69.7	5	3	US-09-406-532-5
21	23	69.7	5	3	US-08-479-089A-7
22	23	69.7	5	4	US-07-669-545B-7
23	23	69.7	5	4	US-09-091-071-6
24	23	69.7	5	4	US-09-269-921-6
25	20	60.6	4	1	US-07-869-933-21
26	20	60.6	4	3	US-09-103-663-21
27	20	60.6	5	2	US-08-476-176B-50

28	20	60.6	5	3	US-08-127-721A-50	Sequence 50, Appl
29	20	60.6	5	3	US-08-485-246A-50	Sequence 50, Appl
30	20	60.6	5	4	US-09-424-712-20	Sequence 20, Appl
31	20	60.6	5	4	US-09-688-188B-40	Sequence 40, Appl
32	20	60.6	5	4	US-09-628-665-8	Sequence 8, Appl
33	20	60.6	5	4	US-09-291-417D-40	Sequence 40, Appl
34	20	60.6	5	6	5217869-8	Patent No. 5217869
35	20	60.6	5	6	5217869-8	Patent No. 5217869
36	19	57.6	4	4	US-09-069-827A-173	Sequence 173, Appl
37	19	57.6	5	3	US-08-469-141A-64	Sequence 64, Appl
38	19	57.6	5	3	US-07-987-264-1	Sequence 1, Appl
39	19	57.6	5	3	US-09-382-689A-4	Sequence 4, Appl
40	19	57.6	5	4	US-08-877-605-9	Sequence 9, Appl
41	19	57.6	5	4	US-08-877-605-14	Sequence 14, Appl
42	19	57.6	5	4	US-09-254-180C-1	Sequence 1, Appl
43	19	57.6	5	5	PCT-US95-13794-64	Sequence 64, Appl
44	19	57.6	5	6	5217869-44	Patent No. 5217869
45	19	57.6	5	6	5217869-44	Patent No. 5217869

ALIGNMENTS

RESULT 1  
US-08-480-434-22  
; Sequence 22, Application US/08480434  
; Patent No. 5811248  
; GENERAL INFORMATION:  
; APPLICANT: Charles C. Ditlow, et al.  
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,  
; ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,434  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Albert P. Halluin  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 7606-053  
; TELEPHONE: (415) 854-3660  
; TELEFAX: (415) 854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: N  
; ANTI-SENSE: N  
; US-08-480-434-22

Query Match 87.9%; Score 29; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYWS 5  
|:|

Db 1 GFWMS 5

## RESULT 2

US-08-480-434-31  
; Sequence 31, Application US/08480434  
; Patent No. 5811248  
; GENERAL INFORMATION:  
; APPLICANT: Charles C. Ditlow, et al.  
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,  
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,434  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Albert P. Halluin  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 7606-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-3660  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: N  
; ANTI-SENSE: N  
; US-08-480-434-31

Query Match 87.9%; Score 29; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5

Db 1 GFWMS 5

## RESULT 3

US-08-053-451B-22  
; Sequence 22, Application US/08053451B  
; Patent No. 5955584  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Francis W.  
; APPLICANT: Ditlow, Charles C.  
; APPLICANT: Calenoff, Emanuel  
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC  
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA

Query Match 87.9%; Score 29; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5

Db 1 GFWMS 5

; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,451B  
; FILING DATE: 26-APR-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 7606-033-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA  
; HYPOTHETICAL: N  
; ANTI-SENSE: N  
; US-08-053-451B-22

Query Match 87.9%; Score 29; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5

Db 1 GFWMS 5

## RESULT 4

US-08-053-451B-31  
; Sequence 31, Application US/08053451B  
; Patent No. 5955584  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Francis W.  
; APPLICANT: Ditlow, Charles C.  
; APPLICANT: Calenoff, Emanuel  
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC  
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,451B  
; FILING DATE: 26-APR-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 7606-033-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEX: 66141 PENNIE



INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA  
 HYPOTHETICAL: N  
 ANTI-SENSE: N  
 US-08-053-451B-31

Query Match 87.9%; Score 29; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5  
 |:|  
 Db 1 GFWMS 5

RESULT 5  
 US-08-244-626-12  
 ; Sequence 12, Application US/08244626  
 ; Patent No. 5502167  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Waldmann, Herman  
 ; APPLICANT: Walsh, Louise  
 ; APPLICANT: Crowe, James Scott  
 ; APPLICANT: Lewis, Alan Peter  
 ; TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL  
 ; TITLE OF INVENTION: ANTIBODIES  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.  
 ; STREET: 555 Thirteenth Street, N. W.  
 ; CITY: Washington  
 ; STATE: D. C.  
 ; COUNTRY: USA  
 ; ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/244,626  
 FILING DATE: July 15, 1994

CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/GB92/02251  
 FILING DATE: December 4, 1992  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ernst, Barbara G.  
 REGISTRATION NUMBER: 30,377  
 REFERENCE/DOCKET NUMBER: 1808-153A  
 TELEPHONE: (202) 783-6040  
 TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-244-626-12

Query Match 81.8%; Score 27; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
 ||||

Db 2 YWMS 5

RESULT 6  
 US-08-480-434-32  
 ; Sequence 32, Application US/08480434  
 ; Patent No. 5811248  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charles C. Dittlow, et al.  
 ; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,  
 ; ANTIBODIES THEREOF, AND USES THEREOF  
 ; TITLE OF INVENTION:  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.24  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,434  
 FILING DATE: 07-JUN-1995

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Albert P. Halluin  
 REGISTRATION NUMBER: 25,227  
 REFERENCE/DOCKET NUMBER: 7606-053  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 854-3660  
 TELEFAX: (415) 854-3694  
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 32:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: N  
 ANTI-SENSE: N  
 US-08-480-434-32

Query Match 81.8%; Score 27; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
 ||||  
 Db 2 YWMS 5

RESULT 7  
 US-08-318-157B-23  
 ; Sequence 23, Application US/08318157B  
 ; Patent No. 5874540  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HANSEN, Hans J.  
 ; APPLICANT: ARMOUR, Kathryn L.  
 ; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED  
 ; ANTIBODIES  
 ; NUMBER OF SEQUENCES: 58  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,157B  
FILING DATE: 05-OCT-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/464  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-157B-23

Query Match 81.8%; Score 27; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
Db 2 YWMS 5

RESULT 8  
US-08-053-451B-32  
Sequence 32, Application US/08053451B  
Patent No. 5955584  
GENERAL INFORMATION:  
APPLICANT: Chen, Francis W.  
APPLICANT: Ditlow, Charles C.  
APPLICANT: Calenoff, Emanuel  
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC  
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,451B  
FILING DATE: 26-APR-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 7606-033-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids

TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA  
HYPOTHETICAL: N  
ANTI-SENSE: N  
US-08-053-451B-32

Query Match 81.8%; Score 27; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
Db 2 YWMS 5

RESULT 9  
US-09-253-794-23  
Sequence 23, Application US/09253794  
Patent No. 6676924  
GENERAL INFORMATION:  
APPLICANT: HANSEN, Hans J.  
ARMOUR, Kathryn L.  
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED  
MOUSE MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/253,794  
FILING DATE: 22-Feb-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,157  
FILING DATE: 05-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/464  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-253-794-23

Query Match 81.8%; Score 27; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5  
Db 2 YWMS 5

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RESULT 10
US-08-353-400-27
; Sequence 27, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-353-400-27

Query Match 75.8%; Score 25; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWM 4
Db 1 GYWI 4

RESULT 11
US-09-948-004-32
; Sequence 32, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; TITLE OF INVENTION: immunological disorders
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; US-09-948-004-32

Query Match 72.7%; Score 24; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
Db 1 YWMN 4

RESULT 12
US-08-753-750B-38
; Sequence 38, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y. C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; TITLE OF INVENTION: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Pasteurella haemolytica
; US-08-753-750B-38

Query Match 72.7%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3
Db 3 GYW 5

RESULT 13
US-09-508-413A-2
; Sequence 2, Application US/09508413A
; Patent No. 6667035
; GENERAL INFORMATION:
; APPLICANT: von Eichel-Streiber, Christoph
; APPLICANT: Moos, Michael
; TITLE OF INVENTION: AMINO ACID SEQUENCES FOR THERAPEUTIC AND
; TITLE OF INVENTION: PROPHYLACTIC USE AGAINST DISEASES DUE TO CLOSTRIDIUM
; TITLE OF INVENTION: DIFFICILE TOXINS
; FILE REFERENCE: 415142000200
; CURRENT APPLICATION NUMBER: US/09/508,413A
; CURRENT FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: PCT/EP98/05759
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-508-413A-2

Query Match 72.7%; Score 24; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
Db 2 YWMN 5

RESULT 14
US-09-192-854-151
; Sequence 151, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
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; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-192-854-151

Query Match      72.7%; Score 24; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. NO. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWMS 5
      |||.||
Db      1 GYWS 5

RESULT 15
US-09-155-106-1
; Sequence 1, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-155-106-1

Query Match      72.7%; Score 24; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. NO. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWMS 5
      |||.
Db      2 YWMT 5

Search completed: April 18, 2005, 15:39:49
Job time : 41 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 13:59:59 ; Search time 37.5581 Seconds  
(without alignments)  
48.674 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLKSDNYATHYAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	101	2 S26460	Ig heavy chain V r
2	98	100.0	115	2 S38714	Ig heavy chain V r
3	93	94.9	106	2 S24521	Ig heavy chain V r
4	93	94.9	115	1 AVMS06	Ig heavy chain V-I
5	91	92.9	113	1 AVMS09	Ig heavy chain V-I
6	91	92.9	113	1 AVMS61	Ig heavy chain V-I
7	91	92.9	113	1 AVMSAB	Ig heavy chain V-I
8	91	92.9	113	1 AVMSB7	Ig heavy chain V-I
9	91	92.9	115	1 AVMS82	Ig heavy chain V-I
10	89	90.8	115	2 A25803	Ig heavy chain V r
11	86	87.8	113	1 AVMS57	Ig heavy chain V-I
12	85	86.7	113	1 HVMSAM	Ig heavy chain V r
13	75.5	77.0	111	1 MHMS76	Ig heavy chain V-I
14	73	74.5	139	2 PC1213	Ig heavy chain pre
15	68	69.4	64	2 I77394	Ig heavy chain V r
16	68	69.4	121	2 S09958	Ig heavy chain V-D
17	67	68.4	100	2 S26462	Ig heavy chain V r
18	67	68.4	110	2 PH1092	Ig heavy chain V r
19	67	68.4	110	2 PH1091	Ig heavy chain V r
20	67	68.4	119	2 A27630	Ig heavy chain pre
21	67	68.4	121	2 A41940	Ig heavy chain V r
22	67	68.4	141	2 I32513	Ig heavy chain pre
23	66	67.3	125	2 S67945	Ig heavy chain BrE
24	65	66.3	139	2 G29380	Ig heavy chain pre
25	64	65.3	110	2 PH1093	Ig heavy chain V r
26	63	64.3	220	2 S68211	Ig heavy chain (Ma
27	63	64.3	444	2 FC4436	monoclonal antibod
28	61	62.2	119	2 PH1293	Ig heavy chain pre
29	61	62.2	137	2 S42467	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S26460

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S26460

R;Kavaler, J

submitted to the EMBL Data Library, April 1991

A;Reference number: S26459

A;Accession: S26460

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-101 <KAV>

A;Cross-references: EMBL:X59106; NID:G51707; PIDN:CAA41832.1; PID:G51708

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 98; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 9.2e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19

|||||

Db 32 EIRLKSDNYATHYAESVKG 50

RESULT 2

S38714

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000

C;Accession: S38714

R;Cimanis, A.Y.

submitted to the EMBL Data Library, November 1993

A;Reference number: S38713

A;Accession: S38714

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-115 <CIM>

A;Cross-references: EMBL:X76014; NID:G416092; PIDN:CAA53601.1; PID:G1334076

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;14-99/Domain: immunoglobulin homology <IMV>

Query Match 100.0%; Score 98; DB 2; Length 115;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19

|||||

Db 49 EIRLKSDNYATHYAESVKG 67

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RESULT 3
S24521
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S24521
R;Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24490
A;Accession: S24521
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <KAA>
A;Cross-references: EMBL:X66664; NID:G51247; PIDN:CAA47226.1; PID:G51248
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;21-106/Domain: immunoglobulin homology <IMM>

Query Match 94.9%; Score 93; DB 2; Length 106;
Best Local Similarity 94.7%; Pred. No. 6.3e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 56 EIRLKSNNYATHYAESVKG 74

RESULT 4
AVMS06
Ig heavy chain V-III region (J606) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: C92811; A02072
R;Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
J. Immunol. 128, 302-307, 1982
A;Title: The complete V domain amino acid sequences of two myeloma inulin-binding proteins
A;Reference number: A92811; MUID:82099361; PMID:679811
A;Accession: C92811
A;Molecule type: protein
A;Residues: 1-115 <JOH>
A;Cross-references: UNIPROT:P01801
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted

Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 6.9e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 5
AVMS09
Ig heavy chain V-III region (E109) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: C93818; A02072
R;Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A;Reference number: A93818; MUID:78158406; PMID:417344
A;Accession: C93818
A;Molecule type: protein
A;Residues: 1-113 <VRA>
A;Cross-references: UNIPROT:P01798
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 6
AVMS61
Ig heavy chain V-III region (U61) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: B93818; A02072
R;Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A;Reference number: A93818; MUID:78158406; PMID:417344
A;Accession: B93818
A;Molecule type: protein
A;Residues: 1-113 <VRA>
A;Cross-references: UNIPROT:P01797
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 7
AVMSAB
Ig heavy chain V-III region (A4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A93818; A02072
R;Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A;Reference number: A93818; MUID:78158406; PMID:417344
A;Accession: A93818
A;Molecule type: protein
A;Residues: 1-113 <VRA>
A;Cross-references: UNIPROT:P01796
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 8
AVMSB7

```

C;Keywords: heterotetramer; immunoglobulin  
F;15-100/Domain: immunoglobulin homology <IMM>  
F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;  
Best Local Similarity 94.7%; Pred. No. 1.4e-07;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
|||||:|||||  
Db 50 EIRLKSNNYATHYAESVKG 68

#### RESULT 6

AVMS61  
Ig heavy chain V-III region (U61) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
C;Accession: B93818; A02072  
R;Vrana, M.; Rudikoff, S.; Potter, M.  
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978  
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.  
A;Reference number: A93818; MUID:78158406; PMID:417344  
A;Accession: B93818  
A;Molecule type: protein  
A;Residues: 1-113 <VRA>  
A;Cross-references: UNIPROT:P01797  
C;Comment: This chain was isolated from a myeloma protein that binds inulin.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-100/Domain: immunoglobulin homology <IMM>  
F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;  
Best Local Similarity 94.7%; Pred. No. 1.4e-07;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
|||||:|||||  
Db 50 EIRLKSNNYATHYAESVKG 68

#### RESULT 7

AVMSAB  
Ig heavy chain V-III region (A4) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 24-Apr-1984 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
C;Accession: A93818; A02072  
R;Vrana, M.; Rudikoff, S.; Potter, M.  
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978  
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.  
A;Reference number: A93818; MUID:78158406; PMID:417344  
A;Accession: A93818  
A;Molecule type: protein  
A;Residues: 1-113 <VRA>  
A;Cross-references: UNIPROT:P01796  
C;Comment: This chain was isolated from a myeloma protein that binds inulin.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-100/Domain: immunoglobulin homology <IMM>  
F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;  
Best Local Similarity 94.7%; Pred. No. 1.4e-07;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
|||||:|||||  
Db 50 EIRLKSNNYATHYAESVKG 68

#### RESULT 8

AVMSB7

C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1980 #sequence revision 30-Sep-1980 #text\_change 09-Jul-2004

Search completed: April 18, 2005, 14:23:34  
Job time : 41.5581 secs

Query Match 69.4%; Score 68; DB 2; Length 64;  
Best Local Similarity 72.2%; Pred. No. 0.00042;  
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:57:43 ; Search time 172.767 seconds  
(without alignments)  
56.316 Million cell updates/sec

Title: US-09-674-716B-11  
Perfect score: 98  
Sequence: 1 EIRLKSNDYATHYAESVKG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	93	94.9	115	1	HV32_MOUSE	P01801 mus musculus
2	92	93.9	464	2	Q6P1P8	Q6P1P8 mus musculus
3	91	92.9	113	1	HV27_MOUSE	P01796 mus musculus
4	91	92.9	113	1	HV28_MOUSE	P01797 mus musculus
5	91	92.9	113	1	HV29_MOUSE	P01798 mus musculus
6	91	92.9	113	1	HV30_MOUSE	P01799 mus musculus
7	91	92.9	115	1	HV33_MOUSE	P01802 mus musculus
8	90	91.8	487	2	Q80Z17	Q80Z17 mus musculus
9	86	87.8	113	1	HV31_MOUSE	P01800 mus musculus
10	85	86.7	113	1	HV34_MOUSE	P01803 mus musculus
11	75.5	77.0	111	1	HV35_MOUSE	P01804 mus musculus
12	68	69.4	64	2	Q61750	Q61750 mus musculus
13	67	68.4	471	2	Q66K04	Q66K04 mus musculus
14	64	65.3	458	2	Q65ZQ1	Q65ZQ1 homo sapien
15	57	58.2	142	1	HV01_RAT	P01805 rattus norv
16	57	58.2	479	2	Q7TMK4	Q7TMK4 mus musculus
17	52	53.1	493	2	Q6GMX2	Q6GMX2 homo sapien
18	51	52.0	480	2	Q91XE1	Q91XE1 mus musculus
19	49	50.0	357	2	Q6J2D0	Q6J2D0 pseudomonas
20	49	50.0	361	2	Q9RBZ2	Q9RBZ2 pseudomonas
21	49	50.0	614	2	Q6DDQ7	Q6DDQ7 xenopus lae
22	48	49.0	122	1	HV21_MOUSE	P01790 mus musculus
23	48	49.0	123	1	HV18_MOUSE	P01787 mus musculus
24	48	49.0	123	1	HV19_MOUSE	P01788 mus musculus
25	48	49.0	123	1	HV22_MOUSE	P01791 mus musculus
26	48	49.0	123	1	HV25_MOUSE	P01794 mus musculus
27	47.5	48.5	754	2	Q8CGQ1	Q8CGQ1 mus musculus
28	47	48.0	357	2	Q9RBZ3	Q9RBZ3 pseudomonas
29	47	48.0	398	2	Q88ZK4	Q88ZK4 lactobacill
30	46	46.9	122	1	HV20_MOUSE	P01789 mus musculus
31	46	46.9	144	1	HV26_MOUSE	P01795 mus musculus

32	46	46.9	163	2	Q68WS1	Q68ws1 rickettsia
33	46	46.9	2910	2	Q9FND5	Q9fnd5 arabidopsis
34	45.5	46.4	703	2	Q8COV3	Q8cov3 mus musculus
35	45.5	46.4	756	2	Q6IMH7	Q6imh7 mus musculus
36	45	45.9	121	2	Q9UL71	Q9ul71 homo sapien
37	45	45.9	300	2	Q8ID86	Q8id86 plasmodium
38	45	45.9	422	2	Q8WR61	Q8wr61 lymantria d
39	45	45.9	450	2	Q8U651	Q8u651 agrobacteri
40	45	45.9	485	1	HUNB_CLOAL	Q96785 clogmia alb
41	45	45.9	593	2	Q6INM5	Q6inm5 xenopus lae
42	44	44.9	123	1	HV23_MOUSE	P01792 mus musculus
43	44	44.9	253	2	Q8DZT9	Q8dz16 streptococc
44	44	44.9	253	2	Q8ESI6	Q8esi6 streptococc
45	44	44.9	270	2	Q7VLX9	Q7vlx9 haemophilus

ALIGNMENTS

RESULT 1  
HV32\_MOUSE STANDARD; PRT; 115 AA.  
AC P01801;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE IG heavy chain V-III region J606.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
RX MEDLINE-82099361; PubMed-6798111;  
RA Johnson N., Stankard J., Paul L., Hood L.;  
RT "The complete V domain amino acid sequences of two myeloma inulin-binding proteins."  
RL J. Immunol. 128:302-307(1982).  
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that binds inulin.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; C92811; AVMS06.  
DR HSSP; P01852; INFD.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 114 IG-like.  
FT DISULFID 22 98 By similarity.  
FT NON\_TER 115 115  
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Query Match 94.9%; Score 93; DB 1; Length 115;  
Best Local Similarity 94.7%; Pred. No. 3.3e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EIRLKSNDYATHYAESVKG 19  
|||||:|||||  
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 2  
ID Q6P1P8 PRELIMINARY; PRT; 464 AA.  
AC Q6P1P8;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Czech II; TISSUE=Mammary tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
 RA Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschul S.P., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Czech II; TISSUE=Mammary tumor;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC031470; AAH31470.1; -  
 DR HSSP; P01865; 1KB5.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG.c1.  
 DR InterPro; IPR003006; IG.MHC.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 464 AA; 51246 MW; FDAC40A45B5E1443 CRC64;  
 Query Match 93.9%; Score 92; DB 2; Length 464;  
 Best Local Similarity 89.5%; Pred. No. 2.2e-06;  
 Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EIRLSDNYATHYAESVKG 19  
 Db :|||:|||||  
 69 QIRLSDNYATHYAESVKG 87  
 RESULT 3  
 HV27\_MOUSE  
 ID HV27\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01796;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig heavy chain V-III region A4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 proteins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).  
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
 binds inulin.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; B93818; AVMS61.  
 DR HSSP; P01783; 1IGC.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 >113  
 FT DISULFID 22 98  
 FT NON\_TER 113 113  
 FT SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;  
 Query Match 92.9%; Score 91; DB 1; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 6.9e-07;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIRLSDNYATHYAESVKG 19  
 Db :|||||:|||||  
 50 EIRLSDNYATHYAESVKG 68  
 RESULT 5  
 HV29\_MOUSE  
 ID HV29\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01797;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig heavy chain V-III region U61.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 proteins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).  
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
 binds inulin.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; B93818; AVMS61.  
 DR HSSP; P01783; 1IGC.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 >113  
 FT DISULFID 22 98  
 FT NON\_TER 113 113  
 FT SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;  
 Query Match 92.9%; Score 91; DB 1; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 6.9e-07;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIRLSDNYATHYAESVKG 19  
 Db :|||||:|||||  
 50 EIRLSDNYATHYAESVKG 68

RT proteins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).  
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
 binds inulin.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; B93818; AVMS61.  
 DR HSSP; P01783; 1IGC.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 >113  
 FT DISULFID 22 98  
 FT NON\_TER 113 113  
 FT SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;  
 Query Match 92.9%; Score 91; DB 1; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 6.9e-07;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIRLSDNYATHYAESVKG 19  
 Db :|||||:|||||  
 50 EIRLSDNYATHYAESVKG 68  
 RESULT 4  
 HV28\_MOUSE  
 ID HV28\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01797;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig heavy chain V-III region U61.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 proteins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).  
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
 binds inulin.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; B93818; AVMS61.  
 DR HSSP; P01783; 1IGC.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 >113  
 FT DISULFID 22 98  
 FT NON\_TER 113 113  
 FT SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;  
 Query Match 92.9%; Score 91; DB 1; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 6.9e-07;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIRLSDNYATHYAESVKG 19  
 Db :|||||:|||||  
 50 EIRLSDNYATHYAESVKG 68  
 RESULT 5  
 HV29\_MOUSE  
 ID HV29\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01797;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig heavy chain V-III region U61.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 proteins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).  
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
 binds inulin.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; B93818; AVMS61.  
 DR HSSP; P01783; 1IGC.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 >113  
 FT DISULFID 22 98  
 FT NON\_TER 113 113  
 FT SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;  
 Query Match 92.9%; Score 91; DB 1; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 6.9e-07;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIRLSDNYATHYAESVKG 19  
 Db :|||||:|||||  
 50 EIRLSDNYATHYAESVKG 68  
 RESULT 5  
 HV29\_MOUSE  
 ID HV29\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01797;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig heavy chain V-III region U61.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 proteins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).  
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
 binds inulin.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; B93818; AVMS61.  
 DR HSSP; P01783; 1IGC.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 >113  
 FT DISULFID 22 98  
 FT NON\_TER 113 113  
 FT SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;  
 Query Match 92.9%; Score 91; DB 1; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 6.9e-07;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIRLSDNYATHYAESVKG 19  
 Db :|||||:|||||  
 50 EIRLSDNYATHYAESVKG 68

```
ID HV29_MOUSE STANDARD; PRT; 113 AA.
AC P01798;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region E109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
  proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
  binds inulin.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C93818; AVMS09.
DR HSP; P01783; IIGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 >113
  Ig-like.
FT DISULFID 22 98
  By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 6.9e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
  ||||| ||||| ||||| |||||
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 6
HV30_MOUSE STANDARD; PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
  protein."
RL Biochemistry 16:1170-1175(1977).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
  binds inulin.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90400; AVMSB7.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 >113
  Ig-like.
```

```
FT DISULFID 22 98
  By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 6.9e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
  ||||| ||||| ||||| |||||
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 7
HV33_MOUSE STANDARD; PRT; 115 AA.
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
  binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
  binds inulin.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01852; 1NFD.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 114
  Ig-like.
FT DISULFID 22 98
  By similarity.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 92.9%; Score 91; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
  ||||| ||||| ||||| |||||
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 8
Q802I7 PRELIMINARY; PRT; 487 AA.
AC Q802I7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Colon;
  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
```

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RESULT 9
ID HV31_MOUSE STANDARD; PR7; 113 AA.
AC F01800;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region T957.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
RT evidence for a new heavy chain joining segment." ;
RL J. Immunol. 127:191-194(1981).
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds inulin.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A92810; AVMS57.
DR HSSP; P01783; IIGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.

```

Query Match	86.7%	Score 85;	DB 1;	Length 113;
Best Local Similarity	89.5%	Pred. No. 6.6e-06;		
Matches	17.	Conservative	0;	Mismatches 2;
				Indels 0;
				Gaps 0

Qy	1	EIRLKSNDNYATHYAESVKG	19
Dd	50	EIRLKSHNYATHYAESVKG	68
RESULT 11			
ID	HV35	MOUSE	
ID	HV35	STANDARD;	PRT; 111 AA.
AC	P01804;		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	10-OCT-2003	(Rel. 42, Last annotation update)	
DE	Ig heavy chain V-III region HPC76	(Fragment).	
OS	Mus musculus	(Mouse).	
OC	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria;	Rodentia; Sciurognathi; Muridae; Mus.	

```
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP MEDLINE=81013937; PubMed=6251474;
RA Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
between translocated VH and mu constant regions genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC -1- MISCELLANEOUS: The sequence of the first 197 residues of the C
region was also determined and differs in only 3 positions from
the corresponding portion of the mouse MOPC 104e mu chain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02074; MMS76.
DR HSSP; P01852; INFD.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT NON_TER 1 1
FT DOMAIN <1 110 Ig-like.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 13304 MW; 0EDE98EC7348056A CRC64;

Query Match 77.0%; Score 75.5; DB 1; Length 111;
Best Local Similarity 89.5%; Pred. No. 0.00023;
Matches 17; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EIRKSDNYATHYAESVKG 19
Db 45 EIRLKS-GYATHYAESVKG 62
||||| |||||||||

RESULT 12
Q61750 PRELIMINARY; PRT; 64 AA.
AC Q61750;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE JH-Cdelta locus, partial cds. (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP MEDLINE=92017847; PubMed=1922069;
RA Owens J.D.Jr., Finkelman F.D., Mountz J.D., Mushinski J.F.;
RT "Nonhomologous recombination at sites within the mouse JH-C delta
locus accompanies C mu deletion and switch to immunoglobulin D
secretion.";
RL Mol. Cell. Biol. 11:5660-5670(1991).
DR EMBL; M64568; AAA39341.1; -.
DR PIR; I77394; I77394.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
FT NON_TER 64
FT SEQUENCE 64 AA; 7594 MW; FE83625079AC3F28 CRC64;

Query Match 69.4%; Score 68; DB 2; Length 64;
Best Local Similarity 72.2%; Pred. No. 0.0021;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IRLKSDNYATHYAESVKG 19
Db 9 ITVKSDNYGANYAESVKG 26
|:|||||:|||||

RESULT 13
Q66K04
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ID Q66K04 PRELIMINARY; PRT; 471 AA.
AC Q66K04;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=CZECH II; TISSUE=Mammary tumor;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smalish J., Schnerch A., Schein J.E.,
RA Jones S.J., Maiz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN SEQUENCE FROM N.A.
RP STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC080671; AAH80671.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 52258 MW; 81BB7C3228315AC2 CRC64;

Query Match 68.4%; Score 67; DB 2; Length 471;
Best Local Similarity 76.5%; Pred. No. 0.027;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IRLKSDNYATHYAESVKG 18
Db 70 IRKSNNYATYVADSVK 86
||:||||:|||||

RESULT 14
Q65ZQ1 PRELIMINARY; PRT; 458 AA.
AC Q65ZQ1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Anti-colorectal carcinoma heavy chain.
OS Homo sapiens (Human).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93383497; PubMed=8372513;  
RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;  
RT "Cloning and characterization of I16NS19.9 heavy and light chain  
cDNAs and expression of antibody fragments in Escherichia coli.";  
RL Year Immunol. 7:56-62(1993).  
DR EMBL; S65761; AAB28159.1; -.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF00047; IG; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 2.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
SQ SEQUENCE 458 AA; 50602 MW; 4AE29F9981D8DFF CRC64;

Query Match 65.3%; Score 64; DB 2; Length 458;  
Best Local Similarity 68.4%; Pred. No. 0.08;  
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 EIRKSDNYATHYAESVKG 19  
Db 69 EIGNKGNHATYAESVKG 87

Oy 1 EIRKSDNYATHYAESVKG 19  
Db 69 EIRKANNVYVYTKSLKG 87

Search completed: April 18, 2005, 14:21:57  
Job time : 174.767 secs

RESULT 15  
HV01\_RAT  
ID HV01\_RAT STANDARD; PRT; 142 AA.  
AC F01805;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region IR2 precursor.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83064537; PubMed=6292865;  
RA Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;  
RT "Structure and evolution of the heavy chain from rat immunoglobulin  
E.";  
RL Nucleic Acids Res. 10:6041-6049(1982).  
CC -!- MISCELLANEOUS: The mRNA was isolated from an IgE-secreting  
immunocytoma that arises spontaneously in LOU/CwSL rats.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02075; EVRIR2.  
DR HSP; F01789; IMCP.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 19  
FT CHAIN 20 142 Ig heavy chain V region IR2.  
FT DOMAIN 20 133 Ig-like.  
FT NON\_TER 142 142  
SQ SEQUENCE 142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;

Query Match 58.2%; Score 57; DB 1; Length 142;  
Best Local Similarity 52.6%; Pred. No. 0.32;  
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:32:07 ; Search time 200.163 Seconds  
(without alignments)  
36.712 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLKSDNYATHVAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	19	3	AAY32258
2	98	100.0	123	6	ABO10742
3	98	100.0	123	6	ABR44686
4	98	100.0	123	8	ADQ90820
5	98	100.0	137	3	AAY32260
6	98	100.0	286	4	AAB50426
7	98	100.0	444	3	AAY32263
8	95	96.9	100	4	AAE06973
9	95	96.9	100	8	ADQ89258
10	95	96.9	299	4	AAB50425
11	93	94.9	115	2	AAR34018
12	93	94.9	116	2	AAY03869
13	93	94.9	119	2	AAW46958
14	93	94.9	119	7	ABR82775
15	93	94.9	119	7	ABR82885
16	93	94.9	120	2	AAW01589
17	93	94.9	122	3	AAY90812
18	93	94.9	142	2	AAW06212
19	93	94.9	142	2	AAW85059
20	93	94.9	142	6	ABU58893
21	93	94.9	143	3	AAW09423
22	93	94.9	255	5	AAU72870
23	93	94.9	256	5	AAU72866
24	93	94.9	503	5	AAU72874
25	93	94.9	570	2	AAY39451

26	91	92.9	19	4	AAB35297	Aab35297 Murine PS
27	91	92.9	151	4	AAU76696	Aau76696 Mouse hea
28	91	92.9	151	4	AAU76696	Aau76696 Mouse hea
29	90	91.8	123	6	ABO10743	Abol0743 Consensus
30	90	91.8	123	6	ABR44687	AbR44687 Murine J4
31	90	91.8	123	8	ADQ90821	Adq90821 Kabat sub
32	89	90.8	117	8	ADRI9267	Adri9267 Glycoeyla
33	89	90.8	117	8	ADRI9296	Adri9296 Mucin 1 r
34	89	90.8	255	8	ADRI9322	Adri9322 Mucin 1 a
35	89	90.8	256	8	ADRI9321	Adri9321 Mucin 1 a
36	89	90.8	257	8	ADRI9320	Adri9320 Mucin 1 a
37	89	90.8	258	8	ADRI9319	Adri9319 Mucin 1 a
38	89	90.8	259	8	ADRI9318	Adri9318 Mucin 1 a
39	89	90.8	260	8	ADRI9317	Adri9317 Mucin 1 a
40	89	90.8	261	8	ADRI9316	Adri9316 Mucin 1 a
41	89	90.8	262	8	ADRI9315	Adri9315 Mucin 1 a
42	89	90.8	263	8	ADRI9314	Adri9314 Mucin 1 a
43	89	90.8	264	8	ADRI9313	Adri9313 Mucin 1 a
44	89	90.8	265	8	ADRI9312	Adri9312 Mucin 1 a
45	89	90.8	274	8	ADRI9311	Adri9311 Mucin 1 a

#### ALIGNMENTS

##### RESULT 1

AAV32258

ID AAY32258 standard; peptide; 19 AA.

XX AC AAY32258;

XX DT 15-FEB-2000 (first entry)

XX DE Light chain CDR H2 of mouse anti-CD23 Mab C11.

XX XX

CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.

XX OS Mus musculus.

XX PN WO958679-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001434.

XX PR 09-MAY-1998; 98GB-00009839.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX DR WPI; 2000-053101/04.

XX XX N-PSDB; AA234743.

Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

Claim 1; Page 40; 81pp; English.

This sequence represents complementarity determining region 2 (CDR H2) of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also AAY32263). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents  
 XX  
 XX Sequence 19 AA;

Query Match 100.0%; Score 98; DB 3; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHAESVKG 19  
 |||||  
 DB 1 EIRLSDNYATHAESVKG 19

RESULT 2  
 ABO10742  
 ID ABO10742 standard; protein; 123 AA.

XX AC ABO10742;

XX DT 20-AUG-2003 (first entry)

XX DE Variable region of murine antibody MuVHIIIC.

XX KW Modified antibody; deimmunised antibody; anti-PSMA antibody;  
 KW prostate specific membrane antigen; immunogenic; CDR; murine;  
 KW complementarity determining region; J591; J415; J533; E99; mouse;  
 KW prostatic disorder; cancerous disorder; genitourinary inflammation;  
 KW prostatitis; benign enlargement; prostatic cancer; testicular cancer;  
 KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;  
 KW antiinflammatory; cytostatic; framework region; variable heavy chain;  
 KW variable light chain; VH; VL; variable region.  
 XX  
 XX Mus musculus.

XX OS Mus musculus.

XX XX WO200298897-A2.

XX PD 12-DEC-2002.

XX PF 30-MAY-2002; 2002WO-US017068.

XX PR 01-JUN-2001; 2001US-0295214P.

XX PR 20-SEP-2001; 2001US-0323585P.

XX PR 08-MAR-2002; 2002US-0362810P.

XX PA (CORR ) CORNELL RES FOUND INC.

XX PI Bander N, Carr FJ, Hamilton A;

XX PS WPI; 2003-156839/15.

XX PT New modified anti-prostate specific membrane antigen (PSMA)  
 PT immunoglobulins, useful for treating or preventing a prostatic or  
 PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or  
 PT prostatic or testicular cancer.

XX PS Disclosure; Fig 7C; 254pp; English.

XX CC The present invention relates to modified (e.g. deimmunised) antibodies  
 CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA  
 CC antibodies are less immunogenic compared to the unmodified anti-PSMA  
 CC antibodies. The modified antibodies comprise complementarity determining  
 CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,

CC J533 or E99), and framework sequences that are less immunogenic in humans  
 CC (e.g. less antigenic than the murine frameworks in which a murine CDR  
 CC naturally occurs). The modified antibodies bind with PSMA, preferably  
 CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies  
 CC are useful for treating or preventing a prostatic or cancerous disorder,  
 CC e.g. genitourinary inflammation, prostatitis, benign enlargement,  
 CC prostatic cancer or testicular cancer, or solid tumours, soft tissue  
 CC tumours or metastatic lesions, and its associated pain. The present  
 CC sequence represents a variable region from a murine antibody  
 XX

SQ Sequence 123 AA;

Query Match 100.0%; Score 98; DB 6; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 3e-08;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHAESVKG 19  
 |||||  
 DB 50 EIRLSDNYATHAESVKG 68

RESULT 3

ABR44686

ID ABR44686 standard; protein; 123 AA.

XX AC ABR44686;

XX DT 25-JUL-2003 (first entry)

XX DE Murine MuVHIIIC amino acid sequence SEQ ID NO:69.

XX KW Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;  
 KW prostate specific membrane antigen; antipsoriatic; antiarthritic;  
 KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;  
 KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;  
 KW neoplastic disorder.

XX XX Mus musculus.

XX OS WO2003024388-A2.

XX PN 27-MAR-2003.

XX PD 30-MAY-2002; 2002WO-US017204.

XX PF 20-SEP-2001; 2001US-0324100P.

XX PR 08-MAR-2002; 2002US-0362612P.

XX XX (CORR ) CORNELL RES FOUND INC.

XX PI Bander N;

XX DR WPI; 2003-313319/30.

XX PT Ablating/killing aberrant prostate specific membrane antigen-expressing  
 PT cells for treating skin disorders, by contacting the cell with an  
 PT antibody that binds to the extracellular domain of prostate specific  
 PT membrane antigen.

XX PS Disclosure; Page 37; 225pp; English.

XX CC The present invention describes a method (M1) for ablating or killing an  
 CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.  
 CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a  
 CC vascular endothelial cell proximate to the cell, with an antibody (or its  
 CC antigen-binding fragment), which binds specifically to the extracellular  
 CC domain of PSMA in an amount sufficient to ablate or kill the cell. The  
 CC antibodies have antipsoriatic, antiarthritic, dermatological, cytostatic,  
 CC antiinflammatory and antiallergic activities, and can be used in  
 CC vaccines. M1 is useful for treating a skin disorder in a subject, by  
 CC administering to the subject, an amount of an antibody which binds  
 CC specifically to the extracellular domain of PSMA (the subject is a  
 CC mammal, preferably human and is having, or at risk of, a skin disorder).



CC The skin disorder is a dermal or an epidermal disorder, and is selected  
 CC from psoriasis (preferably chronic stationary psoriasis, psoriasis  
 CC vulgaris, eruptive (glutamate) psoriasis, psoriatic erythroderma,  
 CC generalised pustular psoriasis (Von Zumbusch), annular pustular  
 CC psoriasis, and localised pustular psoriasis), psoriatic arthritis,  
 CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis rosea,  
 CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,  
 CC ichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis,  
 CC preferably psoriasis. M1 is useful for treating a skin disorder such as  
 CC an inflammatory or neoplastic disorder of the epidermis or dermis,  
 CC preferably an epidermal precancerous or cancerous lesion. M1 is also  
 CC useful to treat or prevent disorders involving aberrant activity of PSMA-  
 CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837  
 CC and ABR44613 to ABR44733 represent sequences used in the exemplification  
 CC of the present invention

XX SQ Sequence 123 AA;

Query Match 100.0%; Score 98; DB 6; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 3e-08;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19

Db 50 EIRLKSDNYATHYAESVKG 68

RESULT 4

ADQ90820  
 ID ADQ90820 standard; protein; 123 AA.

XX AC

XX ADQ90820;

XX DT 07-OCT-2004 (first entry)

XX DE

XX Kabat subgroup murine VHIIIC.

XX insulin-related disorder; prostate specific membrane antigen; PSMA;  
 KW obesity; hyperglycaemia; hypoglycaemia; hyperinsulinaemia;  
 KW insulin-resistance; impaired glucose tolerance; impaired fasting glucose;  
 KW Type 1 diabetes mellitus; Type 2 diabetes mellitus; gestational diabetes;  
 KW antibody; mouse.

XX OS Mus musculus.

XX US2004136998-A1.

XX PD 15-JUL-2004.

XX PF 17-OCT-2003; 2003US-00688015.

XX PR 30-OCT-2002; 2002US-0422396P.

XX PR

XX PA (BAND/) BANDER N H.

XX PI

XX Bander NH;

XX DR

XX WPI; 2004-533338/51.

XX XX

PT Use of anti-prostate specific membrane antigen antibodies for treating or  
 PT preventing insulin-related disorders, e.g. obesity, hyperglycemia,  
 PT hypoglycemia, hyperinsulinemia, insulin-resistance, or Type 1 or 2  
 PT diabetes mellitus.

XX XX

PS Disclosure; SEQ ID NO 69; 89pp; English.

XX XX

CC The invention relates to a method of treating or preventing an insulin-  
 CC related disorder in a subject which comprises administering an antibody  
 CC or its antigen-binding portion specific for prostate specific membrane  
 CC antigen (PSMA). The method is useful for treating an insulin-related  
 CC disorder, including obesity, hyperglycaemia, hypoglycaemia,  
 CC hyperinsulinaemia, insulin-resistance, impaired glucose tolerance,  
 CC impaired fasting glucose, Type 1 diabetes mellitus, Type 2 diabetes

CC mellitus, and gestational diabetes. The present sequence represents Kabat  
 CC subgroup murine VHIIIC.

XX SQ Sequence 123 AA;

Query Match 100.0%; Score 98; DB 8; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 3e-08;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19

Db 50 EIRLKSDNYATHYAESVKG 68

RESULT 5

AAY32260

ID AAY32260 standard; protein; 137 AA.

XX AC

XX AAY32260;

XX DT 15-FEB-2000 (first entry)

XX XX

DE Mouse anti-CD23 MAb C11 heavy chain variable region.

XX XX

KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.

XX OS Mus musculus.

XX Key Location/Qualifiers  
 FT Region 59..63  
 FT /note= "CDR H1"

FT Region 78..96

FT /note= "CDR H2"

FT Region 129..131

FT /note= "CDR H3"

XX WO9598679-A1.

XX XX

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001434.

XX PR 09-MAY-1998; 98GB-00009839.

XX XX

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI

XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX DR

XX WPI; 2000-053101/04.

XX N-PSDB; AAZ34745.

XX XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 PT XX

PS Claim 8; Fig 1; 81pp; English.

XX XX

CC This sequence represents the heavy chain variable region (VH) of murine  
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides  
 CC altered antibodies, such as chimeric or humanised antibodies (see  
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions (see AAY32254-59) to render them capable of binding to the CD23  
 CC type II molecule expressed on haematopoietic cells. The antibodies are  
 CC used to block soluble CD23 formation in human therapy, for the treatment

CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents  
 XX  
 SQ Sequence 137 AA;

Query Match 100.0%; Score 98; DB 3; Length 137;

Best Local Similarity 100.0%; Pred. No. 3.4e-08; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0;

QY 1 EIRLSDNYATHYAESVKG 19  
 DB 78 EIRLSDNYATHYAESVKG 96  
 |||||

## RESULT 6

AAB50426  
 ID AAB50426 standard; protein; 286 AA.

AC AAB50426;

DT 13-MAR-2001 (first entry)

DE Antibody 33F12 catalytic fragment.

KW Antibody 33F12; ketone compound; antitumour; cytotoxic;  
 KW targeted drug delivery.

XX Unidentified.

PN WO200071556-A1.

XX 30-NOV-2000.

PF 24-MAY-2000; 2000WO-US014366.

XX 25-MAY-1999; 99US-00318661.

XX (SCRI ) SCRIPPS RES INST.

XX Barbas CF, Shabat D, Rader C, List B, Lerner RA;

XX WPI; 2001-061339/07.

DR N-PSDB; AAC90472.

XX New ketone compounds containing active agents useful as carriers for e.g.  
 PT antitumor agents, antibiotics or fluorescent molecules.

XX Disclosure; Fig 10; 45pp; English.

XX The present sequence may be used in the activation of new ketone produg  
 CC compounds containing active agents. The ketone derivatives are useful as  
 CC carriers for antitumor agents such as cytotoxic agents, where the  
 CC antitumor agent is a microtubule stabilising agent such as paclitaxel,  
 CC epothilone or its therapeutically active analogue or an anthracycline  
 CC antibiotic such as doxorubicin or its therapeutically active analogue.  
 CC The ketone derivatives are useful for targeted drug delivery. The  
 CC inactive molecules in the ketone compounds are converted to active  
 CC molecules by retro-Michael reaction. The antibody has bifunctional  
 CC activity and specifically immunoreacts with cell surface antigen of a  
 CC target cell. The active ingredients can be mixed effectively with  
 CC excipients as per desired amount along with the buffering agent to  
 CC enhance the effectiveness and activity of the compound

XX Sequence 286 AA;

Query Match 100.0%; Score 98; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 8.2e-08;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19  
 DB 203 EIRLSDNYATHYAESVKG 221  
 |||||

## RESULT 7

AAAY32263  
 ID AAY32263 standard; protein; 444 AA.

XX AC AAY32263;

DT 15-FEB-2000 (first entry)

XX Humanised anti-CD23 MAb C11 heavy chain.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.

XX Homo sapiens.  
 OS Synthetic.

XX Key  
 FT Region

Location/Qualifiers  
 1..30  
 /note= "framework region 1"

31..35  
 /note= "CDR 1"

36..49  
 /note= "framework region 2"

50..68  
 /note= "CDR 2"

69..100  
 /note= "framework region 3"

101..103  
 /note= "CDR 3"

104..111  
 /note= "framework region 4"

112..444  
 /note= "constant region"

WO9958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX ) GLAXO GROUP LTD.

XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX N-PSDB; AAZ34748.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 XX diabetes, multiple sclerosis and psoriasis.

XX Claim 9; Fig 4; 81pp; English.

XX This amino acid sequence represents the heavy chain of humanised anti-  
 CC CD23 (FCERII) monoclonal antibody C11, composed of a human framework  
 CC (H5IGKVII) and the heavy chain complementarity determining regions (see

The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a

The invention relates to humanised immunoglobulin heavy and light chains which have specificity for the CC-chemokine receptor 2 (CCR2) and an

CC immunoglobulin or its antigen binding fragment comprising the chains. The  
 CC humanised immunoglobulin or its antigen binding fragment preferably  
 CC comprises two heavy chains and two light chains. The humanised  
 CC immunoglobulin and its heavy and light chains are useful for the  
 CC diagnosis, prevention and/or treatment of diseases or conditions  
 CC associated with aberrant expression or activity of the CCR2 polypeptide,  
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
 CC infection and atherosclerosis. This sequence represents a mouse  
 CC immunoglobulin protein of the invention.

XX SQ Sequence 100 AA;

Query Match 96.9%; Score 95; DB 8; Length 100;

Best Local Similarity 94.7%; Pred. No. 7.5e-08;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

Db 50 QIRLSDNYATHYAESVKG 68

RESULT 10

AAB50425

ID AAB50425 standard; protein; 299 AA.

AC AAB50425;

XX 13-MAR-2001 (first entry)

DT Mouse antibody 38C2 catalytic fragment.

DE Mouse; antibody 38C2; ketone compound; antitumour; cytotoxic;

KW targeted drug delivery.

XX Mus sp.

XX WO200071556-A1.

XX 30-NOV-2000.

XX 24-MAY-2000; 2000WO-US014366.

XX 25-MAY-1999; 99US-00318661.

XX (SCRI ) SCRIPPS RES INST.

XX Barbas CF, Shabat D, Rader C, List B, Lerner RA;

XX WPI; 2001-061339/07.

XX N-PSDB; AAC90471.

XX New ketone compounds containing active agents useful as carriers for e.g.

XX antitumor agents, antibiotics or fluorescent molecules.

XX Disclosure; Fig 9; 45pp; English.

XX The present sequence may be used in the activation of new ketone prodnug

XX compounds containing active agents. The ketone derivatives are useful as

XX carriers for antitumour agents such as cytotoxic agents, where the

XX antitumour agent is a microtubule stabilising agent such as paclitaxel,

XX epothilone or its therapeutically active analogue or an anthracycline

XX antibiotic such as doxorubicin or its therapeutically active analogue.

XX The ketone derivatives are useful for targeted drug delivery. The

XX inactive molecules in the ketone compounds are converted to active

XX molecules by retro-Michael reaction. The antibody has bifunctional

XX activity and specifically immunoreacts with cell surface antigen of a

XX target cell. The active ingredients can be mixed effectively with

XX excipients as per desired amount along with the buffering agent to

XX enhance the effectiveness and activity of the compound

XX SQ Sequence 299 AA;

Query Match 96.9%; Score 95; DB 4; Length 299;

Best Local Similarity 94.7%; Pred. No. 2.7e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

Db 205 EIRLSDNYATHYAESVKG 223

RESULT 11

AAR34018

ID AAR34018 standard; protein; 115 AA.

AC AAR34018;

XX 25-MAR-2003 (revised)

DT 02-AUG-1993 (first entry)

DE BW 835 VH.

XX Monoclonal antibody; Mab; hybridoma; lung; adenocarcinoma; mammary;

KW ovary; prostate; polymorphic epithelial mucin; PEM.

XX Synthetic.

OS DE4133791-A1.

XX 15-APR-1993.

XX 11-OCT-1991; 91DE-04133791.

XX 11-OCT-1991; 91DE-04133791.

XX (BEHW ) BEHRINGWERKE AG.

XX Bosslet K, Pfeleiderer P, Seemann G;

XX WPI; 1993-127068/16.

XX N-PSDB; AAQ40046.

XX New monoclonal antibody BW835 specific for tumour antigens - useful for

XX diagnosis and treatment of tumours affecting the breasts, ovaries,

XX prostate and lungs.

XX Disclosure; Fig 1a; 24pp; German.

XX Monoclonal antibody BW 835 is produced by hybridoma cell line BW 835. The

XX antibody strongly reacts with lung adenocarcinomas and human mammary-;

XX ovary- and prostate carcinomas. It additionally reacts with polymorphic

XX epithelial mucin (PEM) but does not react with normal human tissue.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 115 AA;

Query Match 94.9%; Score 93; DB 2; Length 115;

Best Local Similarity 94.7%; Pred. No. 1.9e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

Db 46 EIRLSDNYATHYAESVKG 64

RESULT 12

AAY03869

ID AAY03869 standard; protein; 116 AA.

AC AAY03869;

XX 16-JUN-1999 (first entry)

XX SM3 heavy chain variable region.

XX SM3 antibody; epitope; mimic; crystal; tumour; MUC1 epitope; allergy;

KW immune response; arthritis; multiple sclerosis; asthma; diabetes;  
 KW inflammatory disorder; transplant rejection; graft versus host disease.  
 XX Unidentified.  
 XX WO9910379-A1.  
 XX 04-MAR-1999.  
 XX 24-AUG-1998; 98WO-GB002542.  
 XX 22-AUG-1997; 97GB-00017946.  
 XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
 XX Freemont PS, Snary D, Sternberg MJE, Bates PA, Dokurno P;  
 XX WPI; 1999-204650/17.  
 XX N-PSDB; AAX31971.  
 XX New SM3 antibody crystal structures - used to develop agents for treating  
 PT e.g. tumors, autoimmune disorders, allergies, inflammatory disorders or  
 PT transplant rejection.  
 XX Disclosure; Page 279-280; 316pp; English.  
 CC The invention relates to a process for preparing a crystal using cadmium.  
 CC Structure factors or structural coordinates obtained from the crystal of  
 CC SM3 antibody bound to an epitope can be used to design mimics of the  
 CC antibody or the epitope. The crystals comprise at least an epitope  
 CC binding fragment of the SM3 antibody bound to a peptide recognised by the  
 CC epitope binding site of SM3. The products and methods can be used to  
 CC develop agents for the detection of tumour cells and for therapy against  
 CC tumours. MUC1 epitope mimics can also be used to prevent or decrease an  
 CC immune response, e.g. in the therapy of diseases caused by autoimmune  
 CC responses (such as arthritis, multiple sclerosis, asthma or diabetes),  
 CC allergies, inflammatory disorders or transplant rejections such as graft  
 CC versus host disease. The present sequence represents the amino acid  
 CC sequence of a heavy chain variable region of SM3 antibody  
 XX  
 SQ Sequence 116 AA;  
 Query Match 94.9%; Score 93; DB 2; Length 116;  
 Best Local Similarity 94.7%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EIRLKSDNYATHYAESVKG 19  
 DB 50 EIRLKSNYATHYAESVKG 68  
 RESULT 13  
 AAW46958  
 ID AAW46958 standard; protein; 119 AA.  
 XX AC AAW46958;  
 XX 06-JUL-1998 (first entry)  
 XX Amino acid sequence of a synthetic branched mucin type glycolipid.  
 DE Branched mucin type glycolipid; V region; heavy chain; antibody;  
 KW cancer treatment; diagnosis.  
 XX Synthetic.  
 OS  
 XX JP10084963-A.  
 XX 07-APR-1998.  
 XX 12-SEP-1996; 96JP-00241725.  
 XX 12-SEP-1996; 96JP-00241725.  
 PR

XX (TOYJ ) TOSOH CORP.  
 XX WPI; 1998-264850/24.  
 DR N-PSDB; AAV22331.  
 XX Recognising branched mucin type synthetic glycolipid - using gene  
 PT fragment of an antibody, useful in cancer treatment and diagnosis.  
 XX Disclosure; Page 4-5; 6pp; Japanese.  
 XX The present sequence represents a branched mucin type synthetic  
 CC glycolipid. A gene fragment encoding the V region of the heavy chain of  
 CC an antibody recognising the present protein is claimed. The antibody gene  
 CC fragment is useful for the development of cancer treatments and  
 CC diagnosing agents  
 XX  
 SQ Sequence 119 AA;  
 Query Match 94.9%; Score 93; DB 2; Length 119;  
 Best Local Similarity 94.7%; Pred. No. 2e-07;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EIRLKSDNYATHYAESVKG 19  
 DB 50 EIRLKSNYATHYAESVKG 68  
 RESULT 14  
 ABR82775  
 ID ABR82775 standard; protein; 119 AA.  
 XX AC ABR82775;  
 XX 18-DEC-2003 (first entry)  
 DE Hybridoma HB22-23 anti-CD22 MAb heavy chain Vh-D-Jh junction sequence.  
 XX CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-23.  
 XX Homo sapiens.  
 XX WO2003072036-A2.  
 XX 04-SEP-2003.  
 XX 20-FEB-2003; 2003WO-US005323.  
 XX 21-FEB-2002; 2002US-0359419P.  
 PR 21-OCT-2002; 2002US-0420472P.  
 XX (UYDU-) UNIV DUKE.  
 PA (REGC ) UNIV CALIFORNIA.  
 XX Tedder T, Tuscano J;  
 XX WPI; 2003-712652/67.  
 DR N-PSDB; ACF36425.  
 XX Treating a human patient diagnosed with a B-cell malignancy by  
 PT administering a blocking anti-CD22 monoclonal antibody binding to the  
 PT first two Ig-like domains of native human CD22 (hCD22).  
 XX Claim 31; Fig 14; 72pp; English.  
 XX The invention relates to treating a human patient diagnosed with a B-cell  
 CC malignancy. The method involves (a) administering to the human patient a  
 CC blocking anti-CD22 monoclonal antibody binding to the first two Ig-like  
 CC domains, or to an epitope within the first two Ig-like domains of native  
 CC human CD22 (hCD22) (ABR82771) and (b) monitoring the response of the  
 CC malignancy to the treatment. The method is useful for treating a human  
 CC patient diagnosed with a B-cell malignancy comprising Hodgkin's lymphoma,  
 CC Burkitt's lymphoma, multiple myeloma, chronic lymphocytic leukemia, hairy

Db 50 EIRLKSNNYATHYAESVKG 68  
Search completed: April 18, 2005, 14:15:21  
Job time : 202.163 secs

CC cell leukemia or polymphocytic leukemia. The present sequence represents  
CC the amino acid sequence for heavy chain Vh-D-Jh junction for anti-CD22  
CC antibody from hybridoma HB22-23  
XX  
SQ Sequence 119 AA;

Query Match 94.9%; Score 93; DB 7; Length 119;  
Best Local Similarity 94.7%; Pred. No. 2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19  
|||||:|||||  
DB 50 EIRLKSNNYATHYAESVKG 68

RESULT 15  
ABR82885  
ID ABR82885 standard; protein; 119 AA.  
XX  
AC ABR82885;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Hybridoma HB22-23 anti-CD22 Mab heavy chain (VH) fragment.  
XX  
KW CD22; autoimmune disease; anti-CD22 antibody; immunosuppressive;  
KW cytostatic; nephrotropic; dermatological; antiinflammatory; anti-ulcer;  
KW antirheumatic; antiarthritic; antipsoriatic; thyromimetic; antianemic;  
KW antidiabetic; antiallergic; gene therapy; HB22-23.  
XX  
OS Homo sapiens.

XX WO2003072736-A2.  
XX  
XX 04-SEP-2003.  
XX 21-FEB-2003; 2003WO-US005549.  
XX 21-FEB-2002; 2002US-0359419P.  
XX 21-OCT-2002; 2002US-0420472P.  
XX (UYDU-) UNIV DUKE.  
XX  
XX Tedder TF;  
XX  
XX WPI; 2003-721765/68.  
XX N-PSDB; ACF36493.  
XX  
XX Treating an autoimmune disease or a B-cell malignancy in a human patient  
XX comprises administering an amount of an anti-CD22 monoclonal antibody to  
XX the patient and monitoring the response of the disease to the treatment.  
XX  
XX Claim 1; Fig 14; 69pp; English.

XX The invention relates to treating a human patient diagnosed with an  
XX autoimmune disease. The method involves administering to the patient an  
XX amount of a blocking anti-CD22 monoclonal antibody and monitoring the  
XX response of the autoimmune disease to the treatment. The method is useful  
XX in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus  
XX erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis,  
XX Hashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or  
XX allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The  
XX present sequence represents the amino acid sequence for heavy chain Vh-D-  
XX Jh junction for anti-CD22 antibody from hybridoma HB22-23

XX Sequence 119 AA;  
XX  
XX Query Match 94.9%; Score 93; DB 7; Length 119;  
XX Best Local Similarity 94.7%; Pred. No. 2e-07;  
XX Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19  
|||||:|||||

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:22:17 ; Search time 143.605 Seconds  
(without alignments)  
43.975 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLKSNDNYATHYAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	123	14	US-10-160-506-69
2	98	100.0	123	16	US-10-449-379-69
3	98	100.0	123	16	US-10-688-015-69
4	98	100.0	285	9	US-09-883-758-4
5	95	96.9	100	9	US-09-840-459-36
6	95	96.9	100	16	US-10-766-773-36
7	95	96.9	100	16	US-10-766-610-36
8	95	96.9	100	16	US-10-733-563-36
9	95	96.9	298	9	US-09-883-758-2
10	93	94.9	119	15	US-10-372-481-15
11	93	94.9	119	15	US-10-371-797-15
12	93	94.9	122	17	US-10-879-994-66
13	93	94.9	255	15	US-10-239-656-69

14	93	94.9	256	15	US-10-239-656-61	Sequence 61, Appl
15	93	94.9	503	15	US-10-239-656-77	Sequence 77, Appl
16	91	92.9	19	16	US-10-769-308-32	Sequence 32, Appl
17	91	92.9	19	17	US-10-769-074-32	Sequence 32, Appl
18	91	92.9	151	9	US-09-564-329A-15	Sequence 15, Appl
19	91	92.9	151	9	US-09-855-153-15	Sequence 15, Appl
20	91	92.9	151	9	US-09-854-811-15	Sequence 15, Appl
21	91	92.9	151	9	US-09-934-773-15	Sequence 15, Appl
22	91	92.9	151	9	US-09-963-620-15	Sequence 15, Appl
23	91	92.9	151	10	US-09-855-632-15	Sequence 15, Appl
24	91	92.9	151	14	US-10-225-784-15	Sequence 15, Appl
25	91	92.9	151	14	US-10-224-720-15	Sequence 15, Appl
26	91	92.9	151	14	US-10-225-779-15	Sequence 15, Appl
27	91	92.9	151	15	US-10-374-381-15	Sequence 15, Appl
28	91	92.9	151	15	US-10-446-542-15	Sequence 15, Appl
29	91	92.9	151	16	US-10-769-308-27	Sequence 27, Appl
30	91	92.9	151	17	US-10-769-074-27	Sequence 27, Appl
31	90	91.8	123	14	US-10-160-506-70	Sequence 70, Appl
32	90	91.8	123	16	US-10-449-379-70	Sequence 70, Appl
33	90	91.8	123	16	US-10-688-015-70	Sequence 70, Appl
34	85	86.7	114	14	US-10-422-049-11	Sequence 11, Appl
35	85	86.7	114	14	US-10-422-049-12	Sequence 11, Appl
36	82	83.7	17	17	US-10-879-994-68	Sequence 68, Appl
37	82	83.7	117	14	US-10-277-471A-7	Sequence 7, Appl
38	82	83.7	262	14	US-10-277-471A-5	Sequence 5, Appl
39	79	80.6	19	14	US-10-160-506-30	Sequence 30, Appl
40	79	80.6	19	16	US-10-449-379-30	Sequence 30, Appl
41	79	80.6	19	16	US-10-688-015-30	Sequence 30, Appl
42	79	80.6	116	14	US-10-160-506-47	Sequence 47, Appl
43	79	80.6	116	14	US-10-160-506-49	Sequence 49, Appl
44	79	80.6	116	14	US-10-160-506-60	Sequence 60, Appl
45	79	80.6	116	14	US-10-160-506-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1  
US-10-160-506-69  
; Sequence 69, Application US/10160506  
; Publication No. US20030161832A1  
; GENERAL INFORMATION:  
; APPLICANT: Bander, Neil H.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR PROSTATE SPECIFIC MEMBRANE ANTIGEN  
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR PROSTATE SPECIFIC MEMBRANE ANTIGEN  
; FILE REFERENCE: 10448-162001  
; CURRENT APPLICATION NUMBER: US/10/160,506  
; CURRENT FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/324,100  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/362,612  
; PRIOR FILING DATE: 2002-03-08  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-160-506-69

Query Match 100.0%; Score 98; DB 14; Length 123;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
|||||  
Db 50 EIRLKSNDNYATHYAESVKG 68

RESULT 2  
US-10-449-379-69  
; Sequence 69, Application US/10449379

; Publication No. US20040120958A1  
; GENERAL INFORMATION:  
; APPLICANT: Bander, Neil H.  
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC  
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 10448-163002  
; CURRENT APPLICATION NUMBER: US/10/449,379  
; CURRENT FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: 10/160,505  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/323,585  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/362,810  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/295,214  
; PRIOR FILING DATE: 2001-06-01  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-10-449-379-69

Query Match 100.0%; Score 98; DB 16; Length 123;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
Db 50 EIRLKSNDNYATHYAESVKG 68  
|||||

RESULT 3  
US-10-688-015-69  
; Sequence 69, Application US/10688015  
; Publication No. US20040136998A1  
; GENERAL INFORMATION:  
; APPLICANT: Bander, Neil H.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING  
; TITLE OF INVENTION: INSULIN-RELATED DISORDERS USING BINDING AGENTS SPECIFIC FOR  
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN  
; FILE REFERENCE: 10448-196001  
; CURRENT APPLICATION NUMBER: US/10/688,015  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/422,396  
; PRIOR FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-10-688-015-69

Query Match 100.0%; Score 98; DB 16; Length 123;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
Db 50 EIRLKSNDNYATHYAESVKG 68  
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RESULT 4  
US-09-883-758-4  
; Sequence 4, Application US/09883758  
; Patent No. US20020058804A1  
; GENERAL INFORMATION:  
; APPLICANT: Barbas III, Carlos F.  
; APPLICANT: Shabat, Doron  
; APPLICANT: Rader, Christoph  
; APPLICANT: List, Benjamin

; APPLICANT: Lerner, Richard A.  
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
; FILE REFERENCE: PLF00115  
; CURRENT APPLICATION NUMBER: US/09/883,758  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US/09/318,661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 285  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
; OTHER INFORMATION: residue sequence of catalytic fragment  
; US-09-883-758-4

Query Match 100.0%; Score 98; DB 9; Length 285;  
Best Local Similarity 100.0%; Pred. No. 3.1e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
Db 203 EIRLKSNDNYATHYAESVKG 221  
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RESULT 5  
US-09-840-459-36  
; Sequence 36, Application US/09840459  
; Patent No. US20020150576A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-840-459-36

Query Match 96.9%; Score 95; DB 9; Length 100;  
Best Local Similarity 94.7%; Pred. No. 2.9e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
Db 50 EIRLKSNDNYATHYAESVKG 68  
:|||||

RESULT 6  
US-10-766-773-36  
; Sequence 36, Application US/10766773  
; Publication No. US20040126851A1  
; GENERAL INFORMATION:



APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 1855.1052-028  
CURRENT APPLICATION NUMBER: US/10/766,773  
CURRENT FILING DATE: 2004-01-27  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 36  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-766-773-36

Query Match 96.9%; Score 95; DB 16; Length 100;  
Best Local Similarity 94.7%; Pred. No. 2.9e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDYATHYAESVKG 19  
DB 50 QIRLKSNDYATHYAESVKG 68

RESULT 7  
US-10-766-610-36  
Sequence 36, Application US/10766610  
Publication No. US20040132980A1  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 1855.1052-029  
CURRENT APPLICATION NUMBER: US/10/766,610  
CURRENT FILING DATE: 2004-01-27  
PRIOR APPLICATION NUMBER: 09/840,459  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 36  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-766-610-36

Query Match 96.9%; Score 95; DB 16; Length 100;  
Best Local Similarity 94.7%; Pred. No. 2.9e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDYATHYAESVKG 19

DB 50 QIRLKSNDYATHYAESVKG 68

RESULT 8  
US-10-733-563-36  
Sequence 36, Application US/10733563  
Publication No. US20040151721A1  
GENERAL INFORMATION:  
APPLICANT: O'Keefe, Theresa  
APPLICANT: Ponath, Paul  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 10448-213001  
CURRENT APPLICATION NUMBER: US/10/733,563  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: US 10/272,899  
PRIOR FILING DATE: 2002-10-17  
PRIOR APPLICATION NUMBER: US 60/392,364  
PRIOR FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: US 60/350,166  
PRIOR FILING DATE: 2001-10-19  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 36  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-733-563-36

Query Match 96.9%; Score 95; DB 16; Length 100;  
Best Local Similarity 94.7%; Pred. No. 2.9e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDYATHYAESVKG 19  
DB 50 QIRLKSNDYATHYAESVKG 68

RESULT 9  
US-09-883-758-2  
Sequence 2, Application US/09883758  
Patent No. US20020058804A1  
GENERAL INFORMATION:  
APPLICANT: Barbas III, Carlos F.  
APPLICANT: Shabat, Doron  
APPLICANT: Rader, Christoph  
APPLICANT: List, Benjamin  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
FILE REFERENCE: PLF00115  
CURRENT APPLICATION NUMBER: US/09/883,758  
CURRENT FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: US/09/318,661  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-883-758-2

Query Match 96.9%; Score 95; DB 9; Length 298;  
Best Local Similarity 94.7%; Pred. No. 9.6e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDYATHYAESVKG 19  
DB 205 EIRLKSNDYATHYAESVKG 223

RESULT 10

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US-10-372-481-15
; Sequence 15, Application US/10372481
; Publication No. US20030202975A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405,306
; CURRENT APPLICATION NUMBER: US/10/372,481
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-372-481-15
Query Match          94.9%; Score 93; DB 15; Length 119;
Best Local Similarity 94.7%; Pred. No. 7.3e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSNYYATHYAESVKG 68
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RESULT 11
US-10-371-797-15
; Sequence 15, Application US/10371797
; Publication No. US20040001828A1
; GENERAL INFORMATION:
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 119
; TYPE: PRT
; ORGANISM: homo sapiens
;
US-10-371-797-15
Query Match          94.9%; Score 93; DB 15; Length 119;
Best Local Similarity 94.7%; Pred. No. 7.3e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSNYYATHYAESVKG 68
|||||:|||||

RESULT 12
US-10-879-994-66
; Sequence 66, Application US/10879994
; Publication No. US20050032175A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; APPLICANT: KUFER, PETER
```

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; APPLICANT: Katow, Margaret
; APPLICANT: Smith, Eric
; TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC METH
; TITLE OF INVENTION: USE
; FILE REFERENCE: REG 203E2
; CURRENT APPLICATION NUMBER: US/10/879,994
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/610,452
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 122
; TYPE: PRT
; ORGANISM: mus musculus
;
US-10-879-994-66
Query Match          94.9%; Score 93; DB 17; Length 122;
Best Local Similarity 94.7%; Pred. No. 7.5e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSNYYATHYAESVKG 68
|||||:|||||

RESULT 13
US-10-239-656-69
; Sequence 69, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HORMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-11 single
; OTHER INFORMATION: chain Fv
;
US-10-239-656-69
Query Match          94.9%; Score 93; DB 15; Length 255;
Best Local Similarity 94.7%; Pred. No. 1.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 51 EIRKSNYYATHYAESVKG 69
|||||:|||||

RESULT 14
US-10-239-656-61
; Sequence 61, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
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Db 298 EIRLKSNNYATHYAESVKG 316  
Search completed: April 18, 2005, 14:54:43  
Job time : 144.605 secs

APPLICANT: RIETHMULLER, GERT  
APPLICANT: LUTTERBUSE, RALF  
APPLICANT: BORSCHERT, KATRIN  
APPLICANT: KISCHEL, ROMAN  
APPLICANT: MAYER, MONIKA  
APPLICANT: HOFMEISTER, ROBERT  
TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE  
FILE REFERENCE: 029776/0106  
CURRENT APPLICATION NUMBER: US/10/239,656  
CURRENT FILING DATE: 2003-03-06  
PRIOR APPLICATION NUMBER: PCT/EP01/03414  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: EP 00106467.4  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 61  
LENGTH: 256  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-2 single chain Fv  
US-10-239-656-61

Query Match 94.9%; Score 93; DB 15; Length 256;  
Best Local Similarity 94.7%; Pred. No. 1.7e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19  
|||||:|||||  
Db 51 EIRLKSNNYATHYAESVKG 69

RESULT 15  
US-10-239-656-77  
Sequence 77, Application US/10239656  
Publication No. US20040038339A1  
GENERAL INFORMATION:  
APPLICANT: KUPER, PETER  
APPLICANT: RIETHMULLER, GERT  
APPLICANT: LUTTERBUSE, RALF  
APPLICANT: BORSCHERT, KATRIN  
APPLICANT: KISCHEL, ROMAN  
APPLICANT: MAYER, MONIKA  
APPLICANT: HOFMEISTER, ROBERT  
TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE  
FILE REFERENCE: 029776/0106  
CURRENT APPLICATION NUMBER: US/10/239,656  
CURRENT FILING DATE: 2003-03-06  
PRIOR APPLICATION NUMBER: PCT/EP01/03414  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: EP 00106467.4  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 77  
LENGTH: 503  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic 3B10XP5-2 bispecific single chain Fv  
US-10-239-656-77

Query Match 94.9%; Score 93; DB 15; Length 503;  
Best Local Similarity 94.7%; Pred. No. 3.5e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19  
|||||:|||||

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:01:43 ; Search time 51.6977 Seconds  
(without alignments)  
27.435 Million cell updates/sec

**Title:** US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLKSDNYATHYAESVKG 19

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scoring cable: 25030M02  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs. 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum Match 100%  
Listing first 45 summaries

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2: /cqn2_6/ptodata/1/1aa/5B_COMB.per.*
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3: /cqn2_6/ptodata/1/iaa/6A_COMB.pcp:

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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	98	100.0	285	3	US-09-318-661-4	Sequence 4, Appli
2	98	100.0	285	4	US-09-883-758-4	Sequence 4, Appli
3	95	96.9	100	4	US-09-840-459-36	Sequence 36, Appl
4	95	96.9	100	4	US-09-497-625A-36	Sequence 36, Appl
5	95	96.9	298	3	US-09-318-661-2	Sequence 2, Appli
6	95	96.9	298	4	US-09-883-758-2	Sequence 2, Appli
7	93	94.9	115	1	US-08-468-661-1	Sequence 1, Appli
8	93	94.9	115	1	US-08-466-272A-1	Sequence 1, Appli
9	93	94.9	115	1	US-08-478-877-1	Sequence 1, Appli
10	93	94.9	115	2	US-08-471-771-1	Sequence 1, Appli
11	93	94.9	115	3	US-09-130-783-1	Sequence 1, Appli
12	93	94.9	120	3	US-08-767-128-28	Sequence 28, Appl
13	93	94.9	122	3	US-08-483-749A-2	Sequence 2, Appli
14	91	92.9	151	4	US-09-564-329A-15	Sequence 15, Appl
15	91	92.9	151	4	US-09-963-620-15	Sequence 15, Appl
16	91	92.9	151	4	US-09-855-632-15	Sequence 15, Appl
17	91	92.9	151	4	US-09-934-773-15	Sequence 15, Appl
18	85	86.7	114	3	US-08-483-749A-10	Sequence 10, Appl
19	80.5	82.1	119	3	US-08-767-128-26	Sequence 26, Appl
20	74	75.5	119	1	US-08-192-103-5	Sequence 5, Appli
21	74	75.5	119	1	US-08-324-799-5	Sequence 5, Appli
22	74	75.5	119	2	US-08-192-861A-5	Sequence 5, Appli
23	74	75.5	119	3	US-09-133-119-5	Sequence 5, Appli
24	74	75.5	119	3	US-08-192-093A-5	Sequence 5, Appli
25	74	75.5	119	4	US-09-756-301B-5	Sequence 5, Appli
26	74	75.5	119	4	US-09-756-398B-5	Sequence 5, Appli
27	72	73.5	119	1	US-08-442-542-45	Sequence 45, Appl

## ALIGNMENTS

## RESULT 1

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US-09-318-661-4
; Sequence 4, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING C
; FILE REFERENCE: PLF00118
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial S
; OTHER INFORMATION: residue sequence of catalyt
US-09-318-661-4

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Query Match      100.0%; Score 98; DB 3; Length 285;
Best Local Similarity 100.0%; Pred. No. 5.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 EIRLKSDNYATHAESVKG 19  
Db 203 EIRLKSDNYATHAESVKG 221

## RESULT 2

RESOLUT 2  
US-09-883-758-4  
; Sequence 4, Application US/09883758  
; Patent No. 6677435  
; GENERAL INFORMATION:  
; APPLICANT: Barbas III, Carlos F.  
; APPLICANT: Shabat, Doron  
; APPLICANT: Rader, Christoph  
; APPLICANT: List, Benjamin  
; APPLICANT: Leiner, Richard A.  
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES  
; FILE REFERENCE: PLF00115  
; CURRENT APPLICATION NUMBER: US/09/883,758  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US/09/318,661  
; PRIOR FILING DATE: 1999-05-25

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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment
US-09-883-758-4

Query Match          100.0%; Score 98; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 5.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIRLKSNDNYATHYAESVKG 19
Db      203 EIRLKSNDNYATHYAESVKG 221

RESULT 3
US-09-840-459-36
; Sequence 36, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-36

Query Match          96.9%; Score 95; DB 4; Length 100;
Best Local Similarity 94.7%; Pred. No. 5e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIRLKSNDNYATHYAESVKG 19
Db      50 QIRLKSNDNYATHYAESVKG 68

RESULT 4
US-09-497-625A-36
; Sequence 36, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
```

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; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-36

Query Match          96.9%; Score 95; DB 4; Length 100;
Best Local Similarity 94.7%; Pred. No. 5e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIRLKSNDNYATHYAESVKG 19
Db      50 QIRLKSNDNYATHYAESVKG 68

RESULT 5
US-09-318-661-2
; Sequence 2, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-318-661-2

Query Match          96.9%; Score 95; DB 3; Length 298;
Best Local Similarity 94.7%; Pred. No. 1.7e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIRLKSNDNYATHYAESVKG 19
Db      205 EIRLKSNDNYATHYAESVKG 223

RESULT 6
US-09-883-758-2
; Sequence 2, Application US/09883758
; Patent No. 6677435
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
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; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-883-758-2

Query Match 96.9%; Score 95; DB 4; Length 298;  
Best Local Similarity 94.7%; Pred. No. 1.7e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19  
|||||:|||||  
Db 205 EIRLSDNYATHYAESVKG 223

## RESULT 7

US-08-468-661-1  
; Sequence 1, Application US/08468661  
; Patent No. 5639621  
; GENERAL INFORMATION:  
; APPLICANT: Bosslet, Klaus  
; APPLICANT: Pfeleiderer, Peter  
; APPLICANT: Seeman, Gerhard  
; TITLE OF INVENTION: Monoclonal Antibodies Against  
; TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the  
; TITLE OF INVENTION: Preparation Thereof and the Use Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,661  
; FILING DATE: 06-JUNE-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/957,827  
; FILING DATE: 08-OCT-1992  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Forman, David S.  
; REGISTRATION NUMBER: 35,694  
; REFERENCE/DOCKET NUMBER: 05552-1227-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 115 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-468-661-1

Query Match 94.9%; Score 93; DB 1; Length 115;  
Best Local Similarity 94.7%; Pred. No. 1.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19  
|||||:|||||  
Db 46 EIRLSDNYATHYAESVKG 64

## RESULT 8

US-08-466-272A-1  
; Sequence 1, Application US/08466272A  
; Patent No. 5674994  
; GENERAL INFORMATION:  
; APPLICANT: Bosslet, Klaus  
; APPLICANT: Pfeleiderer, Peter  
; APPLICANT: Seeman, Gerhard  
; TITLE OF INVENTION: Monoclonal Antibodies Against  
; TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the Preparation  
; TITLE OF INVENTION: Thereof and the Use Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,272A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/957,827  
; FILING DATE: 08-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bugalsky, Lawrence B.  
; REGISTRATION NUMBER: 35,086  
; REFERENCE/DOCKET NUMBER: 02481-1227-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 115 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-466-272A-1

Query Match 94.9%; Score 93; DB 1; Length 115;  
Best Local Similarity 94.7%; Pred. No. 1.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19  
|||||:|||||  
Db 46 EIRLSDNYATHYAESVKG 64

## RESULT 9

US-08-478-857-1  
; Sequence 1, Application US/08478857  
; Patent No. 5695758  
; GENERAL INFORMATION:  
; APPLICANT: Bosslet, Klaus  
; APPLICANT: Pfeleiderer, Peter  
; APPLICANT: Seeman, Gerhard  
; TITLE OF INVENTION: Monoclonal Antibodies Against  
; TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the Preparation  
; TITLE OF INVENTION: Thereof and the Use Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington

STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,857  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/957,827  
FILING DATE: 08-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 02481-1227-00000  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-478-857-1

Query Match 94.9%; Score 93; DB 1; Length 115;  
Best Local Similarity 94.7%; Pred. No. 1.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHVAESVKG 19  
Db 46 EIRKSNYYATHVAESVKG 64

RESULT 10  
US-08-471-771-1  
Sequence 1, Application US/08471771  
Patent No. 5837824  
GENERAL INFORMATION:  
APPLICANT: Bossett, Klaus  
APPLICANT: Pfeleiderer, Peter  
APPLICANT: Seeman, Gerhard  
TITLE OF INVENTION: Monoclonal Antibodies Against  
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the  
TITLE OF INVENTION: Preparation Thereof and the Use Thereof  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,771  
FILING DATE: 06-JUNE-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/957,827  
FILING DATE: 08-OCT-1992  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:

NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 05552-1227-01000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-471-771-1

Query Match 94.9%; Score 93; DB 2; Length 115;  
Best Local Similarity 94.7%; Pred. No. 1.2e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHVAESVKG 19  
Db 46 EIRKSNYYATHVAESVKG 64

RESULT 11  
US-09-130-783-1  
Sequence 1, Application US/09130783  
Patent No. 6030797  
GENERAL INFORMATION:  
APPLICANT: Bossett, Klaus  
APPLICANT: Pfeleiderer, Peter  
APPLICANT: Seeman, Gerhard  
TITLE OF INVENTION: Monoclonal Antibodies Against  
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the  
TITLE OF INVENTION: Preparation Thereof and the Use Thereof  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/130,783  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/471,771  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 05552-1227-01000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-130-783-1

Query Match 94.9%; Score 93; DB 3; Length 115;  
Best Local Similarity 94.7%; Pred. No. 1.2e-07;



Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
|||||:|||||  
Db 46 EIRLKSNNYATHYAESVKG 64

RESULT 12  
US-08-767-128-28  
; Sequence 28, Application US/08767128  
; Patent No. 6111079  
; GENERAL INFORMATION:  
; APPLICANT: WYLIE, DWANE E.  
; APPLICANT: LOPEZ, OSVALDO  
; APPLICANT: MURRAY, PETER JOSEPH  
; APPLICANT: GOEBEL, PETER  
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND  
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 3100 No. 6111079west Center, 90 South Seventh St  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/767,128  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 04-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/09258  
; FILING DATE: 05-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/541,373  
; FILING DATE: 10-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/462,798  
; FILING DATE: 05-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.49USF1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/371-5278  
; TELEFAX: 612/332-9081  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-767-128-28

Query Match 94.9%; Score 93; DB 3; Length 120;  
Best Local Similarity 94.7%; Pred. No. 1.3e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
|||||:|||||  
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 13  
US-08-483-749A-2  
; Sequence 2, Application US/08483749A  
; Patent No. 6054561  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
; CITY: EMERYVILLE  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,749A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL B.  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0508.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-749A-2

Query Match 94.9%; Score 93; DB 3; Length 122;  
Best Local Similarity 94.7%; Pred. No. 1.3e-07;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19  
|||||:|||||  
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 14  
US-09-564-329A-15  
; Sequence 15, Application US/09564329A  
; Patent No. 6541212  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 30435.54US14  
; CURRENT APPLICATION NUMBER: US/09/564,329A  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/359,326  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: 60/074,675

Tue Apr 19 06:14:46 2005

ORGANISM: SCID Mice  
US-09-963-620-15  
Query Match 92.9%; Score 91; DB 4; Length 151;  
Best Local Similarity 89.5%; Pred. No. 3.5e-07;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EIRLKSNDNYATHYAESVKG 19  
Db 69 EIRLRSENYATHYAESVKG 87  
Search completed: April 18, 2005, 14:25:39  
Job time : 59.6977 secs

PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: 60/113,230  
PRIOR FILING DATE: 1998-12-21  
PRIOR APPLICATION NUMBER: 60/120,536  
PRIOR FILING DATE: 1999-02-17  
PRIOR APPLICATION NUMBER: 60/124,658  
PRIOR FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 09/038,261  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 09/203,939  
PRIOR FILING DATE: 1998-12-02  
PRIOR APPLICATION NUMBER: 09/251,835  
PRIOR FILING DATE: 1999-02-17  
PRIOR APPLICATION NUMBER: 09/308,503  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 151  
TYPE: PRT  
ORGANISM: SCID Mice  
US-09-564-329A-15

Query Match 92.9%; Score 91; DB 4; Length 151;  
Best Local Similarity 89.5%; Pred. No. 3.5e-07;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLKSNDNYATHYAESVKG 19  
Db 69 EIRLRSENYATHYAESVKG 87

RESULT 15  
US-09-963-620-15  
Sequence 15, Application US/09963620  
Patent No. 6756036  
GENERAL INFORMATION:  
APPLICANT: Reiter, Robert E.  
APPLICANT: Witte, Owen N.  
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF  
FILE REFERENCE: 30435.54US14  
CURRENT APPLICATION NUMBER: US/09/963,620  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 09/564,329  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 09/359,326  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 08/814,279  
PRIOR FILING DATE: 1997-03-10  
PRIOR APPLICATION NUMBER: 60/071,141  
PRIOR FILING DATE: 1998-01-12  
PRIOR APPLICATION NUMBER: 60/074,675  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: 60/113,230  
PRIOR FILING DATE: 1998-12-21  
PRIOR APPLICATION NUMBER: 60/120,536  
PRIOR FILING DATE: 1999-02-17  
PRIOR APPLICATION NUMBER: 60/124,658  
PRIOR FILING DATE: 1999-03-16  
PRIOR APPLICATION NUMBER: 09/038,261  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 09/203,939  
PRIOR FILING DATE: 1998-12-02  
PRIOR APPLICATION NUMBER: 09/251,835  
PRIOR FILING DATE: 1999-02-17  
PRIOR APPLICATION NUMBER: 09/308,503  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 151  
TYPE: PRT

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:48:01 ; Search time 44 Seconds  
(without alignments)  
41.548 Million cell updates/sec

Title: US-09-674-716B-11  
Perfect score: 98  
Sequence: 1 EIRLKSNDNYATHYAESVKG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3436

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26.5	27.0	16	2 A39109	hypothetical prote
2	25	25.5	10	2 S77990	cytochrome-c oxida
3	24	24.5	19	2 S39387	protein kinase GSK
4	23	23.5	15	2 PH1631	Ig H chain V-D-J r
5	23	23.5	16	2 B60278	24K antigen - Myco
6	22	22.4	10	2 D46285	formaldehyde dehyd
7	22	22.4	14	2 S59495	formate dehydrogen
8	22	22.4	15	2 PA0046	protein OA100044
9	22	22.4	15	2 I67325	CD33 antigen homol
10	22	22.4	18	2 F49215	urease (EC 3.5.1.5
11	22	22.4	18	2 PQ0072	T-cell receptor be
12	22	22.4	19	2 A41077	protein-disulfide
13	21	21.4	9	2 B24362	chloramphenicol O-
14	21	21.4	9	2 S30494	cat gene leader pe
15	21	21.4	12	2 PH1587	Ig H chain V-D-J r
16	21	21.4	14	2 PH1471	T-cell receptor be
17	21	21.4	16	2 A29520	amino-acid racemas
18	21	21.4	17	2 A61334	trypsin (EC 3.4.21
19	21	21.4	17	2 PH0768	T-cell receptor be
20	21	21.4	18	4 I56393	lacZ/IS1 mutant fu
21	20	20.4	9	2 PT0238	Ig heavy chain CRD
22	20	20.4	10	2 S65388	cytochrome-c oxida
23	20	20.4	11	2 PT0301	Ig heavy chain CRD
24	20	20.4	12	2 S26546	T-cell receptor be
25	20	20.4	12	4 PC2122	aminotransferase c
26	20	20.4	13	2 PH1595	Ig H chain V-D-J r
27	20	20.4	14	2 A47421	leukotriene B-4 12
28	20	20.4	15	2 I78838	flt3 ligand isofor
29	20	20.4	15	2 A30330	neuropeptide pep -

ribulose-bisphosph  
hypothetical prote  
Ig H chain V-D-J r  
Ig H chain V-D-J r  
hypothetical prote  
Ig H chain V-D-J r  
Tha p 1 - Thaumeto  
26K kidney and gal  
leucosulfakinin-II  
leucosulfakinin II  
ranatachykinin B -  
hypothetical prote  
hypothetical prote  
Ig gamma-2b chain  
proteinase E - bla  
serine proteinase

#### ALIGNMENTS

##### RESULT 1

A39109 hypothetical protein 1 - hepatitis C virus

C;Species: hepatitis C virus  
C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 18-Jun-1993

C;Accession: A39109

R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp

Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identificat

A;Reference number: A39109; MUID:91156678; PMID:1705704

A;Accession: A39109

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-16 <HAN>

A;Cross-references: GB:M58406

Query Match 27.0%; Score 26.5; DB 2; Length 16;

Best Local Similarity 70.0%; Pred. No. 5e+02;

Matches 7; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 8 NYATHYAESV 17

Db 8 NYCLH-AESV 16

##### RESULT 2

S77990

cytochrome-c oxidase (EC 1.9.3.1) chain VIIc - bigeye tuna (fragment)

C;Species: Thunnus obesus (bigeye tuna)

C;Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C;Accession: S77990

R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A;Reference number: S77980

A;Accession: S77990

A;Molecule type: protein

A;Residues: 1-10 <ARN>

A;Cross-references: UNIPROT:P80982

A;Experimental source: heart; liver

C;Genetics:

A;Genome: nuclear

A;Function: oxidative phosphorylation; respiratory chain

C;Keyword: electron transfer; membrane-associated complex; mitochondrial inner membran

Query Match 25.5%; Score 25; DB 2; Length 10;

Best Local Similarity 80.0%; Pred. No. 5.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 THYAE 15

Db 1 SHYAE 5

## RESULT 3

S39387  
 protein kinase GSK-3-beta (EC 2.7.1.1) - rabbit (fragment)  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 19-May-1994 #sequence\_revision 26-Jul-1996 #text\_change 07-May-1999  
 C;Accession: S39387  
 R;Sutherland, C.; Leighton, I.A.; Cohen, P.  
 Biochem. J. 296, 15-19, 1993  
 A;Title: Inactivation of glycogen synthase kinase-3-beta by phosphorylation: new kinase  
 A;Reference number: S39387; MUID:94071817; PMID:8250835  
 A;Accession: S39387  
 A;Molecule type: protein  
 A;Residues: 1-19 <SUT>  
 C;Superfamily: Kinase-related transforming protein; protein kinase homology  
 C;Keywords: phosphotransferase; protein kinase

Query Match 24.5%; Score 24; DB 2; Length 19;  
 Best Local Similarity 62.5%; Pred. No. 1.6e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 THYAESVK 18  
 | : || |  
 DB 2 TSFAESXK 9

## RESULT 4

PH1631  
 IG H chain V-D-J region (clone B-less 202) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C;Accession: PH1631  
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A;Reference number: PH1580; MUID:93301609; PMID:8315387  
 A;Accession: PH1631  
 A;Molecule type: DNA  
 A;Residues: 1-15 <LEV>  
 A;Experimental source: bone marrow pre-B lymphocyte  
 C;Keywords: immunoglobulin

Query Match 23.5%; Score 23; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 SDNYATHY 13  
 | : || |  
 DB 8 TDGYAMDY 15

## RESULT 5

B60278  
 24K antigen - Mycobacterium bovis (fragment)  
 C;Species: Mycobacterium bovis  
 C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 09-Jul-2004  
 C;Accession: B60278  
 R;Fifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.  
 Infect. Immun. 59, 800-807, 1991  
 A;Title: Purification and characterization of major antigens from a Mycobacterium bovis  
 A;Reference number: A60278; MUID:91147217; PMID:1900061  
 A;Accession: B60278  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-16 <FIF>  
 A;Cross-references: UNIPROT:Q7M199

Query Match 23.5%; Score 23; DB 2; Length 16;  
 Best Local Similarity 57.1%; Pred. No. 1.9e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 YAESVKG 19

DB 5 YKELKG 11  
 | : || |

## RESULT 6

D46285  
 formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) class III low activity form - Atla  
 C;Species: Gadus morhua (Atlantic cod)  
 C;Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C;Accession: D46285  
 R;Danielsson, O.; Jornvall, H.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 9247-9251, 1992  
 A;Title: "Enzymogenesis": classical liver alcohol dehydrogenase origin from the glutathi  
 A;Reference number: A46285; MUID:93028441; PMID:1409630  
 A;Accession: D46285  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <DAN>  
 A;Cross-references: UNIPROT:Q9PSQ8  
 A;Note: sequence extracted from NCBI backbone (NCBIP:116272)  
 C;Keywords: NAD; oxidoreductase

Query Match 22.4%; Score 22; DB 2; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 DNYATH 12  
 | : || |  
 DB 1 DEFVTH 6

## RESULT 7

S59495  
 formate dehydrogenase delta chain - Alcaligenes eutrophus (fragment)  
 C;Species: Alcaligenes eutrophus  
 C;Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: S59495  
 R;Friedebold, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowien, B.  
 Biol. Chem. Hoppe-Seyler 376, 561-568, 1995  
 A;Title: Structural and immunological studies on the soluble formate dehydrogenase from  
 A;Reference number: S59492; MUID:96145736; PMID:8561915  
 A;Accession: S59495  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-14 <FRI>  
 A;Cross-references: UNIPROT:Q7M0N7

Query Match 22.4%; Score 22; DB 2; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 LKSDNYATH 12  
 | : || |  
 DB 1 MKIDNIITY 9

## RESULT 8

PA0046  
 protein QA100044 - Arabidopsis thaliana (fragment)  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
 C;Accession: PA0046; PA0042  
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Teugita, A.  
 submitted to JIPID, July 1994  
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional  
 A;Reference number: PA0001  
 A;Accession: PA0046  
 A;Molecule type: protein  
 A;Residues: 1-15 <KAM>  
 A;Experimental source: stem

Query Match 22.4%; Score 22; DB 2; Length 15;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 AESVKG 19  
|||  
Db 1 AESKKG 6

## RESULT 9

I67525  
CD33 antigen homolog - mouse (fragment)  
C;Species: Mus sp. (mouse)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I67525  
R;Chies, J.A.; Lembezat, M.P.; Freitas, A.A.  
Eur. J. Immunol. 24, 1657-1664, 1994  
A;Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is regulated by CD33  
A;Reference number: I53392; MUID:94298870; PMID:8026526  
A;Accession: I67525  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-15 <RES>  
A;Cross-references: UNIPROT:Q7M0G8; GB:S71349; NID:G550037  
C;Genetics:  
A;Gene: I9 VH7183

Query Match 22.4%; Score 22; DB 2; Length 15;  
Best Local Similarity 33.3%; Pred. No. 2.5e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 KSDNYATHY 13  
:|:|:  
Db 4 RRDHYGSSY 12

## RESULT 10

F49215  
urease (EC 3.5.1.5) small chain UreA - Helicobacter mustelae (ATCC 43772) (fragment)  
C;Species: Helicobacter mustelae  
C;Date: 19-Dec-1993 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: F49215  
R;Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.  
Infect. Immun. 60, 5259-5266, 1992  
A;Title: Purification and characterization of the urease enzymes of Helicobacter species  
A;Reference number: A49215; MUID:93084378; PMID:1452359  
A;Cross-references: UNIPROT:Q9R5F6  
A;Note: sequence extracted from NCBI backbone (NCBIP:119487)  
C;Superfamily: urease, fused gamma/beta subunit; urease 11K chain homology; urease 12K chain homology  
C;Keywords: hydrolase

Query Match 22.4%; Score 22; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 3.1e+03;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 DNVATHYA 14  
|  
Db 7 DKMMLHYA 14

## RESULT 11

PQ0072  
T-cell receptor beta chain (BTB98) - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Feb-1995  
C;Accession: PQ0072  
R;Tanaka, A.; Ishiguro, N.; Shinagawa, M.  
submitted to JIPID, May 1990  
A;Description: Sequence analysis of bovine T-cell receptor beta chain genes.  
A;Reference number: JQ0472  
A;Accession: PQ0072

A;Molecule type: mRNA  
A;Residues: 1-18 <TAN>  
A;Experimental source: T cell  
C;Genetics:  
A;Gene: BTB98  
C;Keywords: receptor

Query Match 22.4%; Score 22; DB 2; Length 18;  
Best Local Similarity 38.5%; Pred. No. 3.1e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 6 SDNYATHYAESVK 18  
|||  
Db 4 SDDY--HFGPGTK 14

## RESULT 12

A41077  
protein-disulfide reductase (glutathione) (EC 1.8.4.2) Q-5 - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 23-Jun-1993  
C;Accession: A41077  
R;Srivastava, S.P.; Chen, N.; Liu, Y.; Holtzman, J.L.  
J. Biol. Chem. 266, 20337-20344, 1991  
A;Title: Purification and characterization of a new isozyme of thiol:protein-disulfide isomerase from rat liver  
A;Reference number: A41077; MUID:92041865; PMID:1657921  
A;Accession: A41077  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <SRI>  
C;Keywords: oxidoreductase

Query Match 22.4%; Score 22; DB 2; Length 19;  
Best Local Similarity 57.1%; Pred. No. 3.3e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LKSDNYVA 10  
|||  
Db 12 LKKSNEFA 18

## RESULT 13

B24362  
chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus plasmid pUB1  
C;Species: Staphylococcus aureus  
C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C;Accession: B24362  
R;Bruckner, R.; Matzura, H.  
EMBO J. 4, 2295-2300, 1985  
A;Title: Regulation of the inducible chloramphenicol acetyltransferase gene of the Staphylococcus aureus plasmid pUB1  
A;Reference number: A24362; MUID:86081739; PMID:3865770  
A;Accession: B24362  
A;Molecule type: DNA  
A;Residues: 1-9 <BRU>  
A;Cross-references: UNIPROT:P36884; GB:X02872; NID:G46536; PIDN:CAA26630.1; PID:G581555  
C;Comment: Ribosome stalling in the translation of this leader peptide, caused by the translation of the chloramphenicol O-acetyltransferase from a ribosome binding site located upstream of the chloramphenicol O-acetyltransferase gene.

Query Match 21.4%; Score 21; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 KSDNYAT 11  
|||  
Db 3 KSEDYSS 9

## RESULT 14

S30494

cat gene leader peptide - Streptococcus agalactiae plasmid pIP501  
C;Species: Streptococcus agalactiae  
C;Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 16-Aug-2004  
C;Accession: S30494  
R;Trieu-Cuot, P.; de Cespedes, G.; Haraud, T.  
Plasmid 28, 272-276, 1992  
A;Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Streptococcus agalactiae plasmid pIP501  
A;Reference number: JQ1950; MUID:93096867; PMID:1461942  
A;Accession: S30494  
A;Molecule type: DNA  
A;Residues: 1-9 <TRI>  
A;Cross-references: UNIPROT:P36884; EMBL:X65462; NID:G49071; PIDN:CAA46454.1; PID:G58153  
C;Genetics:  
A;Genome: plasmid pIP501

Query Match 21.4%; Score 21; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 5 KSDNYAT 11  
||::||:  
Db 3 KSEDYSS 9

RESULT 15  
PHI587  
IG H chain V-D-J region (wild-type clone 11) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1587  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1587  
A;Molecule type: DNA  
A;Residues: 1-12 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 21.4%; Score 21; DB 2; Length 12;  
Best Local Similarity 44.4%; Pred. No. 2.9e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 5 KSDNYATHY 13  
: || || |  
Db 4 RGDLYAMDY 12

Search completed: April 18, 2005, 15:57:40  
Job time : 47 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:39:55 ; Search time 178 Seconds  
(without alignments)  
54.660 Million cell updates/sec

Title: US-09-674-716B-11  
Perfect score: 98  
Sequence: 1 EIRLKSNDYATHYAESVKG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 10410

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	32.7	19	2 Q73129	Q73129 human immun
2	29	29.6	15	2 Q91BM5	Q91BM5 human immun
3	28	28.6	13	2 Q9UC27	Q9UC27 homo sapien
4	27	27.6	14	1 NEJ2_FASHE	P80526 fasciola he
5	27	27.6	15	2 Q7BVD9	Q7BVD9 borrelia bu
6	27	27.6	17	2 Q7BVD5	Q7BVD5 borrelia bu
7	27	27.6	19	2 Q9L434	Q9L434 salmonella
8	26	26.5	13	2 Q9KHJ4	Q9KHJ4 caulobacter
9	26	26.5	14	2 Q85CA1	Q85CA1 strongyloce
10	26	26.5	15	2 Q9UWH6	Q9UWH6 thermococcu
11	26	26.5	15	2 Q9TRT4	Q9TRT4 sus scrofa
12	26	26.5	15	2 Q9TRT6	Q9TRT6 sus scrofa
13	26	26.5	19	2 Q84863	Q84863 unidentified
14	25	25.5	10	1 COXO_THUOB	P80982 thunnus obe
15	25	25.5	17	2 Q9V2K3	Q9V2K3 methanobact
16	25	25.5	19	2 Q86DB6	Q86DB6 halocynthia
17	24	24.5	13	2 Q9TWR4	Q9TWR4 titiyus serr
18	24	24.5	14	2 Q93057	Q93057 homo sapien
19	24	24.5	14	2 P70319	P70319 mus musculu
20	23	23.5	9	2 Q93LE4	Q93LE4 heliobacill
21	23	23.5	10	2 P96423	P96423 pseudomonas
22	23	23.5	14	2 P96347	P96347 helicobacte
23	23	23.5	15	2 Q8UF12	Q8UF12 human immun
24	23	23.5	16	2 Q7MI99	Q7MI99 mycobacteri
25	23	23.5	17	2 Q9R4H9	Q9R4H9 bordetella
26	23	23.5	18	2 Q9UWJ7	Q9UWJ7 archaeoglob
27	23	23.5	18	2 Q70ZU6	Q70ZU6 bradyrhizob
28	23	23.5	18	2 Q9PRX1	Q9PRX1 struthio ca
29	22	22.4	9	2 Q7RHC2	Q7RHC2 plasmodium
30	22	22.4	10	2 Q67B26	Q67B26 bacterioph
31	22	22.4	12	1 LOSK_LOCM1	P47733 locusta mig

32	22	22.4	14	2 Q7MON7	Q7MON7 alcaligenes
33	22	22.4	15	2 Q6SLH8	Q6SLH8 caenorhabdi
34	22	22.4	15	2 Q6QOR4	Q6QOR4 helicobacte
35	22	22.4	15	2 Q7M0G8	Q7M0G8 mus sp. cd3
36	22	22.4	16	2 Q9R4J4	Q9R4J4 pseudomonas
37	22	22.4	17	2 Q7RGD8	Q7RGD8 plasmodium
38	22	22.4	17	2 Q9R4P9	Q9R4P9 pseudomonas
39	22	22.4	18	2 Q9TRF1	Q9TRF1 bos taurus
40	22	22.4	18	2 Q78379	Q78379 theileria a
41	22	22.4	18	2 Q9R5F6	Q9R5F6 helicobacte
42	22	22.4	18	2 Q7ZFR2	Q7ZFR2 human immun
43	21	21.4	7	2 Q8K3H6	Q8K3H6 rattus norv
44	21	21.4	9	1 LPCA_STAAU	P36884 staphylococ
45	21	21.4	9	2 Q6LDI6	Q6LDI6 staphylococ

ALIGNMENTS

RESULT 1					
Q73129	PRELIMINARY;	PRT;	19	AA.	
AC	Q73129				
DT	01-NOV-1996 (Tremblrel. 01, Created)				
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)				
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)				
DE	Envelope glycoprotein (Fragment).				
GN	Name-env;				
OS	Human immunodeficiency virus 1.				
OC	Viruses; Retrovird viruses; Retroviridae; Lentivirus.				
ON	NCBI_TaxID=11676;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RA	Wolinsky S.M., Korber B.T.M., Neumann A.U., Daniels M., Kunstman K.J.,				
RA	Whetzel A.J., Cao Y., Ho D.D., Safritz J.T., Koup R.A.;				
RL	Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	McDonald D.;				
RL	Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; U36027; AA97722.1; -				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0019028; C:viral capsid; IEA.				
DR	GO; GO:0019031; C:viral envelope; IEA.				
DR	GO; GO:0005198; F:structural molecule activity; IEA.				
DR	InterPro: IPR000777; GP120.				
DR	Pfam: PF00516; GP120; 1.				
KW	AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.				
FT	NON_TER 1				
SQ	SEQUENCE 19 AA; 2066 MW; E117102D52800EF4 CRC64;				
Query Match 32.7%; Score 32; DB 2; Length 19;					
Best Local Similarity 50.0%; Pred. No. 4.4e+02;					
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;					
QY	1 EIRLKSNDYNA 10				
DB	7 EVVIRSDNFA 16				
RESULT 2					
Q91BM5	PRELIMINARY;	PRT;	15	AA.	
ID	Q91BM5				
AC	Q91BM5				
DT	01-OCT-2000 (Tremblrel. 15, Created)				
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)				
DT	01-OCT-2002 (Tremblrel. 22, Last annotation update)				
DE	Envelope glycoprotein, V3 region (Fragment).				
GN	Name-env;				
OS	Human immunodeficiency virus 1.				
OC	Viruses; Retrovird viruses; Retroviridae; Lentivirus.				
ON	NCBI_TaxID=11676;				
RN	[1]				

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RP SEQUENCE FROM N.A.
RX MEDLINE=95115054; PubMed=7815476;
RA Ahmad N., Baroudy B.M., Baker R.C., Chappey C.;
RT "Genetic analysis of human immunodeficiency virus type 1 envelope V3
RT region isolates from mothers and infants after perinatal
RT transmission.";
RL J. Virol. 69:1001-1012(1995).
DR EMBL; U16595; AAA64161.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1794 MW; 747C6A62800BF4A1 CRC64;

Query Match 29.6%; Score 29; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDYA 10
DB 4 EVIIRSDNFS 13

RESULT 3
Q9UC27 PRELIMINARY; PRT; 13 AA.
AC Q9UC27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 94 kDa epididymal cytokeatin-like protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95226590; PubMed=7536047;
RA Boue F., Duquenne C., Lassalle B., Lefevre A., Finaz C.;
RT "FLB1, a human protein of epididymal origin that is involved in the
RT sperm-oocyte recognition process.";
RL Biol. Reprod. 52:267-278(1995).
SQ SEQUENCE 13 AA; 1610 MW; 000A683B81B7A45B CRC64;

Query Match 28.6%; Score 28; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 NYATHY 13
DB 1 NYSTY 6

RESULT 4
NEJ2_FASHE STANDARD; PRT; 14 AA.
AC P80526;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Newly excysted juvenile protein 2 (Fragment).
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Tkalcovic J., Ashman K., Meusen E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proteins.";
RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC -!- DEVELOPMENTAL STAGE: Expressed at the newly excysted juvenile
stage.

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KW Direct protein sequencing.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1581 MW; 9E0F0090CC8C0DF1 CRC64;

Query Match 27.6%; Score 27; DB 1; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 DNYATHYA 14
DB 3 DNGRTHWA 10

RESULT 5
Q7BVD9 PRELIMINARY; PRT; 15 AA.
AC Q7BVD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Borrelia burgdorferi plasmid cp32-2, possible partition proteins,
DE complete cds. (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp32-2.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=B31;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Casjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RT Erp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879(1998).
DR EMBL; AF022479; AAC35441.1; -.
KW Plasmid.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1817 MW; 90E468E030E20078 CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 YATHYAESVK 18
DB 6 YRTYNIESIK 15

RESULT 6
Q7BVD5 PRELIMINARY; PRT; 17 AA.
AC Q7BVD5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Borrelia burgdorferi plasmid cp32-7, possible partition proteins,
DE complete cds. (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp32-7.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=B31;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Casjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RT Erp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879(1998).
DR EMBL; AF022483; AAC35457.1; -.
KW Plasmid.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2060 MW; 6B5830E468E030E2 CRC64;

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Query Match 27.6%; Score 27; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 2.6e+03;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 YATHYAESVK 18  
DB 6 YRTYNIESIK 15

RESULT 7  
Q9L434 PRELIMINARY; PRT; 19 AA.  
AC Q9L434;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein putative yciE (Fragment).  
GN Namesputative yciE;  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=602;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C52;  
RX MEDLINE=21160188; PubMed=11260470;  
RA Robbe-Saule V., Coynault C., Ibanez-Ruiz M., Hermant D., Norel F.;  
RT "Identification of a non-haem catalase in Salmonella and its  
regulation by RpoS (sigmas).";  
RL Mol. Microbiol. 39:1533-1545(2001).  
DR EMBL; AJ251362; CAB71038.1; -.  
DR InterPro; IPR010287; DUF892.  
DR Pfam; PF05974; DUF892; 1.  
KW Hypothetical protein.  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2448 MW; 05D3DB83C7CBE7E5 CRC64;

Query Match 27.6%; Score 27; DB 2; Length 19;  
Best Local Similarity 66.7%; Pred. No. 2.9e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 NYATHY 13  
DB 2 NYTEHY 7

RESULT 8  
Q9KHJ4 PRELIMINARY; PRT; 13 AA.  
AC Q9KHJ4;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Proteolysis tag (Fragment).  
OS Caulobacter crescentus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;  
OC Caulobacteraceae; Caulobacter.  
OX NCBI\_TaxID=155892;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20345063; PubMed=10884408; DOI=10.1073/pnas.97.14.7778;  
RA Keiler K.C., Shapiro L., Williams K.P.;  
RT "mRNAs that encode proteolysis-inducing tags are found in all known  
bacterial genomes: A two-piece tmRNA functions in Caulobacter.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:7778-7783(2000).  
DR EMBL; AF255738; AAF87998.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 13 AA; 1368 MW; CE5F60C57FCE1B1D CRC64;

Query Match 26.5%; Score 26; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 2.8e+03;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 SDNYATHYA 14  
DB 2 NDNFAEFA 10

RESULT 9  
Q85CA1 PRELIMINARY; PRT; 14 AA.  
AC Q85CA1;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
GN Name=COII;  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
OC Strongylocentrotus.  
OX NCBI\_TaxID=7668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22707965; PubMed=12823452;  
RA Biermann C.H., Kessing B.D., Palumbi S.R.;  
RT "Phylogeny and development of marine model species: strongylocentrotid  
sea urchins.";  
RL Evol. Dev. 5:360-371(2003).  
DR EMBL; AY221017; AAP21733.1; -.  
DR EMBL; AY221018; AAP21736.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1820 MW; 2CB850A51E616CD3 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 14;  
Best Local Similarity 44.4%; Pred. No. 3e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 DNYATHYAE 15  
DB 5 ENWVTQYLE 13

RESULT 10  
Q9UWH6 PRELIMINARY; PRT; 15 AA.  
AC Q9UWH6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha  
(Fragment).  
OS Thermococcus litoralis.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Thermococcus.  
OX NCBI\_TaxID=2265;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96146528; PubMed=8550513;  
RA Heider J., Mai X., Adams M.W.;  
RT "Characterization of 2-ketolysvalerate ferredoxin oxidoreductase, a  
new and reversible coenzyme A-dependent enzyme involved in peptide  
fermentation by hyperthermophilic archaea.";  
RL J. Bacteriol. 178:780-787(1996).  
SQ SEQUENCE 15 AA; 1549 MW; 0C1766910B222944 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 15;  
Best Local Similarity 45.5%; Pred. No. 3.3e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHY 13  
DB 3 RLKSDNYATHY 13

Db 3 KVVSGNYAAAY 13

## RESULT 11

Q9TRT4 PRELIMINARY; PRT; 15 AA.  
 AC Q9TRT4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Pyruvate dehydrogenase (BC 1.2.4.1) (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92144618; PubMed=1737046; DOI=10.1016/0167-4838(92)90279-M;  
 RA Koike K., Urata Y., Goto S.;  
 RT "Proteinase-catalyzed activation of porcine heart muscle pyruvate  
 RT dehydrogenase and identification of its cleavage site."  
 RL Biochim. Biophys. Acta 1118:223-230(1992).  
 DR GO; GO:0004739; F:pyruvate dehydrogenase (acetyl-transferring. . .; IEA.  
 SQ SEQUENCE 15 AA; 1757 MW; 94D6BFE4B126598 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 15;

Best Local Similarity 71.4%; Pred. No. 3.3e+03; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSD 7

|:| |||

Db 3 EVRSKSD 9

## RESULT 12

Q9TRT6 PRELIMINARY; PRT; 15 AA.  
 AC Q9TRT6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Pyruvate dehydrogenase (BC 1.2.4.1) (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92144618; PubMed=1737046; DOI=10.1016/0167-4838(92)90279-M;  
 RA Koike K., Urata Y., Goto S.;  
 RT "Proteinase-catalyzed activation of porcine heart muscle pyruvate  
 RT dehydrogenase and identification of its cleavage site."  
 RL Biochim. Biophys. Acta 1118:223-230(1992).  
 DR GO; GO:0004739; F:pyruvate dehydrogenase (acetyl-transferring. . .; IEA.  
 SQ SEQUENCE 15 AA; 1787 MW; DB1265CDF7737E16 CRC64;

Query Match

Best Local Similarity 71.4%; Pred. No. 3.3e+03; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSD 7

|:| |||

Db 7 EVRSKSD 13

## RESULT 13

Q84863 PRELIMINARY; PRT; 19 AA.  
 AC Q84863;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein (Fragment).

OS unidentified human poliovirus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Enterovirus.  
 OX NCBI\_TaxID=40278;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87169734; PubMed=3031313;  
 RA Kuge S., Saito I., Nomoto A.;  
 RT "Primary structure of poliovirus defective-interfering particle  
 RT genomes and possible generation mechanisms of the particles."  
 RL J. Mol. Biol. 192:473-487(1986).  
 DR EMBL; M30221; AAA66829.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2106 MW; F774197992500AC8 CRC64;

## RESULT 14

CXOXO\_THUOB STANDARD; PRT; 10 AA.  
 AC P80982;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).  
 OS Thunnus obesus (Bigeye tuna).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
 OC Scombridae; Thunnus.  
 OX NCBI\_TaxID=8241;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 RX MEDLINE=97454291; PubMed=9310366;  
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,  
 RA Kadenbach B.;  
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and  
 RT liver."  
 RL Eur. J. Biochem. 248:99-103(1997).  
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide  
 CC chains of cytochrome c oxidase, the terminal oxidase in  
 CC mitochondrial electron transport.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.  
 DR PIR; S77990; S77990.  
 KW Direct protein sequencing; Inner membrane; Mitochondrion;  
 KW Oxidoreductase.  
 FT NON\_TER 10  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;

## Query Match

Best Local Similarity 25.5%; Score 25; DB 1; Length 10;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 THYAE 15

:||||

Db 1 SHYAE 5

## RESULT 15

Q9V2X3

ID Q9V2X3 PRELIMINARY; PRT; 17 AA.  
AC Q9V2X3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE RNA polymerase subunit B'', (Fragment).  
OS Methanobacterium thermoformicicum.  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=145262;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88198019; PubMed=2834336;  
RA Schallenberg J., Moes M., Truss M., Reiser W., Thomm M., Stetter K.O.,  
RA Klein A.;  
RT "Cloning and physical mapping of RNA polymerase genes from  
RT Methanobacterium thermoautotrophicum and comparison of homologies and  
RT gene orders with those of RNA polymerase genes from other methanogenic  
RT archaeobacteria.",  
RL J. Bacteriol. 170:2247-2253(1988).  
DR EMBL; M20391; AAA72654.1; -.  
FT NON TER  
SQ SEQUENCE 17 AA; 2137 MW; 0C03CD9E6D780560 CRC64;  
Query Match 25.5%; Score 25; DB 2; Length 17;  
Best Local Similarity 66.7%; Pred. No. 5.5e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 THYAES 16  
Db 4 THYPEN 9

Search completed: April 18, 2005, 15:56:48  
Job time : 180 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:39:15 ; Search time 168 Seconds  
(without alignments)  
43.741 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLSKSDNYTHYAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 691830

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	19	3 AAY32258	Aay32258 Light cha
2	91	92.9	19	4 AAB35297	Aab35297 Murine PS
3	89	90.8	19	8 ADR19267	Adri9267 Glycosyla
4	84	85.7	19	8 ADR19286	Adri9286 Glycosyla
5	83	84.7	19	8 ADR19285	Adri9285 Glycosyla
6	80	81.6	17	3 AAB30033	Aab30033 Scaffold
7	79	80.6	19	6 ABO10709	Abol0709 Murine J4
8	79	80.6	19	6 ABR44653	Abra44653 Murine J4
9	78	79.6	19	8 ADR19284	Adri9284 Glycosyla
10	76	77.6	19	8 ADQ92379	Adq92379 Human hul
11	76	77.6	19	8 ADQ80568	Adq80568 TNF-alpha
12	74	75.5	16	2 AAY40694	Aay40694 A3 deriva
13	74	75.5	19	8 ADH89399	Adh89399 Human tra
14	74	75.5	19	8 ADQ92375	Adq92375 Human hul
15	74	75.5	19	8 ADQ92377	Adq92377 Human hul
16	74	75.5	19	8 ADQ80564	Adq80564 TNF-alpha
17	74	75.5	19	8 ADQ80566	Adq80566 TNF-alpha
18	73	74.5	19	8 ADR19266	Adri9266 Glycosyla
19	70	71.4	19	3 AAB10002	Aab10002 H. pylori
20	69	70.4	19	8 ADQ92387	Adq92387 Human hul
21	69	70.4	19	8 ADQ92381	Adq92381 Human hul
22	69	70.4	19	8 ADQ80570	Adq80570 TNF-alpha
23	69	70.4	19	8 ADQ80576	Adq80576 TNF-alpha
24	68	69.4	19	2 AAR84529	Aar84529 CDRH2 of
25	68	69.4	19	8 ADM73987	Adm73987 Antigen/a

26	68	69.4	19	8 ADQ92383	Adq92383 Human hul
27	68	69.4	19	8 ADQ80572	Adq80572 TNF-alpha
28	65	66.3	19	5 AAO14988	Aao14988 Mouse mAb
29	65	66.3	19	5 ADF98248	Adf98248 Murine mAb
30	64	65.3	19	2 AAW94737	Aaw94737 Anti-Stop
31	64	65.3	19	8 ADL35119	Adl35119 CDR2 of m
32	57	58.2	15	7 ADI57829	Adi57829 Monoclonal
33	54	55.1	15	7 ADI57828	Adi57828 Monoclonal
34	52	53.1	15	7 ADI57830	Adi57830 Monoclonal
35	52	53.1	17	5 AAU82539	Aau82539 Lama CDR
36	52	53.1	19	8 ADE85719	Ade85719 Human Eph
37	51	52.0	13	7 ADI57890	Adi57890 Monoclonal
38	51	52.0	13	7 ADI57995	Adi57995 Anti-TNF-
39	50	51.0	15	7 ADI57827	Adi57827 Monoclonal
40	49	50.0	17	6 ADA90054	Ada90054 Anti-Abet
41	49	50.0	17	6 ADA90708	Ada90708 MS-Roche
42	49	50.0	17	6 ADA90083	Ada90083 Anti-Abet
43	49	50.0	17	6 ADA90835	Ada90835 MS-Roche
44	49	50.0	19	2 AAR74934	Aar74934 H-CDR-2 o
45	49	50.0	19	5 AAU70371	Aau70371 Human hea

ALIGNMENTS

RESULT 1

AAV32258

ID AAY32258 standard; peptide; 19 AA.

XX AC AAY32258;

XX DT 15-FEB-2000 (first entry)

XX DE Light chain CDR H2 of mouse anti-CD23 MAb C11.

KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;

KW monoclonal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinis;

KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

KW therapy.

XX OS Mus musculus.

XX PN WO9958679-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001434.

XX PR 09-MAY-1998; 98GB-00009839.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Bonney JWP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX XX WPI; 2000-053101/04.

XX DR N-PSDB; AA234743.

XX XX Cell receptor specific antibodies useful for treating e.g. arthritis,

XX PT diabetes, multiple sclerosis and psoriasis.

XX PS Claim 1; Page 40; 81pp; English.

XX CC This sequence represents complementarity determining region 2 (CDR H2)

XX CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11

XX CC (see also AAY32263). The invention provides altered antibodies, such as

XX CC chimeric or humanised antibodies, which comprise sufficient of the amino

XX CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents  
 CC  
 XX Sequence 19 AA;

Query Match 100.0%; Score 98; DB 3; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHVAESVKG 19  
 |||||:|||||  
 Db 1 EIRLKSNDNYATHVAESVKG 19

RESULT 2  
 AAB35297  
 ID AAB35297 standard; peptide; 19 AA.

AC AAB35297;

DT 08-MAY-2001 (first entry)

DE Murine PSCA antibody fragment #5.

KW Prostate stem cell antigen; PSCA; human; mouse; prostate cancer;  
 diagnosis; treatment; chromosome 8q24.2.

OS Mus sp.

XX WO200105427-A1.

XX 25-JAN-2001.

XX 20-JUL-2000; 2000WO-US019967.

XX 20-JUL-1999; 99US-00359326.

XX 03-MAY-2000; 2000US-00564329.

XX (REGC ) UNIV CALIFORNIA.

XX (UROG-) UROGENESYS.

XX Reiter R, Witte O, Saffran DC, Jakobovits A;

XX WPI; 2001-159478/16.

XX Antibodies binding to prostate stem cell antigen inhibit the growth of  
 XX cancer cells and are used to detect and treat prostate, pancreatic or  
 XX bladder cancers.

XX Example 21; Fig 61; 229pp; English.

XX The present invention describes a method of treating cancer associated  
 XX with prostate stem cell antigen (PSCA) by administering an antibody which  
 XX selectively binds to PSCA and inhibits the growth of the cancer cells.  
 XX The PSCA gene is found on human chromosome 8q24.2. The invention provides  
 XX the human and murine PSCA protein and coding sequences, which can be used  
 XX not only in the treatment of, but also in detection and prognosis of  
 XX prostate cancer

XX Sequence 19 AA;

Query Match 92.9%; Score 91; DB 4; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 4.6e-08;

Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EIRLKSNDNYATHVAESVKG 19  
 |||||:|||||  
 Db 1 EIRLSENATHVAESVKG 19

RESULT 3

ADRI9267  
 ID ADRI9267 standard; peptide; 19 AA.

XX AC ADRI9267;

XX DT 21-OCT-2004 (first entry)

XX DE Glycosylated MUC1 tumour epitope recognition peptide, SEQ ID 4.

XX Recognition molecule; bind; glycosylated MUC1 tumour epitope; mucin 1;  
 KW tumour; metastatic; carcinoma; breast; colon; stomach; pancreas; ovary;  
 KW liver; kidney cell; intestinal; lung cancer; multiple myeloma.

XX Unidentified.

XX WO2004065423-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-DE000132.

XX 23-JAN-2003; 2003DE-01003664.

XX (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.

XX Goletz S, Danielczyk A, Stahn R, Karsten U;

XX WPI; 2004-593433/57.

XX New recognition molecules that bind the glycosylated MUC1 tumour epitope,  
 XX useful for prevention, diagnosis, treatment and monitoring of tumors.

XX Claim 1; SEQ ID NO 4; 158pp; German.

XX The invention relates to novel recognition molecules comprising sequences  
 XX that bind specifically to a glycosylated MUC1 tumour epitope. The novel  
 XX recognition molecules comprise: sequences ADRI9264 or ADRI9265; sequences  
 XX ADRI9266 or ADRI9267 and sequences ADRI9268 and ADRI9269, and bind  
 XX specifically to the glycosylated mucin 1 (MUC1) tumour epitope. The  
 XX invention further comprises: a construct comprising the recognition  
 XX molecule fused, chemically coupled or non-covalently associated with  
 XX additional sequences and/or structures; an isolated nucleic acid that  
 XX encodes the recognition molecule or construct; expression cassette or  
 XX vector that contains the isolated nucleic acid, operatively linked to a  
 XX promoter; virus or host cell comprising at least one cassette or vector  
 XX of ADRI9266; an organism containing at least one host cell of ADRI9267; a  
 XX method for preparing the recognition molecule and construct; and a kit  
 XX containing the recognition molecule and/or construct. The recognition  
 XX molecules have cytostatic activity. The recognition molecules, constructs  
 XX containing them, the nucleic acid encoding them, and derived viruses,  
 XX cells and organisms, are used for prevention, diagnosis, treatment and  
 XX monitoring of tumours and/or metastases, specifically where MUC1  
 XX positive, particularly carcinoma of breast, colon, stomach, pancreas,  
 XX ovary, liver or kidney cells; (gastro)intestinal or lung cancers and  
 XX multiple myeloma. The recognition molecules show little or no binding to  
 XX MUC1 in either the serum or normal tissue, so provides simple, safe and  
 XX efficient detection of tumours, even at an early stage (carcinoma in  
 XX situ), and can differentiate between tumours and benign diseases. This  
 XX sequence represents one of the novel glycosylated MUC1 tumour epitope  
 XX recognition molecules of the invention.

XX Sequence 19 AA;

Query Match 90.8%; Score 89; DB 8; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 1e-07;

Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHAESVKG 19  
|||||:|||||  
Db 1 EIRLKSNYYTHAESVKG 19

## RESULT 4

ADRI9286  
ID ADR19286 standard; peptide; 19 AA.

XX AC ADR19286;

XX DT 21-OCT-2004 (first entry)

XX Glycosylated MUC1 tumour epitope recognition variant peptide, SEQ ID 23.

XX Recognition molecule; bind; glycosylated MUC1 tumour epitope; mucin 1;  
KW tumour; metastatic; carcinoma; breast; colon; stomach; pancreas; ovary;  
KW liver; kidney cell; intestinal; lung cancer; multiple myeloma; variant.

XX OS Synthetic; Unidentified.

XX PN WO2004065423-A2.

XX PD 05-AUG-2004.

XX PF 23-JAN-2004; 2004WO-DE000132.

XX PR 23-JAN-2003; 2003DE-01003664.

XX PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.

XX PI Goletz S, Danielczyk A, Stahn R, Karsten U;

XX DR WPI; 2004-593433/57.

XX New recognition molecules that bind the glycosylated MUC1 tumour epitope,  
PT useful for prevention, diagnosis, treatment and monitoring of tumors.

XX PS Claim 9; SEQ ID NO 23; 158pp; German.

XX The invention relates to novel recognition molecules comprising sequences  
CC that bind specifically to a glycosylated MUC1 tumour epitope. The novel  
CC recognition molecules comprise: sequences ADR19264 or ADR19265; sequences  
CC ADR19266 or ADR19267 and sequences ADR19268 and ADR19269, and bind  
CC specifically to the glycosylated mucin 1 (MUC1) tumour epitope. The  
CC invention further comprises: a construct comprising the recognition  
CC molecule fused, chemically coupled or non-covalently associated with  
CC additional sequences and/or structures; an isolated nucleic acid that  
CC encodes the recognition molecule or construct; expression cassette or  
CC vector that contains the isolated nucleic acid, operatively linked to a  
CC promoter; virus or host cell comprising at least one cassette or vector  
CC of ADR19266; an organism containing at least one host cell of ADR19267; a  
CC method for preparing the recognition molecule and construct; and a kit  
CC containing the recognition molecule and/or construct. The recognition  
CC molecules have cytostatic activity. The recognition molecules, constructs  
CC containing them, the nucleic acid encoding them, and derived viruses,  
CC cells and organisms, are used for prevention, diagnosis, treatment and  
CC monitoring of tumours and/or metastases, specifically where MUC1  
CC positive, particularly carcinoma of breast, colon, stomach, pancreas,  
CC ovary, liver or kidney cells; (gastro)intestinal or lung cancers and  
CC multiple myeloma. The recognition molecules show little or no binding to  
CC MUC1 in either the serum or normal tissue, so provides simple, safe and  
CC efficient detection of tumours, even at an early stage (carcinoma in  
CC situ), and can differentiate between tumours and benign diseases. This  
CC sequence represents a variant glycosylated MUC1 tumour epitope  
CC recognition peptide of the invention.

XX SQ Sequence 19 AA;

Query Match 85.7%; Score 84; DB 8; Length 19;  
Best Local Similarity 84.2%; Pred. No. 7.1e-07;

Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHAESVKG 19  
|||||:|||||  
Db 1 EIRLKSNYYTHAESVKG 19

## RESULT 5

ADRI9285  
ID ADR19285 standard; peptide; 19 AA.

XX AC ADR19285;

XX DT 21-OCT-2004 (first entry)

XX Glycosylated MUC1 tumour epitope recognition variant peptide, SEQ ID 22.

XX Recognition molecule; bind; glycosylated MUC1 tumour epitope; mucin 1;  
KW tumour; metastatic; carcinoma; breast; colon; stomach; pancreas; ovary;  
KW liver; kidney cell; intestinal; lung cancer; multiple myeloma; variant.

XX OS Synthetic; Unidentified.

XX PN WO2004065423-A2.

XX PD 05-AUG-2004.

XX PF 23-JAN-2004; 2004WO-DE000132.

XX PR 23-JAN-2003; 2003DE-01003664.

XX PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.

XX PI Goletz S, Danielczyk A, Stahn R, Karsten U;

XX DR WPI; 2004-593433/57.

XX New recognition molecules that bind the glycosylated MUC1 tumour epitope,  
PT useful for prevention, diagnosis, treatment and monitoring of tumors.

XX PS Claim 9; SEQ ID NO 22; 158pp; German.

XX The invention relates to novel recognition molecules comprising sequences  
CC that bind specifically to a glycosylated MUC1 tumour epitope. The novel  
CC recognition molecules comprise: sequences ADR19264 or ADR19265; sequences  
CC ADR19266 or ADR19267 and sequences ADR19268 and ADR19269, and bind  
CC specifically to the glycosylated mucin 1 (MUC1) tumour epitope. The  
CC invention further comprises: a construct comprising the recognition  
CC molecule fused, chemically coupled or non-covalently associated with  
CC additional sequences and/or structures; an isolated nucleic acid that  
CC encodes the recognition molecule or construct; expression cassette or  
CC vector that contains the isolated nucleic acid, operatively linked to a  
CC promoter; virus or host cell comprising at least one cassette or vector  
CC of ADR19266; an organism containing at least one host cell of ADR19267; a  
CC method for preparing the recognition molecule and construct; and a kit  
CC containing the recognition molecule and/or construct. The recognition  
CC molecules have cytostatic activity. The recognition molecules, constructs  
CC containing them, the nucleic acid encoding them, and derived viruses,  
CC cells and organisms, are used for prevention, diagnosis, treatment and  
CC monitoring of tumours and/or metastases, specifically where MUC1  
CC positive, particularly carcinoma of breast, colon, stomach, pancreas,  
CC ovary, liver or kidney cells; (gastro)intestinal or lung cancers and  
CC multiple myeloma. The recognition molecules show little or no binding to  
CC MUC1 in either the serum or normal tissue, so provides simple, safe and  
CC efficient detection of tumours, even at an early stage (carcinoma in  
CC situ), and can differentiate between tumours and benign diseases. This  
CC sequence represents a variant glycosylated MUC1 tumour epitope  
CC recognition peptide of the invention.

XX SQ Sequence 19 AA;

Query Match 84.7%; Score 83; DB 8; Length 19;  
Best Local Similarity 84.2%; Pred. No. 1e-06;

Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19  
 DB 1 EIRLSKNKYTHYAESVKG 19

RESULT 6  
 AAB30033  
 ID AAB30033 standard; peptide; 17 AA.  
 XX  
 AC AAB30033;  
 XX  
 DT 09-FEB-2001 (first entry)  
 XX  
 DE Scaffold protein SCA A3 peptide SEQ ID NO: 94.  
 XX  
 DE Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;  
 KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;  
 KW diabetic retinopathy; atherosclerosis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200060070-A1.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 01-APR-1999; 99WO-EP002283.  
 XX  
 PR 01-APR-1999; 99WO-EP002283.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Desmet J, Hufton S, Hoogenboom H, Sablon E;  
 XX  
 DR WPI; 2000-665002/64.  
 XX  
 PT Scaffold composed of single-chain polypeptide having beta sandwich  
 PT architecture carrying new and randomized peptide sequences useful as  
 PT supporting framework and carrying antigen- or receptor binding fragments.  
 XX  
 PS Disclosure; Page 14; 68pp; English.  
 XX  
 CC The present invention is concerned with producing scaffold proteins based  
 CC upon the human CTLA-4 SCA domain. These scaffold proteins can be used as  
 CC a scaffold to bind antigen- or receptor-binding fragments. These can be  
 CC used in the treatment of diseases such as cancer, atherosclerosis,  
 CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.  
 CC Sequences AAB29930-B29939 were used in the production of the proteins of  
 CC the invention  
 XX  
 SQ Sequence 17 AA;

Query Match 81.6%; Score 80; DB 3; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.9e-06;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19  
 DB 1 RLNSDNFATHYAESVKG 17

RESULT 7  
 ABO10709  
 ID ABO10709 standard; peptide; 19 AA.  
 XX  
 AC ABO10709;  
 XX  
 DT 20-AUG-2003 (first entry)  
 XX  
 DE Murine J415 antibody heavy chain CDR2.  
 XX  
 KW Modified antibody; deimmunised antibody; anti-PMSA antibody;

prostate specific membrane antigen; immunogenic; CDR; murine;  
 complementarity determining region; J591; J415; J533; E99; mouse;  
 prostatic disorder; cancerous disorder; genitourinary inflammation;  
 prostatitis; benign enlargement; prostatic cancer; testicular cancer;  
 solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;  
 antiinflammatory; cytostatic; framework region; variable heavy chain;  
 variable light chain; VH; VL; variable region.

Mus musculus.  
 WO200298897-A2.  
 12-DEC-2002.  
 30-MAY-2002; 2002WO-US017068.  
 01-JUN-2001; 2001US-0295214P.  
 20-SEP-2001; 2001US-0323585P.  
 08-MAR-2002; 2002US-0362810P.  
 (CORR ) CORNELL RES FOUND INC.  
 Bander N, Carr FJ, Hamilton A;  
 WPI; 2003-156839/15.  
 New modified anti-prostate specific membrane antigen (PMSA)  
 immunoglobulins, useful for treating or preventing a prostatic or  
 cancerous disorder, e.g. genitourinary inflammation, prostatitis, or  
 prostatic or testicular cancer.  
 Disclosure; Fig 5; 254pp; English.

The present invention relates to modified (e.g. deimmunised) antibodies  
 to prostate specific membrane antigen (PMSA). The modified anti-PMSA  
 antibodies are less immunogenic compared to the unmodified anti-PMSA  
 antibodies. The modified antibodies comprise complementarity determining  
 regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,  
 J533 or E99), and framework sequences that are less immunogenic in humans  
 (e.g. less antigenic than the murine frameworks in which a murine CDR  
 naturally occurs). The modified antibodies bind with PMSA, preferably  
 human PMSA, with high affinity and specificity. The anti-PMSA antibodies  
 are useful for treating or preventing a prostatic or cancerous disorder,  
 e.g. genitourinary inflammation, prostatitis, benign enlargement,  
 prostatic cancer or testicular cancer, or solid tumours, soft tissue  
 tumours or metastatic lesions, and its associated pain. The present  
 sequence represents a CDR from a murine antibody

Sequence 19 AA;

Query Match 80.6%; Score 79; DB 6; Length 19;  
 Best Local Similarity 78.9%; Pred. No. 4.9e-06;  
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19  
 DB 1 EIRSQNNFATHYAESVKG 19

RESULT 8  
 ABR44653  
 ID ABR44653 standard; peptide; 19 AA.  
 XX  
 AC ABR44653;  
 XX  
 DT 25-JUL-2003 (first entry)  
 XX  
 DE Murine J415 antibody VH CDR2 peptide SEQ ID NO:30.  
 XX  
 DE Mouse; murine; antibody; skin disorder; binding agent; PMSA; cytostatic;  
 KW prostate specific membrane antigen; antipsoaric; antiarthritic;  
 KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;  
 KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;



KW neoplastic disorder.  
 XX Mus musculus.  
 OS WO2003024388-A2.  
 XX 27-MAR-2003.  
 PD  
 XX 30-MAY-2002; 2002WO-US017204.  
 XX  
 PF 20-SEP-2001; 2001US-0324100P.  
 XX 08-MAR-2002; 2002US-0362612P.  
 PR  
 XX (CORR ) CORNELL RES FOUND INC.  
 PA  
 XX Bander N;  
 XX WPI; 2003-313319/30.  
 DR  
 XX Ablating/killing aberrant prostate specific membrane antigen-expressing  
 PT cells for treating skin disorders, by contacting the cell with an  
 PT antibody that binds to the extracellular domain of prostate specific  
 PT membrane antigen.  
 XX  
 XX Claim 22; Page 53; 225pp; English.  
 PS  
 XX The present invention describes a method (M1) for ablating or killing an  
 XX aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.  
 CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a  
 CC vascular endothelial cell proximate to the cell, with an antibody (or its  
 CC antigen-binding fragment), which binds specifically to the extracellular  
 CC domain of PSMA in an amount sufficient to ablate or kill the cell. The  
 CC antibodies have antiproliferative, antiarthritic, dermatological, cytostatic,  
 CC antiinflammatory and anti-allergic activities, and can be used in  
 CC vaccines. M1 is useful for treating a skin disorder in a subject, by  
 CC administering to the subject, an amount of an antibody which binds  
 CC specifically to the extracellular domain of PSMA (the subject is a  
 CC mammal, preferably human and is having, or at risk of, a skin disorder).  
 CC The skin disorder is a dermal or an epidermal disorder, and is selected  
 CC from psoriasis (preferably chronic stationary psoriasis, psoriasis  
 CC vulgaris, eruptive (glutamate) psoriasis, psoriatic erythroderma,  
 CC generalised pustular psoriasis (Von Zumbusch), annular pustular  
 CC psoriasis, and localised pustular psoriasis), psoriatic arthritis,  
 CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis rosacea,  
 CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,  
 CC ichthyosiform dermatosis, keratoderma, dermatosis, and prokeratosis,  
 CC preferably psoriasis. M1 is useful for treating a skin disorder such as  
 CC an inflammatory or neoplastic disorder of the epidermis or dermis,  
 CC preferably an epidermal precancerous or cancerous lesion. M1 is also  
 CC useful to treat or prevent disorders involving aberrant activity of PSMA-  
 CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837  
 CC and ABR44613 to ABR44733 represent sequences used in the exemplification  
 CC of the present invention  
 XX  
 SQ Sequence 19 AA;  
 Query Match 80.6%; Score 79; DB 6; Length 19;  
 Best Local Similarity 78.9%; Pred. No. 4.9e-06;  
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIRLKSNDNYATHYAESVKG 19  
 ||| : : : : :  
 Db 1 EIRSQNNPATHYAESVKG 19  
 ||| : : : : :  
 RESULT 9  
 ADR19284  
 ID ADR19284 standard; peptide; 19 AA.  
 XX  
 AC ADR19284;  
 XX  
 XX 21-OCT-2004 (first entry)  
 XX

DE Glycosylated MUC1 tumour epitope recognition variant peptide, SEQ ID 21.  
 XX Recognition molecule; bind; glycosylated MUC1 tumour epitope; mucin 1;  
 KW tumour; metastatic; carcinoma; breast; colon; stomach; pancreas; ovary;  
 KW liver; kidney cell; intestinal; lung cancer; multiple myeloma; variant.  
 XX Synthetic; Unidentified.  
 OS  
 XX WO2004065423-A2.  
 PN  
 XX 05-AUG-2004.  
 PD  
 XX 23-JAN-2004; 2004WO-DE000132.  
 PF  
 XX 23-JAN-2003; 2003DE-01003664.  
 PR  
 XX (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.  
 PA  
 XX Goletz S, Danielczyk A, Stahn R, Karsten U;  
 PI WPI; 2004-593433/57.  
 XX  
 XX New recognition molecules that bind the glycosylated MUC1 tumor epitope,  
 PT useful for prevention, diagnosis, treatment and monitoring of tumors.  
 PT  
 XX Claim 9; SEQ ID NO 21; 158pp; German.  
 PS  
 XX The invention relates to novel recognition molecules comprising sequences  
 CC that bind specifically to a glycosylated MUC1 tumour epitope. The novel  
 CC recognition molecules comprise: sequences ADR19264 or ADR19265; sequences  
 CC ADR19266 or ADR19267 and sequences ADR19268 and ADR19269, and bind  
 CC specifically to the glycosylated mucin 1 (MUC1) tumour epitope. The  
 CC invention further comprises: a construct comprising the recognition  
 CC molecule fused, chemically coupled or non-covalently associated with  
 CC additional sequences and/or structures; an isolated nucleic acid that  
 CC encodes the recognition molecule or construct; expression cassette or  
 CC vector that contains the isolated nucleic acid, operatively linked to a  
 CC promoter; virus or host cell comprising at least one cassette or vector  
 CC of ADR19266; an organism containing at least one host cell of ADR19267; a  
 CC method for preparing the recognition molecule and construct; and a kit  
 CC containing the recognition molecule and/or construct. The recognition  
 CC molecules have cytostatic activity. The recognition molecules, constructs  
 CC containing them, the nucleic acid encoding them, and derived viruses,  
 CC cells and organisms, are used for prevention, diagnosis, treatment and  
 CC monitoring of tumours and/or metastases, specifically where MUC1  
 CC positive, particularly carcinoma of breast, colon, stomach, pancreas,  
 CC ovary, liver or kidney cells; gastrointestinal or lung cancers and  
 CC multiple myeloma. The recognition molecules show little or no binding to  
 CC MUC1 in either the serum or normal tissue, so provides simple, safe and  
 CC efficient detection of tumours, even at an early stage (carcinoma in  
 CC situ), and can differentiate between tumours and benign diseases. This  
 CC sequence represents a variant glycosylated MUC1 tumour epitope  
 CC recognition peptide of the invention.  
 XX  
 SQ Sequence 19 AA;  
 Query Match 79.6%; Score 78; DB 8; Length 19;  
 Best Local Similarity 78.9%; Pred. No. 7.1e-06;  
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIRLKSNDNYATHYAESVKG 19  
 ||| : : : : :  
 Db 1 EIRSKANNYATYAESVKG 19  
 ||| : : : : :  
 RESULT 10  
 ADQ92379  
 ID ADQ92379 standard; peptide; 19 AA.  
 XX  
 AC ADQ92379;  
 XX  
 XX 23-SEP-2004 (first entry)  
 XX

DE Human h1 CDRH2 variant peptide, 153Xaa.

XX Tumour necrosis factor alpha; TNF-alpha; TNF-alpha mediated disease;

KW sepsis; autoimmune disease; rheumatoid arthritis; inflammatory disease;

KW neurodegenerative disease; malignancy; TNF-secreting tumour;

KW alcohol-induced hepatitis; psoriasis; psoriatic arthritis;

KW Wegener's granulomatosis; ankylosing spondylitis; heart failure;

KW reperfusion injury; chronic obstructive pulmonary disease;

KW pulmonary fibrosis; hepatitis C infection; Kawasaki's pathology;

KW Refsum's disease; ataxia; telangiectasia; Alzheimer's disease;

KW Down's syndrome; Parkinson's disease; leukaemia; myelodysplastic syndrome;

KW lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; Burkitt's syndrome;

KW hypokinetic movement disorder; drug-induced movement disorder;

KW Crohn's disease; ulcerative colitis; amyotrophic lateral sclerosis;

KW multiple sclerosis; Grave's disease; diabetes mellitus; atherosclerosis;

KW Shy-drager syndrome; cachexia; infectious disease; antibody therapy;

KW human; heavy chain variable region; VH; CDR;

KW complementarity determining region; variant; mutein; mutant.

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

FT Misc-difference 7

FT /note= "Encoded by NNN"

FT

FT

PN US2004131613-A1.

XX

XX 08-JUL-2004.

PD

XX

XX 08-JAN-2003; 2003US-00338627.

PF

XX

XX 08-JAN-2003; 2003US-00338627.

PR

XX

XX (WATK/) WATKINS J D.

PA (VASS/) VASSEROT A P.

PA (MARQ/) MARQUIS D.

PA (HUSE/) HUSE W D.

XX

XX Watkins JD, Vasserot AP, Marquis D, Huse WD;

PI

XX WPI; 2004-524894/50.

DR N-PSDB; ADQ92380.

DR

XX

XX New composition comprising a tumor necrosis factor alpha (TNF-alpha)

PT binding molecule, useful for treating a TNF-alpha mediated disease such

PT as sepsis, an autoimmune disease, rheumatoid arthritis, and

PT neurodegenerative diseases.

XX

XX Disclosure; SEQ ID NO 47; 60pp; English.

XX

XX The present invention relates to tumour necrosis factor alpha (TNF-alpha)

CC binding polypeptides and their encoding polynucleotides. The invention is

CC useful for treating TNF-alpha mediated disease such as sepsis, an

CC autoimmune disease, rheumatoid arthritis, inflammatory diseases,

CC neurodegenerative diseases, malignant pathologies involving TNF-secreting

CC tumours, alcohol-induced hepatitis, psoriasis, psoriatic arthritis,

CC Wegener's granulomatosis, ankylosing spondylitis, heart failure,

CC reperfusion injury, chronic obstructive pulmonary disease, pulmonary

CC fibrosis, hepatitis C infection, Kawasaki's pathology, Refsum's disease,

CC ataxia, telangiectasia, Alzheimer's disease, Down's syndrome, Parkinson's

CC disease, leukaemias (acute, chronic myelocytic, chronic lymphocytic

CC and/or myelodysplastic syndrome), lymphomas (Hodgkin's, non-Hodgkin's and

CC Burkitt's syndrome), hypokinetic movement disorders, drug-induced

CC movement disorders, Crohn's disease, ulcerative colitis, amyotrophic

CC lateral sclerosis, multiple sclerosis, Grave's disease, diabetes

CC mellitus, atherosclerosis, Shy-drager syndrome, cachexia and infectious

CC diseases. The invention is also useful in antibody therapy. The present

CC sequence is human h1 complementarity determining region (CDR) of heavy

CC chain variable (VH) region (CDRH) variant peptide. This sequence is used

CC in the invention.

XX

XX Sequence 19 AA;

SQ

Query Match 77.6%; Score 76; DB 8; Length 19;

Best Local Similarity 84.2%; Pred. No. 1.5e-05;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRLKSNDYATHVAESVKG 19

Db 1 EIRSKSXNSATHVAESVKG 19

|||||

RESULT 11

ADQ80568

ID ADQ80568 standard; peptide; 19 AA.

XX

AC ADQ80568;

XX

DT 23-SEP-2004 (first entry)

XX

DE TNF-alpha binding molecule heavy chain CDR #7.

XX

XX TNF-alpha binding; complementarity determining region; CDR; TNF-alpha;

KW immunoassay; CDRH-3; sepsis; autoimmune disease;

KW rheumatoid arthritis; allergy; multiple sclerosis;

KW systemic lupus erythematosus; scleroderma; diabetes mellitus; cachexia;

KW parasitic disease; infectious disease; ulcerative colitis; Crohn's disease;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW disseminated intravascular coagulation; Parkinson's disease;

KW Alzheimer's disease; Down's syndrome; psoriasis; ankylosing spondylitis;

KW Wegener's granulomatosis; idiopathic pulmonary fibrosis; asthma;

KW graft-versus-host disease; leukemia.

XX

OS Synthetic.

XX

XX US2004131612-A1.

PN

XX

XX 08-JUL-2004.

PD

XX

XX 08-JAN-2003; 2003US-00338552.

PF

XX

XX 08-JAN-2003; 2003US-00338552.

PR

XX

XX (WATK/) WATKINS J D.

PA (VASS/) VASSEROT A P.

PA (MARQ/) MARQUIS D.

PA (HUSE/) HUSE W D.

XX

XX Watkins JD, Vasserot AP, Marquis D, Huse WD;

PI

XX WPI; 2004-516978/49.

DR N-PSDB; ADQ80569.

DR

XX

XX Composition useful for treating diseases such as leukemia, asthma,

PT rheumatoid arthritis, Alzheimer's disease, psoriasis or multiple

PT sclerosis, comprises TNF-alpha binding molecule.

XX

XX Disclosure; SEQ ID NO 47; 60pp; English.

XX

XX The invention relates to a composition which comprises a TNF-alpha

CC binding molecule having sequence of complementarity determining region

CC (CDR) in light chain variable region (CDRL)-3 and sequence of CDR in

CC heavy chain variable region (CDRH)-3. The composition is useful in the

CC treatment of TNF-alpha mediated diseases. TNF-alpha binding molecule is

CC useful for treating sepsis, autoimmune disease, rheumatoid arthritis,

CC allergy, multiple sclerosis, systemic lupus erythematosus, scleroderma,

CC diabetes mellitus, cachexia, acute and chronic parasitic and/or

CC infectious diseases, sarcoidosis, inflammatory bowel disease, ulcerative

CC colitis, Crohn's disease, disseminated intravascular coagulation,

CC Parkinson's disease, Alzheimer's disease, Down's syndrome, psoriasis,

CC ankylosing spondylitis, Wegener's granulomatosis, idiopathic pulmonary

CC fibrosis, asthma, graft-versus-host disease, or leukemia. TNF-alpha

CC binding molecule is useful in diagnostic methods for detecting TNF-alpha

CC in patients known to be or suspected of having TNF-alpha-mediated

CC disease. TNF-alpha binding molecule is useful in immunoassays for

CC detecting or quantifying TNF-alpha in a sample. The present sequence

CC represents the amino acid sequence of a TNF-alpha binding molecule heavy chain.

XX Sequence 19 AA;

Query Match 77.6%; Score 76; DB 8; Length 19;  
Best Local Similarity 84.2%; Pred. No. 1.5e-05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHVAESVKG 19

Db 1 EIRKSDNYATHVAESVKG 19

RESULT 12

AAV40694

ID AAY40694 standard; peptide; 16 AA.

XX AAY40694;

DT 01-DEC-1999 (first entry)

DE A3 derivative #15, beta strand of scaffold protein structure.

XX Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;  
KW tumour; chemotherapeutic agent.

XX Synthetic.

PN EP947582-A1.

XX 06-OCT-1999.

XX 31-MAR-1998; 98EP-00870065.

XX 31-MAR-1998; 98EP-00870065.

PA (INNO-) INNOGENETICS NV.

PI Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 1999-542958/46.

XX New scaffold protein, useful for stabilizing antigens used as vaccines.

XX Disclosure; Page 6; 105pp; English.

XX Sequences AAY40680-Y40703 are functionally equivalent derivatives of the A3 peptide (AAY40605) which forms part of a scaffold protein. A3 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines

XX Sequence 16 AA;

Query Match 75.5%; Score 74; DB 2; Length 16;  
Best Local Similarity 87.5%; Pred. No. 2.7e-05;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLKSDNYATHVAESVK 18

Db 1 RLKSDNYATHVAESVK 18

RESULT 13

ADH89399

ID ADH89399 standard; peptide; 19 AA.

XX ADH89399;

DT 15-APR-2004 (first entry)

DE Human transferrin fusion protein-related CDR2 peptide SeqID43.

XX fusion protein; transferrin protein; glycosylation;

KW antibody variable region; cytostatic; antibacterial; virucide;

KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;

KW septic shock; endotoxic shock; cachexia syndrome; bacterial infection;

KW viral infection; parasitic infection; neoplasm; autoimmune disease;

XX arthritis; graft rejection.

XX Unidentified.

XX US2003226155-A1.

XX 04-DEC-2003.

XX 10-MAR-2003; 2003US-00384060.

XX 30-AUG-2001; 2001US-0315745P.

XX 30-NOV-2001; 2001US-0334059P.

XX 30-AUG-2002; 2002US-00231494.

XX 30-AUG-2002; 2002US-0406977P.

XX (BIOR-) BIOREXIS PHARM CORP.

XX Sadeghi H, Prior CP, Turner A;

XX WPI; 2004-022093/02.

XX New fusion protein comprising a transferrin protein exhibiting reduced glycosylation fused to at least one antibody variable region, useful for preparing a composition for treating e.g., septic shock, neoplasm or autoimmune disease.

XX Example 2; SEQ ID NO 43; 82pp; English.

XX This invention relates to a novel fusion protein which comprises a transferrin protein exhibiting reduced glycosylation fused to at least one antibody variable region. The invention may be useful for the development of compounds with cytostatic, antibacterial, virucide, antiparasitic, immunosuppressive or antiarthritic activity. In addition, the sequences disclosed may be useful for gene therapy. The fusion protein is useful for preparing a composition for treating a disease or disease symptom in a patient for example septic shock, endotoxic shock, cachexia syndromes associated with bacterial, viral or parasitic infections, neoplasm, autoimmune disease, arthritis or adverse effects associated with treatment for preventing graft rejection. The present sequence is that of a CDR 2 peptide which was used in the exemplification of the invention.

XX Sequence 19 AA;

Query Match 75.5%; Score 74; DB 8; Length 19;  
Best Local Similarity 84.2%; Pred. No. 3.3e-05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIRLKSNDYATHYAESVKG 19  
 |||||  
 Db 1 EIRSKSINSATHYAESVKG 19  
 |||||  
 RESULT 14  
 ID ADQ92375  
 ADQ92375 standard; peptide; 19 AA.  
 XX  
 AC ADQ92375;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Human hul CDRH2 peptide.  
 XX  
 KW Tumour necrosis factor alpha; TNF-alpha; TNF-alpha mediated disease;  
 KW sepsis; autoimmune disease; rheumatoid arthritis; inflammatory disease;  
 KW neurodegenerative disease; malignancy; TNF-secreting tumour;  
 KW alcohol-induced hepatitis; psoriasis; psoriatic arthritis;  
 KW Wegener's granulomatosis; ankylosing spondylitis; heart failure;  
 KW reperfusion injury; chronic obstructive pulmonary disease;  
 KW pulmonary fibrosis; hepatitis C infection; Kawasaki's pathology;  
 KW Refsum's disease; ataxia; telangiectasia; Alzheimer's disease;  
 KW Down's syndrome; Parkinson's disease; leukaemia; myelodysplastic syndrome;  
 KW lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; Burkitt's syndrome;  
 KW hypokinetic movement disorder; drug-induced movement disorder;  
 KW Crohn's disease; ulcerative colitis; amyotrophic lateral sclerosis;  
 KW multiple sclerosis; Grave's disease; diabetes mellitus; atherosclerosis;  
 KW Shy-drager syndrome; cachexia; infectious disease; antibody therapy;  
 KW human; heavy chain variable region; VH; CDR;  
 KW complementarity determining region.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2004131613-A1.  
 XX  
 PD 08-JUL-2004.  
 XX  
 PF 08-JAN-2003; 2003US-00338627.  
 XX  
 PR 08-JAN-2003; 2003US-00338627.  
 XX  
 PA (WATK/) WATKINS J D.  
 PA (VASS/) VASSEROT A P.  
 PA (MARQ/) MARQUIS D.  
 PA (HUSE/) HUSE W D.  
 XX  
 PI Watkins JD, Vasserot AP, Marquis D, Huse WD;  
 DR WPI; 2004-524894/50.  
 DR N-PSDB; ADQ92376.  
 XX  
 XX New composition comprising a tumor necrosis factor alpha (TNF-alpha)  
 PT binding molecule, useful for treating a TNF-alpha mediated disease such  
 PT as sepsis, an autoimmune disease, rheumatoid arthritis, and  
 PT neurodegenerative diseases.  
 XX  
 PS Disclosure; SEQ ID NO 43; 60pp; English.  
 XX  
 CC The present invention relates to tumour necrosis factor alpha (TNF-alpha)  
 CC binding polypeptides and their encoding polynucleotides. The invention is  
 CC useful for treating TNF-alpha mediated disease such as sepsis, an  
 CC autoimmune disease, rheumatoid arthritis, inflammatory diseases,  
 CC neurodegenerative diseases, malignant pathologies involving TNF-secreting  
 CC tumours, alcohol-induced hepatitis, psoriasis, psoriatic arthritis,  
 CC Wegener's granulomatosis, ankylosing spondylitis, heart failure,  
 CC reperfusion injury, chronic obstructive pulmonary disease, pulmonary  
 CC fibrosis, hepatitis C infection, Kawasaki's pathology, Refsum's disease,  
 CC ataxia, telangiectasia, Alzheimer's disease, Down's syndrome, Parkinson's  
 CC disease, leukaemias (acute, chronic myelocytic, chronic lymphocytic  
 CC and/or myelodysplastic syndrome), lymphomas (Hodgkin's, non-Hodgkin's and  
 CC Burkitt's syndrome), hypokinetic movement disorders, drug-induced  
 CC movement disorders, Crohn's disease, ulcerative colitis, amyotrophic

CC lateral sclerosis, multiple sclerosis, Grave's disease, diabetes  
 CC mellitus, atherosclerosis, Shy-drager syndrome, cachexia and infectious  
 CC diseases. The invention is also useful in antibody therapy. The present  
 CC sequence is human hul complementarity determining region (CDR) of heavy  
 CC chain variable (VH) region (CDRH) peptide. This sequence is used in the  
 CC invention.  
 XX  
 SQ Sequence 19 AA;  
 Query Match 75.5%; Score 74; DB 8; Length 19;  
 Best Local Similarity 84.2%; Pred. NO. 3.3e-05;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 EIRLKSNDYATHYAESVKG 19  
 |||||  
 Db 1 EIRSKSINSATHYAESVKG 19  
 |||||  
 RESULT 15  
 ID ADQ92377 standard; peptide; 19 AA.  
 XX  
 AC ADQ92377;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Human hul CDRH2 variant peptide, I53M.  
 XX  
 KW Tumour necrosis factor alpha; TNF-alpha; TNF-alpha mediated disease;  
 KW sepsis; autoimmune disease; rheumatoid arthritis; inflammatory disease;  
 KW neurodegenerative disease; malignancy; TNF-secreting tumour;  
 KW alcohol-induced hepatitis; psoriasis; psoriatic arthritis;  
 KW Wegener's granulomatosis; ankylosing spondylitis; heart failure;  
 KW reperfusion injury; chronic obstructive pulmonary disease;  
 KW pulmonary fibrosis; hepatitis C infection; Kawasaki's pathology;  
 KW Refsum's disease; ataxia; telangiectasia; Alzheimer's disease;  
 KW Down's syndrome; Parkinson's disease; leukaemia; myelodysplastic syndrome;  
 KW lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; Burkitt's syndrome;  
 KW hypokinetic movement disorder; drug-induced movement disorder;  
 KW Crohn's disease; ulcerative colitis; amyotrophic lateral sclerosis;  
 KW multiple sclerosis; Grave's disease; diabetes mellitus; atherosclerosis;  
 KW Shy-drager syndrome; cachexia; infectious disease; antibody therapy;  
 KW human; heavy chain variable region; VH; CDR;  
 KW complementarity determining region; variant; mutant.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2004131613-A1.  
 XX  
 PD 08-JUL-2004.  
 XX  
 PF 08-JAN-2003; 2003US-00338627.  
 XX  
 PR 08-JAN-2003; 2003US-00338627.  
 XX  
 PA (WATK/) WATKINS J D.  
 PA (VASS/) VASSEROT A P.  
 PA (MARQ/) MARQUIS D.  
 PA (HUSE/) HUSE W D.  
 XX  
 PI Watkins JD, Vasserot AP, Marquis D, Huse WD;  
 DR WPI; 2004-524894/50.  
 DR N-PSDB; ADQ92378.  
 XX  
 XX New composition comprising a tumor necrosis factor alpha (TNF-alpha)  
 PT binding molecule, useful for treating a TNF-alpha mediated disease such  
 PT as sepsis, an autoimmune disease, rheumatoid arthritis, and  
 PT neurodegenerative diseases.  
 XX  
 PS Disclosure; SEQ ID NO 45; 60pp; English.  
 XX  
 CC The present invention relates to tumour necrosis factor alpha (TNF-alpha)

CC binding polypeptides and their encoding polynucleotides. The invention is  
 CC useful for treating TNF-alpha mediated disease such as sepsis, an  
 CC autoimmune disease, rheumatoid arthritis, inflammatory diseases,  
 CC neurodegenerative diseases, malignant pathologies involving TNF-secreting  
 CC tumours, alcohol-induced hepatitis, psoriasis, psoriatic arthritis,  
 CC Wegener's granulomatosis, ankylosing spondylitis, heart failure,  
 CC reperfusion injury, chronic obstructive pulmonary disease, pulmonary  
 CC fibrosis, hepatitis C infection, Kawasaki's pathology, Refsum's disease,  
 CC ataxia, telangiectasia, Alzheimer's disease, Down's syndrome, Parkinson's  
 CC disease, leukaemias (acute, chronic myelocytic, chronic lymphocytic  
 CC and/or myelodysplastic syndrome), lymphomas (Hodgkin's, non-Hodgkin's and  
 CC Burkitt's syndrome), hypokinetic movement disorders, drug-induced  
 CC movement disorders, crohn's disease, ulcerative colitis, amyotrophic  
 CC lateral sclerosis, multiple sclerosis, Grave's disease, diabetes  
 CC mellitus, atherosclerosis, Shy-drager syndrome, cachexia and infectious  
 CC diseases. The invention is also useful in antibody therapy. The present  
 CC sequence is human hul complementarity determining region (CDR) of heavy  
 CC chain variable (VH) region (CDRH) variant peptide. This sequence is used  
 CC in the invention.

XX

SQ Sequence 19 AA;

Query Match 75.5%; Score 74; DB 8; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 3.3e-05;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIRLKSNDNVATHYAESVKG 19  
 |||||  
 Db 1 EIRSKSWNSATHYAESVKG 19  
 |||||

Search completed: April 18, 2005, 15:53:43  
 Job time : 170 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 15:56:54 ; Search time 130 Seconds  
(without alignments)  
48.577 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLKSNDYATHYAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 284765

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	92.9	19	16	US-10-769-308-32
2	91	92.9	19	17	US-10-769-074-32
3	82	83.7	17	17	US-10-879-994-68
4	79	80.6	19	14	US-10-160-506-30
5	79	80.6	19	16	US-10-449-379-30
6	79	80.6	19	16	US-10-688-015-30
7	76	77.6	19	16	US-10-338-552-47
8	76	77.6	19	16	US-10-338-627-47
9	74	75.5	19	15	US-10-384-060-43
10	74	75.5	19	16	US-10-338-552-43
11	74	75.5	19	16	US-10-338-552-45
12	74	75.5	19	16	US-10-338-627-43
13	74	75.5	19	16	US-10-338-627-45

14	71	72.4	19	10	US-09-791-551-87	Sequence 87, Appl
15	70	71.4	19	11	US-09-842-776A-14	Sequence 14, Appl
16	69	70.4	19	16	US-10-338-552-49	Sequence 49, Appl
17	69	70.4	19	16	US-10-338-552-55	Sequence 55, Appl
18	69	70.4	19	16	US-10-338-627-49	Sequence 49, Appl
19	69	70.4	19	16	US-10-338-627-55	Sequence 55, Appl
20	68	69.4	19	9	US-09-839-666-4	Sequence 4, Appl
21	68	69.4	19	14	US-10-234-579-4	Sequence 4, Appl
22	68	69.4	19	15	US-10-372-735-46	Sequence 46, Appl
23	68	69.4	19	16	US-10-338-552-51	Sequence 51, Appl
24	68	69.4	19	16	US-10-338-627-51	Sequence 51, Appl
25	66	67.3	19	10	US-09-947-839-78	Sequence 78, Appl
26	65	66.3	19	9	US-09-835-087-18	Sequence 18, Appl
27	64	65.3	19	14	US-10-230-880-125	Sequence 125, Appl
28	55	56.1	17	17	US-10-879-994-20	Sequence 20, Appl
29	53	54.1	11	17	US-10-879-994-71	Sequence 71, Appl
30	52	53.1	17	14	US-10-031-874A-105	Sequence 105, Appl
31	52	53.1	19	15	US-10-436-782-23	Sequence 23, Appl
32	49	50.0	19	10	US-09-563-222-51	Sequence 51, Appl
33	49	50.0	19	16	US-10-783-950-51	Sequence 51, Appl
34	48	49.0	17	9	US-09-192-854-60	Sequence 60, Appl
35	48	49.0	17	9	US-09-968-561A-98	Sequence 98, Appl
36	48	49.0	17	10	US-09-968-744A-98	Sequence 98, Appl
37	48	49.0	17	11	US-09-968-561A-98	Sequence 98, Appl
38	48	49.0	19	10	US-09-563-222-60	Sequence 60, Appl
39	48	49.0	19	16	US-10-783-950-60	Sequence 60, Appl
40	46	46.9	17	9	US-09-192-854-164	Sequence 164, Appl
41	46	46.9	17	9	US-09-968-561A-290	Sequence 290, Appl
42	46	46.9	17	10	US-09-968-744A-290	Sequence 290, Appl
43	46	46.9	17	11	US-09-968-561A-290	Sequence 290, Appl
44	46	46.9	17	16	US-10-327-598-481	Sequence 481, Appl
45	45	45.9	17	17	US-10-725-962-85	Sequence 85, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-769-308-32  
; Sequence 32, Application US/10769308  
; Publication No. US20050003465A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Robert E.  
; APPLICANT: Witte, Owen N.  
; APPLICANT: Saffran, Douglas C.  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: The Regents of the University of California  
; APPLICANT: Agensys, Inc.  
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof  
; FILE REFERENCE: 02307K-141589US  
; CURRENT APPLICATION NUMBER: US/10/769,308  
; CURRENT FILING DATE: 2004-01-29  
; PRIOR APPLICATION NUMBER: US 08/814,279  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: US 60/228,816  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: US 60/071,141  
; PRIOR FILING DATE: 1998-01-12  
; PRIOR APPLICATION NUMBER: US 60/074,675  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 09/038,261  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: US 09/203,939  
; PRIOR FILING DATE: 1998-12-02  
; PRIOR APPLICATION NUMBER: US 60/113,230  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: US 09/251,835  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: US 60/120,536  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: US 60/124,658  
; PRIOR FILING DATE: 1999-03-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.

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; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PSCA mab 2H9
; OTHER INFORMATION: CDR2
US-10-769-308-32

Query Match          92.9%; Score 91; DB 16; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
    ||||:|||||||
Db 1 EIRLSENATHYAESVKG 19

RESULT 2
US-10-769-074-32
; Sequence 32, Application US/10769074
; Publication No. US2005005909A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safiran, Douglas C.
; APPLICANT: Jakobovits, Aya
; APPLICANT: The Regents of the University of California
; APPLICANT: Agensys, Inc.
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof
; FILE REFERENCE: 02307K-141589US
; CURRENT APPLICATION NUMBER: US/10/769,074
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US/10/769,308
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/228,816
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: US 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: US 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/120,536
; PRIOR FILING DATE: 1999-02-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PSCA mab 2H9
; OTHER INFORMATION: CDR2
US-10-769-074-32

Query Match          92.9%; Score 91; DB 17; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
    ||||:|||||||
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Db 1 EIRLSENATHYAESVKG 19

RESULT 3
US-10-879-994-68
; Sequence 68, Application US/10879994
; Publication No. US20050032175A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Iancopoulos, George D.
; APPLICANT: Karow, Margaret
; APPLICANT: Smith, Eric
; TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC MET
; FILE REFERENCE: REG 203E2
; CURRENT APPLICATION NUMBER: US/10/879,994
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/610,452
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 17
; TYPE: PRT
; ORGANISM: mus musculus
US-10-879-994-68

Query Match          83.7%; Score 82; DB 17; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESV 17
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Db 1 EIRLSDNYATHYAESV 17

RESULT 4
US-10-160-506-30
; Sequence 30, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-162001
; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-160-506-30

Query Match          80.6%; Score 79; DB 14; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.6e-05;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
    ||||:|||||||
Db 1 EIRSDNNFATHYAESVKG 19

RESULT 5
US-10-449-379-30
; Sequence 30, Application US/10449379
; Publication No. US20040120958A1
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: GENERAL INFORMATION:
: APPLICANT: Bander, Neil H.
: TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
: FILE REFERENCE: 10448-163002
: CURRENT APPLICATION NUMBER: US/10/449,379
: CURRENT FILING DATE: 2003-05-30
: PRIOR APPLICATION NUMBER: 10/160,505
: PRIOR FILING DATE: 2002-05-30
: PRIOR APPLICATION NUMBER: 60/323,585
: PRIOR FILING DATE: 2001-09-20
: PRIOR APPLICATION NUMBER: 60/362,810
: PRIOR FILING DATE: 2002-03-08
: PRIOR APPLICATION NUMBER: 60/295,214
: PRIOR FILING DATE: 2001-06-01
: NUMBER OF SEQ ID NOS: 128
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 30
: LENGTH: 19
: TYPE: PRT
: ORGANISM: Mus musculus
: US-10-449-379-30

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Query Match      80.6%; Score 79; DB 16; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.6e-05;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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**Qy**      1 EIRLKSDNYATHAESVKG 19  
         ||| : | : | : | : |  
**Db**      1 EIRSQSNNFATHAESVKG 19

## RESULT 6

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US-10-688-015-30
; Sequence 30, Application US/10688015
; Publication No. US20040036998A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: INSULIN-RELATED DISORDERS USING BINDING AGENTS SPECIFIC FOR
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-196001
; CURRENT APPLICATION NUMBER: US/10/688,015
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/422,396
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-688-015-30

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Query Match 80.6%; Score 79; DB 16; Length 19;  
Best Local Similarity 78.9%; Pred.No. 1.6e-05;  
Matches 15; Conservative 3; Mismatches 1; Indels

Qy 1 EIRLKSDNYATHYAESVKG 19  
||| : : : |||  
Db 1 EIRSQSNFATHYAESVKG 19

## RESULT 7

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US-10-338-552-47
; Sequence 47, Application US/10339552
; Publication No. US20040131612A1
;
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: TNF-alpha Binding Molecules

```

```

; FILE REFERENCE: AWE-06971
; CURRENT APPLICATION NUMBER: US/10/338,552
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-338-552-47

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Query Match	77.6%;	Score 76;	DB 16;	Length 19;
Best Local Similarity	84.2%;	Pred. No. 4.8e-05;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

**Qy**

1 EIRLKSDNYATHYAESVKG 19  
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**Db**

1 EIRSKSXNSATHYAESVKG 19

## RESULT 8

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US-10-338-627-47
; Sequence 47, Application US/10338627
; Publication No. US20040131613A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffery D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: TNF-alpha Binding Molecules
; FILE REFERENCE: AME-07497
; CURRENT APPLICATION NUMBER: US/10/338,627
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: Xaa can be any naturally occ
US-10-338-627-47

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Query Match	77.6%;	Score 76;	DB 16;	Length 19;
Best Local Similarity	84.2%;	Pred. No. 4.8e-05;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

**Qy**

1 EIRLKSDNYATHYAESVKG 19  
||| || | ||| ||| |||  
**Db**

1 EIRSKSXNSATHYAESVKG 19

## RESULT 9

US-10-384-060-43  
; Sequence 43, Application US/10384060  
; Publication No. US20030226155A1  
; GENERAL INFORMATION:  
; APPLICANT: SADEGHI, Homayoun  
; APPLICANT: PRIOR, Christopher P.  
; APPLICANT: TURNER, Andrew  
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS  
; FILE REFERENCE: 54710-5004-US  
; CURRENT APPLICATION NUMBER: US/10/384,060

; CURRENT FILING DATE: 2003-03-10  
; PRIOR APPLICATION NUMBER: US 10/231,494  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US 60/334,059  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: US 60/315,745  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 60/406,977  
; PRIOR FILING DATE: 2002-08-30  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 43  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: P VH CDR2 sequence  
US-10-384-060-43

Query Match 75.5%; Score 74; DB 15; Length 19;  
Best Local Similarity 84.2%; Pred. No. 9.8e-05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHAESVKG 19  
Db 1 EIRKSDNYATHAESVKG 19

RESULT 10  
US-10-338-552-43  
; Sequence 43, Application US/10338552  
; Publication No. US20040131612A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Vasserot, Alain P.  
; APPLICANT: Marquis, David  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: TNF-alpha Binding Molecules  
; FILE REFERENCE: AME-06971  
; CURRENT APPLICATION NUMBER: US/10/338,552  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 43  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-338-552-43

Query Match 75.5%; Score 74; DB 16; Length 19;  
Best Local Similarity 84.2%; Pred. No. 9.8e-05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHAESVKG 19  
Db 1 EIRKSDNYATHAESVKG 19

RESULT 11  
US-10-338-552-45  
; Sequence 45, Application US/10338552  
; Publication No. US20040131612A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Vasserot, Alain P.  
; APPLICANT: Marquis, David  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: TNF-alpha Binding Molecules  
; FILE REFERENCE: AME-06971  
; CURRENT APPLICATION NUMBER: US/10/338,552  
; CURRENT FILING DATE: 2003-01-08

; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 45  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-338-552-45

Query Match 75.5%; Score 74; DB 16; Length 19;  
Best Local Similarity 84.2%; Pred. No. 9.8e-05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHAESVKG 19  
Db 1 EIRKSDNYATHAESVKG 19

RESULT 12  
US-10-338-627-43  
; Sequence 43, Application US/10338627  
; Publication No. US20040131613A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Vasserot, Alain P.  
; APPLICANT: Marquis, David  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: TNF-alpha Binding Molecules  
; FILE REFERENCE: AME-07497  
; CURRENT APPLICATION NUMBER: US/10/338,627  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 43  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-338-627-43

Query Match 75.5%; Score 74; DB 16; Length 19;  
Best Local Similarity 84.2%; Pred. No. 9.8e-05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHAESVKG 19  
Db 1 EIRKSDNYATHAESVKG 19

RESULT 13  
US-10-338-627-45  
; Sequence 45, Application US/10338627  
; Publication No. US20040131613A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Vasserot, Alain P.  
; APPLICANT: Marquis, David  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: TNF-alpha Binding Molecules  
; FILE REFERENCE: AME-07497  
; CURRENT APPLICATION NUMBER: US/10/338,627  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 45  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-338-627-45

**Qy**            1 EIRLKSDNYATHAESVKG 19  
               |||||  
**Dd**            1 EIRSKSMNSATHAESVKG 19

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Query Match          72.4%; Score 71; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 0.00029;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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1 EIRLKSDNYATHYAESVKG 19  
|||:|:|:|:|:|:|  
1 EIRSKAHNHATYYAESVKG 19

Query Match 71.4%; Score 70; DB 11; Length 19;  
Best Local Similarity 82.4%; Pred. No. 0.00042;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

2 IRLKSDNYATHAESVK 18

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:48:43 ; Search time 40 Seconds  
(without alignments)  
35.458 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLSDNYATHYAEVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 187692

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	69.4	19	2	US-08-737-085A-4
2	68	69.4	19	3	US-09-246-258-4
3	68	69.4	19	3	US-09-532-106-4
4	68	69.4	19	4	US-09-839-666-4
5	66	67.3	19	1	US-07-977-696C-78
6	66	67.3	19	1	US-08-129-930B-78
7	66	67.3	19	3	US-08-376-288A-78
8	49	50.0	19	1	US-08-318-970B-6
9	49	50.0	19	4	US-09-563-222C-51
10	48	49.0	17	4	US-09-192-854-60
11	48	49.0	19	4	US-09-563-222C-60
12	47	48.0	19	1	US-08-318-970B-5
13	46	46.9	17	4	US-09-192-854-164
14	45	45.9	17	4	US-09-424-840B-63
15	45	45.9	17	4	US-09-424-840B-74
16	45	45.9	19	2	US-08-765-783A-85
17	45	45.9	19	3	US-09-416-557-85
18	45	45.9	19	4	US-08-407-620A-2
19	44	44.9	17	1	US-08-264-093-22
20	43	43.9	17	4	US-09-192-854-37
21	43	43.9	17	4	US-09-424-840B-64
22	41	41.8	17	4	US-09-192-854-4
23	41	41.8	17	4	US-09-192-854-115
24	41	41.8	17	4	US-09-424-840B-72
25	41	41.8	17	4	US-09-424-840B-88
26	40	40.8	17	4	US-09-192-854-10
27	40	40.8	17	4	US-09-192-854-18

28	40	40.8	17	4	US-09-192-854-96	Sequence 96, Appl
29	40	40.8	17	4	US-09-424-840B-107	Sequence 107, Appl
30	39	39.8	14	2	US-08-452-724A-41	Sequence 41, Appl
31	39	39.8	14	4	US-08-453-623-41	Sequence 41, Appl
32	39	39.8	17	2	US-08-650-262-14	Sequence 14, Appl
33	39	39.8	17	4	US-09-192-854-29	Sequence 29, Appl
34	39	39.8	17	4	US-09-192-854-68	Sequence 68, Appl
35	39	39.8	17	4	US-09-192-854-93	Sequence 93, Appl
36	39	39.8	17	4	US-09-192-854-124	Sequence 124, Appl
37	39	39.8	17	4	US-09-192-854-139	Sequence 139, Appl
38	38	38.8	17	1	US-08-053-171-31	Sequence 31, Appl
39	38	38.8	17	4	US-09-424-840B-76	Sequence 76, Appl
40	37	37.8	16	4	US-09-155-106-2	Sequence 2, Appl
41	37	37.8	17	4	US-09-192-854-22	Sequence 22, Appl
42	37	37.8	17	4	US-09-192-854-64	Sequence 64, Appl
43	37	37.8	17	4	US-09-192-854-71	Sequence 71, Appl
44	37	37.8	17	4	US-09-192-854-86	Sequence 86, Appl
45	37	37.8	17	4	US-09-192-854-99	Sequence 99, Appl

#### ALIGNMENTS

RESULT 1  
US-08-737-085A-4  
; Sequence 4, Application US/08737085A  
; Patent No. 5869232  
; GENERAL INFORMATION:  
; APPLICANT: SALLBERG, MATTI  
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY  
; TITLE OF INVENTION: EXCHANGER  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DARBY & DARBY PC  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/737,085A  
FILING DATE: 27-DEC-1996  
CLASSIFICATION: 426  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Reza  
REGISTRATION NUMBER: 38,475  
REFERENCE/DOCKET NUMBER: 3846/0C569  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7659  
TELEFAX: 212-753-6237  
TELEX: 236687

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-737-085A-4

Query Match 69.4%; Score 68; DB 2; Length 19;  
Best Local Similarity 72.2%; Pred. No. 0.00018;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAEVKG 19



TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-839-666-4

Query Match 69.4%; Score 68; DB 4; Length 19;  
Best Local Similarity 72.2%; Pred. No. 0.00018;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVKG 19  
DB 2 VRSKSFNYATYADSVKG 19

RESULT 5  
US-07-977-696C-78  
Sequence 78, Application US/07977696C  
Patent No. 5792852  
GENERAL INFORMATION:  
APPLICANT: do Couto, Fernando J.R.  
APPLICANT: Ceriani Dr., Roberto L.  
APPLICANT: Peterson Dr., Jerry A.  
APPLICANT: Padlan Dr., Eduardo A.  
TITLE OF INVENTION: Analogue Peptides with Specificity  
TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination  
TITLE OF INVENTION: and Therapeutic Methods.  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,696C  
FILING DATE: 11-16-92  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel Ph.D., Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P66 38227  
TELEPHONE: (510) 748-6868  
TELEFAX: (510) 748-6688  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-977-696C-78

Query Match 67.3%; Score 66; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 0.00038;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
DB 1 EIRNKANNHATYDES VKG 19

RESULT 6  
US-08-129-930B-78  
Sequence 78, Application US/08129930B  
Patent No. 5804187  
GENERAL INFORMATION:  
APPLICANT: do Couto Dr., Fernando J.R.  
APPLICANT: Ceriani Dr., Roberto L.  
APPLICANT: Peterson Dr., Jerry A.  
APPLICANT: Padlan Dr., Eduardo A.  
TITLE OF INVENTION: Analogue Peptides With Broad  
TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
TITLE OF INVENTION: Diagnostic Vaccination and  
TITLE OF INVENTION: Therapeutic Methods  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: V. AMZEL & ASSOC.  
STREET: 2055 No. 5804187th Broadway, Suite 201  
CITY: Walnut Creek  
STATE: California  
COUNTRY: USA  
ZIP: 94596  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/129,930B  
FILING DATE: September 30, 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel Ph.D., Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: CRECC-008A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 521-1333  
TELEFAX: (510) 521-3541  
TELEX: n.a.  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-129-930B-78

Query Match 67.3%; Score 66; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 0.00038;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19  
DB 1 EIRNKANNHATYDES VKG 19

RESULT 7  
US-08-976-288A-78  
Sequence 78, Application US/08976288A  
Patent No. 6315997  
GENERAL INFORMATION:  
APPLICANT: do Couto Dr., Fernando J.R.  
APPLICANT: Ceriani Dr., Roberto L.  
APPLICANT: Peterson Dr., Jerry A.  
APPLICANT: Padlan Dr., Eduardo A.  
TITLE OF INVENTION: Analogue Peptides With Broad  
TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
TITLE OF INVENTION: Diagnostic Vaccination and  
TITLE OF INVENTION: Therapeutic Methods  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder & Poplawski

```
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-78

Query Match 67.3%; Score 66; DB 3; Length 19;
Best Local Similarity 68.4%; Pred. No. 0.00038;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHVAESVKG 19
||| |::|||:|||||
Db 1 EIRKANNHATYYDES VKG 19

RESULT 8
US-08-318-970B-6
; Sequence 6, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg

; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,288A
; FILING DATE: No. 6315997ember 21, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/129,930
; FILING DATE: September 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. 6315997ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-976-288A-78

; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR2-3
; OTHER INFORMATION: hypervariable region
; US-08-318-970B-6

Query Match 50.0%; Score 49; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 0.21;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHVAESVKG 19
||| |::|||:|||||
Db 2 IRNKANYTTEYSASVKG 19

RESULT 9
US-09-563-222C-51
; Sequence 51, Application US/09563222C
; Patent No. 6696820
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-563-222C-51

Query Match 50.0%; Score 49; DB 4; Length 19;
Best Local Similarity 60.0%; Pred. No. 0.21;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 KSDNYATHVAESVKG 19
||| |::|||:|||||
Db 5 KTDGGSTTYADSVKG 19

RESULT 10
US-09-192-854-60
; Sequence 60, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-60

Query Match          49.0%; Score 48; DB 4; Length 17;
Best Local Similarity 52.9%; Pred. No. 0.28;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAEVSKG 19
   | : | | | | | | | |
Db 1 RIPARGTVHYADSVKG 17

RESULT 11
US-09-563-222C-60
; Sequence 60, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 60
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-60

Query Match          49.0%; Score 48; DB 4; Length 19;
Best Local Similarity 52.9%; Pred. No. 0.31;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAEVSKG 19
   | : | | | | | | | |
Db 3 RKNKANDYTEYSASVKG 19

RESULT 12
US-08-318-970B-5
; Sequence 5, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
```

```
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR2-2
; OTHER INFORMATION: hypervariable region
US-08-318-970B-5

Query Match          48.0%; Score 47; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 0.45;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRKSDNYATHYAEVSKG 19
   | | : | | : | | | |
Db 2 IRKKNLYTTDYSVKG 19

RESULT 13
US-09-192-854-164
; Sequence 164, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 164
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-164

Query Match          46.9%; Score 46; DB 4; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.58;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 SDNYATHYAEVSKG 19
   | | | | | | | | | |
Db 4 SSGYGTGYADSVKG 17

RESULT 14
US-09-424-840B-63
; Sequence 63, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
```

```

; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-424-840B-63

```

```

Query Match      45.9%; Score 45; DB 4; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 THYAESVKG 19
      ||||:||||
Db      9 THYADSVKG 17

```

```

RESULT 15
US-09-424-840B-74
; Sequence 74, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-424-840B-74

```

```

Query Match      45.9%; Score 45; DB 4; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 THYAESVKG 19
      ||||:||||
Db      9 THYADSVKG 17

```

Search completed: April 18, 2005, 15:58:24  
Job time : 40 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 13:59:59 ; Search time 5.93023 Seconds  
(without alignments)  
48.674 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	18	2 S43834	DNA topoisomerase
2	16	100.0	21	2 D48518	PEB1 5'-region hyp
3	16	100.0	23	1 S20453	pyrroloquinoline q
4	16	100.0	25	2 F84666	hypothetical prote
5	16	100.0	30	2 A26188	lipocortin I - pig
6	16	100.0	30	2 A44682	nitrobenzene nitro
7	16	100.0	31	2 H82818	hypothetical prote
8	16	100.0	32	2 PQ0413	nonstructural prot
9	16	100.0	33	2 PQ0416	RNA-directed RNA p
10	16	100.0	33	2 A95119	hypothetical prote
11	16	100.0	33	2 H82096	hypothetical prote
12	16	100.0	33	2 S33646	hypothetical prote
13	16	100.0	35	2 PS0363	protein-tyrosine-p
14	16	100.0	35	2 PS0364	protein-tyrosine-p
15	16	100.0	36	2 D87544	hypothetical prote
16	16	100.0	37	2 C70186	hypothetical prote
17	16	100.0	37	2 G95919	probable transposa
18	16	100.0	38	2 S33402	Ig heavy chain V r
19	16	100.0	38	2 B19803	proline-rich phosph
20	16	100.0	39	2 D82085	hypothetical prote
21	16	100.0	39	2 A96026	hypothetical prote
22	16	100.0	40	2 A23098	probable transposa
23	16	100.0	43	1 ZDBPT9	larvicidal toxin -
24	16	100.0	43	2 B97505	gene 55.4 protein
25	16	100.0	45	2 H83816	hypothetical prote
26	16	100.0	45	2 C34669	calmodulin-related
27	16	100.0	46	2 B82461	hypothetical prote
28	16	100.0	47	2 FC4133	hypothetical 47 pr
29	16	100.0	48	2 T07316	hypothetical prote

30 16 100.0 48 2 C95060 hypothetical prote  
31 16 100.0 50 2 AB0367 hypothetical prote  
32 16 100.0 51 2 S00576 hypothetical prote  
33 16 100.0 52 2 S15922 hypothetical prote  
34 16 100.0 52 2 C83621 hypothetical prote  
35 16 100.0 52 2 AF0293 hypothetical prote  
36 16 100.0 52 2 PN0481 cell division cycl  
37 16 100.0 52 2 A71002 hypothetical prote  
38 16 100.0 53 2 A82862 hypothetical prote  
39 16 100.0 53 2 H98094 hypothetical prote  
40 16 100.0 54 2 E95230 hypothetical prote  
41 16 100.0 54 2 S46848 gene A52K protein  
42 16 100.0 54 2 T04034 hypothetical prote  
43 16 100.0 54 2 D84144 hypothetical prote  
44 16 100.0 54 2 AH1362 Bacteriophage A118  
45 16 100.0 54 2 S32360 SNAP receptor - bo

#### ALIGNMENTS

##### RESULT 1

S43834

DNA topoisomerase (EC 5.99.1.2) - Klebsiella sp. (ATCC 15380) (fragment)

C:Species: Klebsiella sp.

A:Variety: ATCC 15380

C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 07-May-1999

C:Accession: S43834

R:lynch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wilkinson, A.J.

Biochem. J. 299, 129-136, 1994

A:Title: Characterization of the CysB protein of Klebsiella aerogenes: direct evidence

A:Reference number: S43834; MUID:94220019; PMID:8166630

A:Accession: S43834

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-18 <LYN>

A:Experimental source: ATCC 15380

C:Genetics:

A:Gene: topI

C:Function:

A:Description: catalyzes ATP-independent transient breakage of DNA phosphodiester bonds rejoining; this reaction will lead to the conversion of one topological isomer of DNA to C:Superfamily: bacterial type I DNA topoisomerase

C:Keywords: DNA binding; DNA replication; isomerase; zinc finger

Query Match 100.0%; Score 16; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 1 FID 3

DB 8 FID 10

##### RESULT 2

D48518

PEB1 5'-region hypothetical protein A - Campylobacter jejuni (fragment)

C:Species: Campylobacter jejuni

C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 09-Jul-2004

C:Accession: D48518

R:Pei, Z.; Blaser, M.J.

J. Biol. Chem. 268, 18717-18725, 1993

A:Title: PEB1, the major cell-binding factor of Campylobacter jejuni, is a homolog of t

A:Reference number: A48518; MUID:93366784; PMID:8360165

A:Accession: D48518

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-21 <PEI>

A:Cross-references: UNIPROT:Q9PP09; GB:L13662

Query Match 100.0%; Score 16; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

```

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Feb-1997
C;Accession: A26188
R;De, B.K.; Misono, K.S.; Lukas, T.J.; Mroczkowski, B.; Cohen, S.
J. Biol. Chem. 261, 13784-13792, 1986
A;Title: A calcium-dependent 35-kilodalton substrate for epidermal growth factor receptor
A;Reference number: A26188; MUID:87008618; PMID:3020049
A;Accession: A26188
A;Molecule type: protein
A;Residues: 1-30 <DEB>
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: phosphoprotein

Query Match      100.0%; Score 16; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
      |||
Db      1 FID 3
      |||

RESULT 6
A44682
C;Species: Pseudomonas pseudoalcaligenes
C;Title: Nitrobenzene nitroreductase (EC 1.-.-.-) - Pseudomonas pseudoalcaligenes (fragment)
C;Date: 28-Feb-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C;Accession: A44682
R;Somerville, C.C.
A;Submitted to the Protein Sequence Database, February 1995
A;Description: Purification and characterization of nitrobenzene nitroreductase from Pse
F;15-19/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted
F;15-19/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match      100.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
      |||
Db      7 FID 9
      |||

RESULT 4
F84066
hypothetical protein BH3334 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84066
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84066
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25 <STO>
A;Cross-references: UNIPROT:Q9K7M7; GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BA070
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3334

Query Match      100.0%; Score 16; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
      |||
Db     13 FID 15
      |||

RESULT 5
A26188
lipocortin I - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)

```

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A.; Reference number: A59328  
A;Content: annotation  
C;Genetics:  
A;Gene: XF0341

Query Match 100.0%; Score 16; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 16 FID 18

## RESULT 8

PQ0413  
nonstructural protein NS1 - influenza A virus (strain A/Hebei/24/89 [H1N2]) (fragment)  
C;Species: influenza A virus  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: PQ0413  
R;Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerom J. Gen. Virol. 73, 1329-1337, 1992  
A;Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (H1N2) virus  
A;Reference number: PQ0408; MUID:92300326; PMID:1607856  
A;Accession: PQ0413  
A;Molecule type: genomic RNA  
A;Residues: 1-32 <LIA>  
A;Cross-references: UNIPROT:Q7LZX4  
C;Genetics:  
A;Map position: segment 8  
C;Superfamily: influenza virus nonstructural protein NS1  
C;Keywords: nonstructural protein

Query Match 100.0%; Score 16; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 10 FID 12

## RESULT 9

PQ0416  
RNA-directed RNA polymerase (EC 2.7.7.48) 3 - influenza A virus (strain A/Yamagata/120/89 [H1N1])  
N;Alternate names: P2 protein; PA protein  
C;Species: influenza A virus  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: PQ0416  
R;Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerom J. Gen. Virol. 73, 1329-1337, 1992  
A;Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (H1N1) virus  
A;Reference number: PQ0408; MUID:92300326; PMID:1607856  
A;Accession: PQ0416  
A;Molecule type: genomic RNA  
A;Residues: 1-33 <LIA>  
A;Cross-references: UNIPROT:Q7M023  
C;Genetics:  
A;Map position: segment 3  
C;Superfamily: influenza virus RNA-directed RNA polymerase 3  
C;Keywords: nucleotidyltransferase

Query Match 100.0%; Score 16; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 11 FID 13

## RESULT 10

A95119  
hypothetical protein SP1031 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: A95119  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Helon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A.; Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: A95119  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-33 <KUR>  
A;Cross-references: UNIPROT:Q97R10; GB:AE005672; PIDN:AAK75146.1; PID:g14972505; GSPDB:1  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP1031

Query Match 100.0%; Score 16; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 22 FID 24

## RESULT 11

H82096  
hypothetical protein VC2284 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: H82096  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: H82096  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-33 <HEI>  
A;Cross-references: UNIPROT:Q9KP88; GB:AE004299; GB:AE003852; NID:g9656835; PIDN:AAF954  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC2284  
A;Map position: 1

Query Match 100.0%; Score 16; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 19 FID 21

## RESULT 12

S33646  
hypothetical protein 2 - pin mould (Absidia glauca) plasmid PSSP15 (fragment)  
C;Species: Absidia glauca  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: S33646  
R;Haefliger, J.; Woestemeyer, J.; Weigel, C.T.  
submitted to the EMBL Data Library, June 1992  
A;Description: Complete nucleotide sequence of the pAPD9 extrachromosomal DNA element

Query Match 100.0%; Score 16; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 19 FID 21

A:Reference number: S33645  
A:Accession: S33646  
A:Molecule type: DNA  
A:Residues: 1-33 <HAE>  
A:Cross-references: UNIPROT:Q00062; EMBL:M94861  
C:Genetics:  
A:Genome: plasmid

Query Match 100.0%; Score 16; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 22 FID 24

RESULT 13  
PS0363  
protein-tyrosine-phosphatase (EC 3.1.3.48) (clone PTP5) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 20-Mar-1998  
C:Accession: PS0363  
R:den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.  
Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992  
A:Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase  
A:Reference number: JH0609; MUID:92272714; PMID:1590786  
A:Accession: PS0363  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-35 <DEN>  
A:Experimental source: embryonal carcinoma cell, P19 cell  
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat-tyrosine-phosphatase homology  
C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 100.0%; Score 16; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 6 FID 8

RESULT 14  
PS0364  
protein-tyrosine-phosphatase (EC 3.1.3.48) (clone PTP31) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 20-Mar-1998  
C:Accession: PS0364  
R:den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.  
Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992  
A:Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase  
A:Reference number: JH0609; MUID:92272714; PMID:1590786  
A:Accession: PS0364  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-35 <DEN>  
A:Experimental source: embryonal carcinoma cell, P19 cell  
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat-tyrosine-phosphatase homology  
C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 100.0%; Score 16; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 6 FID 8

RESULT 15  
D87544  
hypothetical protein CC2381 [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: D87544  
R:Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolorn, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: D87544  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-36 <STO>  
A:Cross-references: UNIPROT:Q9A5R6; GB:AE005673; MID:gl3423914; PIDN:AAK24352.1; GSPDB:C  
C:Genetics:  
A:Gene: CC2381

Query Match 100.0%; Score 16; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
DB 28 FID 30

Search completed: April 18, 2005, 14:23:36  
Job time : 7.93023 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2005, 13:57:43 ; Search time 27.2791 Seconds  
(without alignments)  
56.316 Million cell updates/sec

Title: US-09-674-716B-13  
Perfect score: 16  
Sequence: 1 FID 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	15	2 Q9KIV5	Q9KIV5 anabaena sp
2	16	100.0	15	2 Q9R4K0	Q9R4K0 nocardia. n
3	16	100.0	16	1 FIBA RABIT	P14461 oryctolagus
4	16	100.0	16	2 Q7R7Y9	Q7R7Y9 plasmodium
5	16	100.0	18	1 TOPI KLEAE	P46155 klebsiella
6	16	100.0	20	2 Q85485	Q85485 avian leuko
7	16	100.0	21	2 Q7RBP5	Q7RBP5 plasmodium
8	16	100.0	23	1 PQQA ENTIT	P59726 enterobacte
9	16	100.0	23	1 PQQA KLEPN	P27503 klebsiella
10	16	100.0	23	2 Q7RDS0	Q7RDS0 plasmodium
11	16	100.0	24	2 Q9R2R0	Q9R2R0 streptococc
12	16	100.0	24	2 Q9Z630	Q9Z630 streptococc
13	16	100.0	24	2 Q8CGM9	Q8CGM9 mus musculu
14	16	100.0	25	2 Q9K7M7	Q9K7M7 bacillus ha
15	16	100.0	28	2 Q8K887	Q8K887 escherichia
16	16	100.0	29	2 Q6JTX2	Q6JTX2 isohypsiabu
17	16	100.0	29	2 Q7RLD1	Q7RLD1 plasmodium
18	16	100.0	29	2 Q7RTA7	Q7RTA7 plasmodium
19	16	100.0	29	2 Q6U204	Q6U204 helicobacte
20	16	100.0	29	2 Q6UNW4	Q6UNW4 vibrio chol
21	16	100.0	29	2 Q87L17	Q87L17 vibrio para
22	16	100.0	29	2 Q8CLJ9	Q8CLJ9 versinia pe
23	16	100.0	30	2 Q9NRC5	Q9NRC5 homo sapien
24	16	100.0	30	2 Q7R8Y6	Q7R8Y6 plasmodium
25	16	100.0	30	2 Q7RB68	Q7RB68 pseudomonas
26	16	100.0	30	2 Q7MI28	Q7MI28 pseudomonas
27	16	100.0	30	2 Q81NQ6	Q81NQ6 bacillus an
28	16	100.0	31	2 Q7R863	Q7R863 plasmodium
29	16	100.0	31	2 Q6UK06	Q6UK06 vibrio chol
30	16	100.0	31	2 Q6WLW6	Q6WLW6 rhizobium s
31	16	100.0	31	2 Q8KGF6	Q8KGF6 chlorobium

32 16 100.0 31 2 Q8EIW8 Q8EIW8 shewanella  
33 16 100.0 31 2 Q9PGG1 Q9PGG1 xylella fas  
34 16 100.0 31 2 Q9S0E6 Q9S0E6 borrelia bu  
35 16 100.0 32 1 RS19 YEREN Q56847 versinia en  
36 16 100.0 32 2 Q501I0 Q501I0 mycobacteri  
37 16 100.0 32 2 Q6V7H0 Q6V7H0 vibrio chol  
38 16 100.0 32 2 Q87IK8 Q87IK8 vibrio para  
39 16 100.0 32 2 Q7LZX4 Q7LZX4 influenza a  
40 16 100.0 33 2 Q7RQV0 Q7RQV0 plasmodium  
41 16 100.0 33 2 Q9S7Y3 Q9S7Y3 picea abies  
42 16 100.0 33 2 Q6JSD0 Q6JSD0 haemophilus  
43 16 100.0 33 2 Q6ZJF9 Q6ZJF9 burkholderi  
44 16 100.0 33 2 Q97R10 Q97R10 streptococc  
45 16 100.0 33 2 Q9KPS8 Q9KPS8 vibrio chol

#### ALIGNMENTS

##### RESULT 1

Q9KIV5 PRELIMINARY; PRT; 15 AA.  
AC Q9KIV5;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
DE Putative deoxyribose-phosphate aldolase (Fragment).  
OS Anabaena sp. (strain PCC 7120).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
OX NCBI\_TaxID=103690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PCC7120;  
RA Matveyev A.V., Young K.T., Elhai J.;  
RT "DNA methyltransferases of the cyanobacterium Anabaena PCC 7120.";  
RL Nucleic Acids Res. 29:1493-1506 (2001).  
DR EMBL; AF220508; AAF75233.1; -.  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1608 MW; 1B1307FDA6850099 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
DB 13 FID 15

##### RESULT 2

Q9R4K0 PRELIMINARY; PRT; 15 AA.  
AC Q9R4K0;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Nitric oxide synthase (EC 4.14.23.-) (Fragment).  
OS Nocardia.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Nocardiaaceae.  
OX NCBI\_TaxID=1817;  
RN [1]  
RP MEDLINE=953394819; PubMed=7545152;  
RA Chen Y., Rosazza J.P.;  
RT "Purification and characterization of nitric oxide synthase (NOSNoc)  
from a Nocardia species.";  
RL J. Bacteriol. 177:5122-5128 (1995).  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1818 MW; 2BD5B859DE288B77 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 15;

```
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 13 FID 15

RESULT 3
FIBA RABIT
ID FIBA RABIT STANDARD; PRT; 16 AA.
AC P14461;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC Blood coagulation; Direct protein sequencing; Plasma.
KW PEPTIDE 1 16 Fibrinopeptide A.
FT NON TER 16
FT SEQUENCE 16 AA; 1651 MW; DB 16; Length 16;
QY 1 FID 3
Db 8 FID 10

Query Match 100.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 8 FID 10

RESULT 4
Q7R7Y9 PRELIMINARY; PRT; 16 AA.
ID Q7R7Y9
AC Q7R7Y9;
DT 01-MAR-2004 (TEMBLrel. 26, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY07435;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XN1;
RX PubMed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002729; EAA19883.1; -.
KW Hypothetical protein.
FT NON TER 16
FT SEQUENCE 16 AA; 1946 MW; B13FDBDB22FD127 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 6 FID 8

RESULT 5
TOPI KLEAE STANDARD; PRT; 18 AA.
ID TOPI KLEAE
AC P46155;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
DE (Untwisting enzyme) (Swivelase) (Fragment).
GN Name=topA;
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 418 / ATCC 15380;
RX MEDLINE=94220019; PubMed=8166630;
RA Lynch A.S., Tyrrell R., Smerdon S.J., Briggs G.S., Wilkinson A.J.;
RT "Characterization of the CysB protein of Klebsiella aerogenes: direct
RT evidence that N-acetylserine rather than O-acetylserine serves as the
RT inducer of the cysteine regulon.";
RL Biochem. J. 299:129-136(1994).
CC -!- FUNCTION: The reaction catalyzed by topoisomerases leads to the
CC conversion of one topological isomer of DNA to another.
CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
CC DNA, followed by passage and rejoining.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA
CC backbone bond, it simultaneously forms a protein-DNA link, in
CC which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus
CC at one end of the enzyme-severed DNA strand.
CC -!- SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase
CC family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
DR EMBL; X78729; -. NOT_ANNOTATED_CDS.
DR HSSP; P06612; IYUA.
DR InterPro; IPR000380; DNA tpisomrase.
DR PROSITE; PS00396; TOPOISOMERASE_I_PROK; PARTIAL.
DR DNA-binding; Isomerase; Topoisomerase.
FT NON TER 1
FT SEQUENCE 18 AA; 2043 MW; 8C1C81238FF0EPA4 CRC64;
```



```
Query Match 100.0%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 8 FID 10

RESULT 6
Q85485 ID Q85485 PRELIMINARY; PRT; 20 AA.
AC Q85485;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag-erbB fusion protein (Fragment).
OS Avian leukosis virus.
OC Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11864;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=RAV1;
RA MEDLINE=86230605; PubMed=2897475;
RX Raines M.A., Maible N.J., Moscovici C., Crittenden L., Kung H.-J.;
RT "Mechanism of c-erbB transduction: newly released transducing viruses
RT retain poly(A) tracts of erbB transcripts and encode C-terminally
RT intact erbB proteins."
RL J. Virol. 62:2437-2443(1998).
DR EMBL; M19970; AAA42586.1; -.
DR InterPro; IPR009030; Grow_fac_recept.
FT NON_TER 1 20
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2167 MW; 2A4EFD2E3A709011 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 11 FID 13

RESULT 7
Q7RBP5 ID Q7RBP5 PRELIMINARY; PRT; 21 AA.
AC Q7RBP5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Names=PY06095;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angioli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegh M., Shoalbi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RT Nature 419:512-519(2002).
```

```
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
DR EMBL; AABL01002024; EAA18247.1; -.
KW Hypothetical protein.
SQ SEQUENCE 21 AA; 2603 MW; 6633105FCS69A116 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 5 FID 7

RESULT 8
PQQA_ENTIT ID PQQA_ENTIT STANDARD; PRT; 23 AA.
AC P59726;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Coenzyme PQQ synthesis protein A (Pyrroloquinoline quinone
DE biosynthesis protein A).
GN Name=pqqa;
OS Enterobacter intermedius.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=61648;
RN [1]
RS SEQUENCE FROM N.A.
RA Kim C.H., Han S.H., Kim K.Y., Cho B.H., Kim Y.H., Gu B.S., Kim Y.C.;
RT "Cloning and expression of pyrroloquinoline (PQQ) genes from a
RT phosphate-solubilizing bacterium Enterobacter intermedius."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ)
CC biosynthesis. Probably provides the glutamate and tyrosine
CC residues that are cross-linked and modified to form the coenzyme
CC (By similarity).
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC -!- SIMILARITY: Belongs to the pqqa family.
CC
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CC
CC EMBL; AY216683; AAP34378.1; -.
DR HAMAP; MF00656; -.
KW PQQ; PQQ Biosynthesis.
FT CROSSLNK 15 19
FT SEQUENCE 23 AA; 2764 MW; ACCB321460871C5D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 7 FID 9

RESULT 9
PQQA_KLEPN ID PQQA_KLEPN STANDARD; PRT; 23 AA.
AC P27503;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
```

05-JUL-2004 (Rel. 44, Last annotation update)  
 Coenzyme PQQ synthesis protein A (pyrroloquinoline quinone biosynthesis protein A).  
 Name: ppgA;  
 Klebsiella pneumoniae.  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Klebsiella.  
 NCBI\_TaxID=573;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCTC 418;  
 RX MEDLINE=92212293; PubMed=1313537;  
 RA Neulenber J.J.M., Sellink E., Kiegan N.H., Postma P.W.;  
 RT "Nucleotide sequence and structure of the Klebsiella pneumoniae ppg operon.";  
 RL Mol. Gen. Genet. 232:284-294(1992).  
 RN [2]  
 RP FUNCTION.  
 RC STRAIN=NCTC 418;  
 RX MEDLINE=95394815; PubMed=7665488;  
 RA Velterop J.S., Sellink E., Meulenber J.J., David S., Bulder I.,  
 RT Postma P.W.;  
 RT "Synthesis of pyrroloquinoline quinone in vivo and in vitro and detection of an intermediate in the biosynthetic pathway.";  
 RL J. Bacteriol. 177:5088-5098(1995).  
 CC -1- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ) biosynthesis. Probably provides the glutamate and tyrosine residues that are cross-linked and modified to form the coenzyme.  
 CC -1- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.  
 CC -1- SIMILARITY: Belongs to the ppgA family.  
 CC -----  
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 CC -----  
 CC EMBL; X58778; CAA41579.1; -.  
 DR PIR; S20453; S20453.  
 DR HAMAP; MF 00656; -; 1.  
 KW PQQ; PQQ Biosynthesis.  
 FT CROSSLINK 15 19  
 FT SEQUENCE 23 AA; 2764 MW; ACCB321460871C5D CRC64;  
 SQ  
 Query Match 100.0%; Score 16; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 FID 3  
 Db |||  
 7 FID 9  
 RESULT 10  
 ID Q7RDS0 PRELIMINARY; PRT; 23 AA.  
 AC Q7RDS0;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=PY05351;  
 OS Plasmodium yoelii yoelii.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=73239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=17XNL;  
 RX PubMed=12368865; DOI=10.1038/nature01099;  
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Persea M.,

RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,  
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.;  
 RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";  
 RL Nature 419:512-519(2002).  
 CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.  
 CC EMBL; AABL01001686; EAA17363.1; -.  
 DR Hypothetical protein.  
 KW SEQUENCE 23 AA; 2779 MW; 338868E33689DBC7 CRC64;  
 SQ  
 Query Match 100.0%; Score 16; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 FID 3  
 Db |||  
 6 FID 8  
 RESULT 11  
 ID Q9R2R0 PRELIMINARY; PRT; 24 AA.  
 AC Q9R2R0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Capsular polysaccharide B (Fragment).  
 GN Name=cpsB;  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D39;  
 RX MEDLINE=99287847; PubMed=10348877;  
 RA Morona J.K., Morona R., Paton J.C.;  
 RT "Analysis of the 5' portion of the type 19A capsule locus identifies two classes of cpsC, cpsD, and cpsE genes in Streptococcus pneumoniae.";  
 RL J. Bacteriol. 181:3599-3605(1999).  
 DR EMBL; AF106134; AAD17979.1; -.  
 DR EMBL; AF106132; AAD17975.1; -.  
 DR EMBL; AF106133; AAD17977.1; -.  
 FT NON\_TER 1  
 FT SEQUENCE 24 AA; 2820 MW; ED047715CF90483B CRC64;  
 SQ  
 Query Match 100.0%; Score 16; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 FID 3  
 Db |||  
 11 FID 13  
 RESULT 12  
 ID Q9Z630 PRELIMINARY; PRT; 24 AA.  
 AC Q9Z630;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Capsular polysaccharide B (Fragment).

```
GN Name=cpsB;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9287847; PubMed=10348877;
RA Morona J.K., Morona R., Paton J.C.;
RT "Analysis of the 5' portion of the type 19A capsule locus identifies
RT two classes of cpsC, cpsD, and cpsE genes in Streptococcus
RT pneumoniae.";
RL J. Bacteriol. 181:3599-3605 (1999).
DR EMBL; AF106135; AAD17981.1; -.
FT NON_TER 1
SQ SEQUENCE 24 AA; 2834 MW; ED047715CF82D83B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 11 FID 13

RESULT 13
Q8CGM9 PRELIMINARY; PRT; 24 AA.
AC Q8CGM9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Retinoblastoma-binding protein 1 (Fragment).
GN Name=Rbbp1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129X1/SvJ;
RA Banda O., Branton P.E.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY163235; AAN84616.1; -.
FT NON_TER 1
FT NON_TER 24
SQ SEQUENCE 24 AA; 2685 MW; BF6991AC3D52BC4E CRC64;

Query Match 100.0%; Score 16; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 20 FID 22

RESULT 14
Q9K7M7 PRELIMINARY; PRT; 25 AA.
AC Q9K7M7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BH3334 protein.
GN OrderedLocusNames=BH3334;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
```

```
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331 (2000).
DR EMBL; AF001518; BAB07053.1; -.
DR PIR; F84066; F84066.
KW Complete proteome.
SQ SEQUENCE 25 AA; 2986 MW; OC21EA93BE976875 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 13 FID 15

RESULT 15
Q8KS87 PRELIMINARY; PRT; 28 AA.
AC Q8KS87;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative oxidoreductase Fe-S subunit (Fragment).
GN Name=b1589; Synonyms=z2577;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOR-9;
RX MEDLINE=22053230; PubMed=12057959;
RX DOI=10.1128/JB.184.13.3640-3648.2002;
RA Sandt C.H., Hopper J.E., Hill C.W.;
RT "Activation of prophage eib genes for immunoglobulin-binding proteins
RT by genes from the IbrAB genetic island of Escherichia coli ECOR-9.";
RL J. Bacteriol. 184:3640-3648 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CB6220;
RA Koch C., Hertwig S., Appel B.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF520223; AAM53254.1; -.
DR EMBL; AJ576011; CAE11225.1; -.
FT NON_TER 28
SQ SEQUENCE 28 AA; 3185 MW; A2F42416487ED57B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 8 FID 10

Search completed: April 18, 2005, 14:22:02
Job time : 32.2791 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:32:07 ; Search time 31.6047 Seconds  
(without alignments)  
36.712 Million cell updates/sec

Title: US-09-674-716B-13  
Perfect score: 16  
Sequence: 1 FID 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1980s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	3	3 AAY32259	Aay32259 Light cha
2	16	100.0	5	1 AAP94794	Rap94794 Periferal
3	16	100.0	5	2 AAW55773	Aaw55773 Immunizat
4	16	100.0	5	5 AAU86974	Aau86974 Estradiol
5	16	100.0	5	5 ABB84336	Abb84336 Human MBP
6	16	100.0	6	2 AAR29321	Aar29321 Endothell
7	16	100.0	6	2 AAR69115	Aar69115 Endothell
8	16	100.0	6	2 AAW31469	Aaw31469 Transcrip
9	16	100.0	7	3 AAB06774	Aab06774 Claudin-6
10	16	100.0	7	3 AAB06594	Aab06594 Claudin-3
11	16	100.0	7	3 AAB06656	Aab06656 Claudin-4
12	16	100.0	7	6 ABU96533	Abu96533 Human cyt
13	16	100.0	7	6 ABU96535	Abu96535 Human cyt
14	16	100.0	7	7 ADL17604	Adl17604 Human MAG
15	16	100.0	8	3 AAB06597	Aab06597 Claudin-3
16	16	100.0	8	3 AAB06777	Aab06777 Claudin-6
17	16	100.0	8	3 AAB06659	Aab06659 Claudin-4
18	16	100.0	8	4 AAU25282	Aau25282 Schizophr
19	16	100.0	8	4 AAU15626	Aau15626 Schizophr
20	16	100.0	8	5 ABG73046	Abg73046 Cryptococ
21	16	100.0	8	5 ABP46831	Abp46831 Human BLY
22	16	100.0	8	5 ABG65708	Abg65708 Plant ICK
23	16	100.0	8	5 ABG65705	Abg65705 Plant ICK
24	16	100.0	8	7 ADG97658	Adg97658 scfVr VHCD
25	16	100.0	8	7 ADL17538	Adl17538 Human MAG

ALIGNMENTS

RESULT 1

AAY32259  
ID AAY32259 standard; peptide; 3 AA.

AC AAY32259;

XX  
XX  
15-FEB-2000 (first entry)

XX  
XX  
Light chain CDR H3 of mouse anti-CD23 Mab C11.

XX  
XX  
CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
monoclonal antibody; chimeric antibody; humanised antibody;  
complementarity determining region; CDR; autoimmune disease;  
inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
urticaria; nephrotic syndrome; glomerulonephritis;  
inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
therapy.

XX  
XX  
Mus musculus.

XX  
XX  
W09958679-A1.

XX  
XX  
18-NOV-1999.

XX  
XX  
07-MAY-1999; 99WO-GB001434.

XX  
XX  
09-MAY-1998; 98GB-00009839.

XX  
XX  
(GLAX ) GLAXO GROUP LTD.

XX  
XX  
Bonnefoy JNP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX  
XX  
WPI; 2000-053101/04.

XX  
XX  
N-PSDB; AA234744.

XX  
XX  
Cell receptor specific antibodies useful for treating e.g. arthritis,

XX  
XX  
diabetes, multiple sclerosis and psoriasis.

XX  
XX  
Claim 1; Page 40; 81pp; English.

XX  
XX  
This sequence represents complementarity determining region 3 (CDR H3)  
of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11  
(see also AAY32263). The invention provides altered antibodies, such as  
chimeric or humanised antibodies, which comprise sufficient of the amino  
acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

Adh35824 Vitamin D  
Adh35805 Kininogen  
Adh35831 Vitamin D  
Ado78893 Schizophr  
Adr72194 PET analy  
Aar48299 Vitamin E  
Aaw13609 HLA-A2.1  
Aab06662 Claudin-4  
Aab06780 Claudin-6  
Aab06600 Claudin-3  
Aab75620 HLA class  
Aab75667 HLA class  
Aab67398 Modified  
Aab67397 Modified  
Aab67395 Tobacco m  
Aam49930 Human D40  
Aau95252 Human nov  
Aau94879 Human nov  
Abm6263 Proptonib  
Abj60588 184P1B2-r

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents

XX Sequence 3 AA;

Query Match 100.0%; Score 16; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 DB 1 FID 3

RESULT 2  
 AAP94794  
 ID AAP94794 standard; protein; 5 AA.

XX AAP94794;

AC 25-MAR-2003 (revised)  
 DT 09-JUL-1990 (first entry)

XX Periferal nervous system myelin protein, proteolipid protein, a PNS CNS  
 DE myelin component and acetyl choline receptor epitope associated motif.

XX Autoantigen; MBP; myelin basic protein; transplantation antigen;  
 KW myasthenia gravis; myasthenics; Transplantation antigen.

XX Synthetic.

XX EP304279-A.

XX 22-FEB-1989.

XX 17-AUG-1988; 88EP-00307608.

XX 17-AUG-1987; 87US-00086694.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Steinman L, Zamvil S;

XX WPI; 1989-055696/08.

XX Oligopeptide and polypeptide compsns. - based on the amino acid sequence  
 PT of an immunogen and used for modulating the immune system.

XX Disclosure; Page; 7pp; English.

XX Sequences will normally be part of 9 to 15 AA sequence, excluded as  
 CC motifs for immunisation but useful in tolerisation. (Updated on 25-MAR-  
 CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 16; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||

DB 3 FID 5

RESULT 3

AAW55773

ID AAW55773 standard; peptide; 5 AA.

XX AAW55773;

AC 25-MAR-2003 (revised)

XX 08-JUL-1998 (first entry)

DE Immunisation motif associated with AChr 4.

XX Myelin basic protein; immunity; immune response; neurological; T-cell;  
 KW human; immunogen; B-cell; transplantation antigen; immunomodulator.

XX Unidentified.

XX EP805162-Al.

XX 05-NOV-1997.

XX 17-AUG-1988; 97EP-00106788.

XX 17-AUG-1987; 87US-00086694.

XX 17-AUG-1988; 88EP-00307608.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Steinman L, Zamvil S;

XX WPI; 1998-034664/04.

XX Polypeptide comprising human myelin basic protein fragment - useful as  
 PT immuno modulator.

XX Disclosure; Page 8; 8pp; English.

XX The present sequence represents an immunisation motif normally excluded,  
 CC but which may be used with advantage for tolerisation by itself or in  
 CC conjunction with other epitope sequences from the present invention. The  
 CC present invention describes a polypeptide comprising a human myelin basic  
 CC protein (hMBP) fragment including P89-101 of hMBP, excluding native hMBP.  
 CC The term P89-101 is not defined but may be intended to mean amino acids  
 CC 89-101 of hMBP. The polypeptide can be used for tolerising a mammalian  
 CC host immune system comprising B and T cells to an immunogen of interest,  
 CC wherein said immunogen is restricted by a transplantation antigen of said  
 CC host. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-  
 CC 2003 to correct PR field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 16; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||

DB 3 FID 5

RESULT 4

AAU86974

ID AAU86974 standard; peptide; 5 AA.

XX AAU86974;

XX 21-MAY-2002 (first entry)

XX Estradiol mimotope peptide #22.

XX Estradiol; mimotope; estrone-3-glucuronide; steroid detection;

KW immunoassay; phage display; immunogen.  
 XX Synthetic.  
 OS  
 XX WO200212270-A1.  
 PN  
 XX 14-FEB-2002.  
 PD  
 XX  
 XX 26-JUL-2001; 2001WO-EP008705.  
 XX  
 XX 03-AUG-2000; 2000EP-00306613.  
 PR  
 XX (UNIL ) UNILEVER PLC.  
 PA (UNIL ) UNILEVER NV.  
 PA (UNIL ) HINDUSTAN LEVER LTD.  
 XX  
 XX Badley RA, Berry MJ, Williams SC;  
 PI  
 XX WPI; 2002-241729/29.  
 DR  
 XX  
 XX Peptide mimotope capable of binding specifically to antibody specific to  
 PT estradiol, useful for assaying presence and/or amount of estradiol,  
 PT especially estrone-3-glucuronide in sample.  
 XX  
 XX Claim 3; Page 22; 57pp; English.  
 PS  
 XX The invention relates to a purified peptide mimotope capable of binding  
 CC specifically to an antibody specific to estradiol. Also included are a  
 CC solid support having immobilised (releasably or non-releasably) peptide  
 CC mimotopes, an immunoassay test device for the detection of estradiol in  
 CC the sample, comprising the mimotopes and an antibody capable of binding  
 CC specifically to the mimotopes to generate a detectable signal and an  
 CC isolated nucleic acid encoding the peptide mimotopes. The mimotope is  
 CC useful for assaying the presence and/or amount of estradiol preferably  
 CC estrone-3-glucuronide in a sample which is urine or serum sample to be  
 CC tested and is also utilised in an immunoassay test device, and further  
 CC can be used as immunogens. The mimotope be used to construct new, or  
 CC improve the performance of old, immunoassay test formats and devices.  
 CC They can, for example, be utilised essentially to tune the signal in  
 CC conventional displacement assays for the detection of estradiol. The  
 CC mimotope can be bound directly to certain assay surfaces which are  
 CC otherwise non-compatible with estradiol on such surfaces needing to be  
 CC bound to the surface by complexing with another - often proteinaceous -  
 CC molecule. The mimotope is capable of being bound to the antigen-binding  
 CC site of an antibody in a selective fashion in the presence of excess  
 CC quantities of other undesired materials, and tightly enough (i.e. with  
 CC high enough affinity) that when used in an immunoassay, it provides a  
 CC useful result). The present sequence is a peptide mimotopes of the  
 CC invention  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 100.0%; Score 16; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FID 3  
 |||  
 Db 3 FID 5  
 RESULT 5  
 ABB84336  
 ID ABB84336 standard; peptide; 5 AA.  
 XX  
 AC ABB84336;  
 XX  
 XX 17-OCT-2002 (first entry)  
 DT  
 DT Human MBP protein derived peptide SEQ ID 36.  
 DE  
 XX MBP; myelin basic protein; human; tolerance; immune system;  
 KW multiple sclerosis; autoimmune response; autoimmune disease;

KW immunosuppressive; neuroprotective.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002076412-A1.  
 XX  
 PD 20-JUN-2002.  
 XX  
 XX 07-JUN-1995; 95US-00484409.  
 XX  
 PR 17-AUG-1987; 87US-00086694.  
 PR 12-JUL-1989; 89US-00379500.  
 PR 01-MAY-1990; 90US-00517245.  
 PR 01-MAY-1991; 91WO-US002991.  
 PR 30-APR-1992; 92US-00877444.  
 PR 21-MAY-1993; 93US-00066325.  
 PR 22-SEP-1993; 93US-00125407.  
 XX  
 XX (STEI/) STEINMAN L.  
 PA (ZAMV/) ZAMVIL S.  
 PA  
 XX Steinman L, Zamvil S;  
 PI  
 XX WPI; 2002-598709/64.  
 DR  
 XX  
 XX Modulating or tolerizing the immune system, useful for treating multiple  
 PT sclerosis, by administering a peptide derived from human myelin binding  
 PT protein.  
 XX  
 XX Disclosure; Page 15; 2lpp; English.  
 PS  
 XX This invention describes a novel method for modulating or tolerizing the  
 CC immune system, and for treating multiple sclerosis comprising  
 CC administering a peptide derived from hMBP (human myelin basic protein).  
 CC The peptide induces an autoimmune response (T cell) to a self-antigen (or  
 CC part of it), and binds to an MHC (major histocompatibility complex)  
 CC antigen of a host susceptible to autoimmune diseases, i.e. competes with  
 CC binding to MBP and inhibit proliferation of MBP-reactive cells. The  
 CC peptide has immunosuppressive and neuroprotective activity. This sequence  
 CC represents a peptide derived from the human MBP protein which can be used  
 CC for tolerization  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 100.0%; Score 16; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FID 3  
 |||  
 Db 3 FID 5  
 RESULT 6  
 AAR29321  
 ID AAR29321 standard; peptide; 6 AA.  
 XX  
 AC AAR29321;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 13-APR-1993 (first entry)  
 DT  
 XX Endothelin antagonist peptide.  
 DE  
 XX Hypertension; myocardial infarction; congestive heart failure;  
 KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;  
 KW acute renal failure; preclampsia; diabetes; metabolic; endocrinological;  
 KW neurological; disorders.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1  
 FT

AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076 are fragments used in an assay to determine novel transcriptional activators.



CC The method involves the production of transcriptional activators  
 CC comprising of a DNA-binding group and a 6-25 amino acid peptide that is  
 CC covalently bonded to the DNA binding group and does not represent a  
 CC fragment of a natural transcription activator. Protein-protein  
 CC interactions are identified in the assay by fusing a DNA-binding domain  
 CC to a library of DNA fragments and introducing this and a fusion of target  
 CC protein and a polypeptide containing a region of Gal4 which interacts  
 CC with Gal4p into a cell containing Gal4p and identifying members of the  
 CC library that interact with the target from activation of transcription.  
 CC Such constructs are used to activate transcription in a cell, e.g. for  
 CC controlling gene activity, particularly in gene therapy (e.g. recognizing  
 CC a site close to a selected therapeutic gene). Transcription can be  
 CC activated without blocking other transcriptional activators. They  
 CC probably act by interacting with a component of the RNA polymerase II  
 CC holoenzyme, Gal11, the strongest known yeast activator, which provides a  
 CC more sensitive assay allowing detection of even weak protein-protein  
 CC interactions. Such activators do not create toxicity problems even when  
 CC overexpressed  
 XX  
 SQ Sequence 6 AA;

Query Match 100.0%; Score 16; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
 |||  
 Db 1 FID 3

## RESULT 9

AAB06774  
 ID AAB06774 standard; peptide; 7 AA.

XX  
 AC AAB06774;

XX 28-SEP-2000 (first entry)

XX Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 345.

XX Claudin-6 modulating agent; claudin-9 modulating agent;  
 KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;  
 KW inflammatory disease; cancer; graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA001029.

XX 03-NOV-1998; 98US-00185908.

XX 30-MAR-1999; 99US-00282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin.

XX Claim 73; Page 103; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins  
 CC are cadherins, which are membrane glycoproteins involved in cell  
 CC adhesion. In some situations, cell adhesion occurs at abnormal levels,  
 CC and these peptides can be used to modulate these levels, and thus treat  
 CC autoimmune diseases, inflammatory diseases and cancer, and aid wound

CC healing and implant adhesion. In addition, they can also be used to  
 CC facilitate drug delivery to the desired target site. The present sequence  
 CC has a cyclic conformation  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 16; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
 |||  
 Db 5 FID 7

## RESULT 10

AAB06594  
 ID AAB06594 standard; peptide; 7 AA.

XX  
 AC AAB06594;

XX 28-SEP-2000 (first entry)

XX Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 227.

XX Claudin-3 modulating agent; cell adhesion recognition sequence;  
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;  
 KW graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA001029.

XX 03-NOV-1998; 98US-00185908.

XX 30-MAR-1999; 99US-00282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing  
 PT vasopermeability, for delivering drugs to tumors and the nervous system  
 PT and across the skin.

XX Claim 55; Page 99; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated  
 CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
 CC which are membrane glycoproteins involved in cell adhesion. In some  
 CC situations, cell adhesion occurs at abnormal levels, and these peptides  
 CC can be used to modulate these levels, and thus treat autoimmune diseases,  
 CC inflammatory diseases and cancer, and aid wound healing and implant  
 CC adhesion. In addition, they can also be used to facilitate drug delivery  
 CC to the desired target site. The present sequence has a cyclic  
 CC conformation

XX Sequence 7 AA;

Query Match 100.0%; Score 16; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
 |||  
 Db 5 FID 7



XX New polymorphic variants of the gene encoding Cytochrome P450 polypeptide  
PT 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.  
PT arachidonic acid metabolism, cancer or cardiovascular diseases.  
XX  
XX Disclosure; Page 58; 178pp; English.  
XX  
CC The invention describes a new polynucleotide comprises a polynucleotide:  
CC (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined  
CC in the specification; (b) encoding any of seven polypeptides having 7  
CC amino acids, or a polypeptide with 3 amino acids; (c) capable of  
CC hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)  
CC encoding a molecular CYP2C8 variant polypeptide or its fragment. The  
CC polynucleotide, gene, vector, polypeptide or antibody is useful for  
CC diagnosing or treating a disease, for preparing a diagnostic composition  
CC for diagnosing a disease, or for preparing a pharmaceutical composition  
CC for treating a disease. This disease includes arachidonic acid  
CC metabolism, cancer or cardiovascular diseases. This is the amino acid  
CC sequence of a human cytochrome P450 polypeptide 2C8 (CYP2C8) wild type  
CC peptide  
XX  
XX Sequence 7 AA;  
  
Query Match 100.0%; Score 16; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FID 3  
DB 3 FID 5  
  
RESULT 14  
ADL17604  
ID ADL17604 standard; peptide; 7 AA.  
XX  
AC ADL17604;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Human MAGI3 PDZ3 domain peptide SEQ ID NO:567.  
XX  
DE 95 kDa post-synaptic density protein/Discs large/ZO-1 domain;  
XX PSD-95/Discs large/ZO-1 domain; PDZ domain; fusion protein;  
XX phage coat protein; PDZ domain binding peptide; cytoskeletal; nontropic;  
XX neuroprotective; antiparkinsonian; neuroleptic; antitumour;  
XX immunosuppressive; pulmonary; muscular; gene therapy;  
XX rickettsial disease; murine typhus; chronic myeloid leukaemia;  
XX Alzheimer's disease; neurological disorder; Parkinson's disease;  
XX schizophrenia; X-linked autoimmune enteropathy; tsutsugamushi disease;  
XX facioscapulohumeral muscular dystrophy; late onset demyelinating disease;  
XX Usher syndrome type 1; USH1; nitric oxide-mediated tissue damage; tumour;  
XX cystic fibrosis; human; MAGI3.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO2003004604-A2.  
XX  
XX 16-JAN-2003.  
XX  
XX 03-JUL-2002; 2002WO-US020993.  
XX  
XX 06-JUL-2001; 2001US-0303634P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Held HA, Lasky LA, Laura RP, Sidhu SS, Wong WL, Wu Y;  
XX WPI; 2003-267930/26.  
XX  
XX New polypeptide that interacts with a 95 kDa post-synaptic density  
PT protein 95/Discs large/ZO-1 (PDZ) domain, useful for producing, selecting

PT and identifying PDZ domain binding peptides.  
XX  
PS Claim 26; SEQ ID NO 567; 228pp; English.  
XX  
XX The present invention describes an isolated polypeptide (I) that  
XX interacts with a 95 kDa post-synaptic density protein (PSD-95)/Discs  
XX large/ZO-1 (PDZ) domain. Also described: (1) a fusion protein (II)  
XX comprising a portion of a phage coat protein bonded through its carboxyl-  
XX terminus, optionally through a peptide linker, to a PDZ domain binding  
XX peptide, where the peptide contains 3-20 amino acid residues; (2) a  
XX library of (II), where the fusion proteins in the library comprise a  
XX number of PDZ domain binding peptides; (3) an assay for a PDZ domain  
XX binding compound; (4) a polypeptide that binds to the same epitope as  
XX (1), or that competes for binding to a PDZ domain with (1); (5) a  
XX polynucleotide (PN) encoding (I); (6) inhibiting a polypeptide-  
XX polypeptide interaction, by contacting a mixture comprising a first and a  
XX second polypeptide with an inhibitor of interaction between a PDZ domain  
XX and its ligand, where the first polypeptide comprises the PDZ domain and  
XX the second polypeptide comprises the ligand; (7) screening for a  
XX substance that modulates interaction between a PDZ domain polypeptide and  
XX a molecule known to bind to the PDZ domain of the polypeptide; and (8)  
XX screening (M) for a substance that inhibits binding of a PDZ domain  
XX polypeptide to a molecule known to bind to the PDZ domain of the  
XX polypeptide. (I) has cytostatic, nontropic, neuroprotective,  
XX antiparkinsonian, neuroleptic, antitumour, immunosuppressive, pulmonary  
XX and muscular activities, and can be used in gene therapy. The library of  
XX a fusion protein (II) is useful for producing a PDZ domain binding  
XX peptide library, and for selecting PDZ domain binding peptides in  
XX recombinant host cells. The library of (II) is also useful for  
XX identifying a PDZ domain binding protein, by selecting PDZ domain binding  
XX peptides using a new method. PN is useful for gene therapy, and in  
XX diagnoses of diseases. (I) and PN are useful for treating a subject at  
XX risk of a disorder or having a disorder associated with aberrant PDZP.  
XX PDZD, PDZ interacting protein (PIP) or PDZ domain binding peptides (PDBP)  
XX expression or activity such as rickettsial diseases, murine typhus,  
XX chronic myeloid leukaemia, Alzheimer's disease, neurological disorders  
XX such as Parkinson's disease and schizophrenia, X-linked autoimmune  
XX enteropathy, tsutsugamushi disease, facioscapulohumeral muscular  
XX dystrophy, late onset demyelinating disease, Usher syndrome type 1  
XX (USH1), nitric oxide-mediated tissue damage, tumours and cystic fibrosis.  
XX (I) is useful to identify cognate protein ligands for the PDZ domains.  
XX Structural analysis of the peptides are useful to understand PDZ domain  
XX structure and function, and also to identify intracellular biological  
XX functions for these motifs and the proteins that contain them. The  
XX peptides are further useful as PDZ domain inhibitors and are also useful  
XX as structural models in the design of small molecule inhibitors/agonists  
XX of the binding interaction between a PDZ domain containing protein and  
XX its cognate ligand. The present sequence represents a peptide which is  
XX used in the exemplification of the present invention.

Sequence 7 AA;

Query Match 100.0%; Score 16; DB 7; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
DB 4 FID 6

RESULT 15  
AAB06597  
ID AAB06597 standard; peptide; 8 AA.  
XX  
XX AAB06597;  
XX  
XX 28-SEP-2000 (first entry)  
XX  
XX Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 230.

XX Claudin-3 modulating agent; cell adhesion recognition sequence;  
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;

KW graft rejection; cyclic.  
XX OS Mammalia.  
XX PN WO200026360-A1.  
XX PD 11-MAY-2000.  
XX PF 03-NOV-1999; 99WO-CA001029.  
XX PR 03-NOV-1998; 98US-00185908.  
XX PR 30-MAR-1999; 99US-00282029.  
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX PI Blaschuck OW, Symonds JM, Gour BJ;  
XX PF 2000-365610/31.  
XX DR WPI; 2000-365610/31.  
XX PT Antibody modulation of claudin-mediated cell adhesion for increasing  
PT vasopermeability, for delivering drugs to tumors and the nervous system  
PT and across the skin.  
XX PS Claim 55; Page 99; 121pp; English.  
XX CC The present invention relates to the use of peptides as claudin-mediated  
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,  
CC which are membrane glycoproteins involved in cell adhesion. In some  
CC situations, cell adhesion occurs at abnormal levels, and these peptides  
CC can be used to modulate these levels, and thus treat autoimmune diseases,  
CC inflammatory diseases and cancer, and aid wound healing and implant  
CC adhesion. In addition, they can also be used to facilitate drug delivery  
CC to the desired target site. The present sequence has a cyclic  
CC conformation  
XX SQ Sequence 8 AA;  
Query Match 100.0%; Score 16; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FID 3  
Db 6 FID 8  
Search completed: April 18, 2005, 14:15:23  
Job time : 33.6047 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 14:22:17 ; Search time 22.6744 Seconds  
(without alignments)  
43.975 Million cell updates/sec

Title: US-09-674-716B-13  
Perfect score: 16  
Sequence: 1 FID 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	5	8	US-08-484-409-36
2	16	100.0	5	11	US-09-920-306-25
3	16	100.0	6	11	US-09-943-944E-130
4	16	100.0	7	9	US-09-185-908-174
5	16	100.0	7	9	US-09-185-908-227
6	16	100.0	7	14	US-10-190-082-567
7	16	100.0	8	9	US-09-946-678-8
8	16	100.0	8	9	US-09-791-378-511
9	16	100.0	8	9	US-09-185-908-177
10	16	100.0	8	9	US-09-185-908-230
11	16	100.0	8	10	US-09-880-748-2842
12	16	100.0	8	11	US-09-791-377-511
13	16	100.0	8	14	US-10-190-082-501

14	16	100.0	8	15	US-10-293-418-2842
15	16	100.0	8	15	US-10-601-100-92
16	16	100.0	8	15	US-10-601-100-108
17	16	100.0	8	16	US-10-712-425-1352
18	16	100.0	8	17	US-10-773-032-1352
19	16	100.0	9	9	US-09-185-908-180
20	16	100.0	9	9	US-09-185-908-233
21	16	100.0	9	10	US-09-932-165-862
22	16	100.0	9	10	US-09-932-165-1235
23	16	100.0	9	15	US-10-363-791-121
24	16	100.0	9	17	US-10-801-990-357
25	16	100.0	9	17	US-10-820-467-241
26	16	100.0	10	9	US-09-757-417-45
27	16	100.0	10	10	US-09-572-404B-644
28	16	100.0	10	10	US-09-572-404B-1464
29	16	100.0	10	10	US-09-572-404B-2015
30	16	100.0	10	10	US-09-572-404B-2017
31	16	100.0	10	10	US-09-572-404B-3882
32	16	100.0	10	10	US-09-572-404B-3883
33	16	100.0	10	10	US-09-932-165-153
34	16	100.0	10	10	US-09-932-165-356
35	16	100.0	10	10	US-09-932-165-563
36	16	100.0	10	10	US-09-932-165-583
37	16	100.0	10	10	US-09-932-165-1361
38	16	100.0	10	10	US-09-573-822C-8
39	16	100.0	10	10	US-09-573-822C-693
40	16	100.0	10	14	US-10-042-945-45
41	16	100.0	10	16	US-10-327-598-462
42	16	100.0	10	17	US-10-833-951-216
43	16	100.0	11	9	US-09-817-310-5
44	16	100.0	11	14	US-10-097-065-560
45	16	100.0	11	15	US-10-372-876-560

#### ALIGNMENTS

#### RESULT 1

US-08-484-409-36  
Sequence 36, Application US/08484409  
Publication No. US20020076412A1  
GENERAL INFORMATION:  
APPLICANT: Steinman, Lawrence  
APPLICANT: Zarnvil, Scott  
TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,409  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 690068.409C1  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid

;  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-484-409-36

Query Match 100.0%; Score 16; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 3 FID 5

## RESULT 2

US-09-920-306-25  
; Sequence 25, Application US/09920306  
; Publication No. US20040029808A1  
; GENERAL INFORMATION:  
; APPLICANT: Unilever PLC  
; APPLICANT: Unilever NV  
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for  
; TITLE OF INVENTION: Hormonal Analyses  
; FILE REFERENCE: Peptide Mimotopes  
; CURRENT APPLICATION NUMBER: US/09/920,306  
; CURRENT FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: EP00306613.1  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-920-306-25

Query Match 100.0%; Score 16; DB 11; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 3 FID 5

## RESULT 3

US-09-943-944E-130  
; Sequence 130, Application US/09943944E  
; Publication No. US20040044036A1  
; GENERAL INFORMATION:  
; APPLICANT: Ptashne, et al.,  
; TITLE OF INVENTION: Transcriptional Activation System, Activators, and Uses  
; TITLE OF INVENTION: Therefor  
; FILE REFERENCE: 0342941-0065  
; CURRENT APPLICATION NUMBER: US/09/943,944E  
; CURRENT FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 238  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 130  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Random peptide  
; OTHER INFORMATION: sequences.  
US-09-943-944E-130

Query Match 100.0%; Score 16; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 1 FID 3

## RESULT 4

US-09-185-908-174  
; Sequence 174, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; TITLE OF INVENTION: FUNCTIONS  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185,908A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 174  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R  
; OTHER INFORMATION: sequences  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-174

Query Match 100.0%; Score 16; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 5 FID 7

## RESULT 5

US-09-185-908-227  
; Sequence 227, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; TITLE OF INVENTION: FUNCTIONS  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185,908A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 227  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-227

Query Match 100.0%; Score 16; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
|||  
Db 5 FID 7

```
RESULT 6
US-10-190-082-567
; Sequence 567, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Laskey, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 567
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-567

Query Match      100.0%; Score 16; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 4 FID 6

RESULT 7
US-09-946-678-8
; Sequence 8, Application US/09946678
; Patent No. US20020106782A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Kotaro
; APPLICANT: KOYAMA, Yasuji
; APPLICANT: UMITSUJI, Genryou
; TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same
; FILE REFERENCE: 0283-0158P
; CURRENT APPLICATION NUMBER: US/09/946,678
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: JP 2000-270371
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Cryptococcus nodaensis
US-09-946-678-8

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 2 FID 4

RESULT 8
US-09-791-378-511
; Sequence 511, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
```

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; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 511
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-511

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 2 FID 4

RESULT 9
US-09-185-908-177
; Sequence 177, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 177
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; OTHER INFORMATION: sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-177

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 6 FID 8

RESULT 10
US-09-185-908-230
; Sequence 230, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 8
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-230

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db       6 FID 8

RESULT 11
US-09-880-748-2842
; Sequence 2842, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2842
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2842

Query Match      100.0%; Score 16; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db       5 FID 7

RESULT 12
US-09-791-377-511
; Sequence 511, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 511
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-791-377-511

Query Match      100.0%; Score 16; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db       2 FID 4

RESULT 13
US-10-190-082-501
; Sequence 501, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Lasky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 501
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-501

Query Match      100.0%; Score 16; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db       5 FID 7

RESULT 14
US-10-293-418-2842
; Sequence 2842, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2842
; LENGTH: 8
; TYPE: PRT
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; ORGANISM: Homo sapiens  
US-10-293-418-2842

Query Match 100.0%; Score 16; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
|||  
Db 5 FID 7

## RESULT 15

US-10-601-100-92  
; Sequence 92, Application US/10601100  
; Publication No. US20040072261A1  
; GENERAL INFORMATION:  
; APPLICANT: INNOGENETICS N.V.  
; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of  
; TITLE OF INVENTION: Neurological Diseases  
; FILE REFERENCE: 11362.0038.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/601,100  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: EP 02447121.1  
; PRIOR FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 60/396,437  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 92  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-601-100-92

Query Match 100.0%; Score 16; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
|||  
Db 2 FID 4

Search completed: April 18, 2005, 14:54:44  
Job time : 23.6744 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:01:43 ; Search time 8.16279 Seconds  
(without alignments)  
27.435 Million cell updates/sec

Title: US-09-674-716B-13  
Perfect score: 16  
Sequence: 1 FID 3

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	7	1	US-08-197-792-25
2	16	100.0	7	1	US-08-459-850-25
3	16	100.0	7	1	US-08-459-214-25
4	16	100.0	7	4	US-09-282-029A-174
5	16	100.0	7	4	US-09-282-029A-227
6	16	100.0	7	4	US-09-282-029A-345
7	16	100.0	7	4	US-09-185-908-174
8	16	100.0	7	4	US-09-185-908-227
9	16	100.0	7	4	US-09-434-355A-174
10	16	100.0	7	4	US-09-434-355A-227
11	16	100.0	7	4	US-09-434-355A-345
12	16	100.0	7	3	US-09-042-071-52
13	16	100.0	8	4	US-09-946-678-8
14	16	100.0	8	4	US-09-282-029A-177
15	16	100.0	8	4	US-09-282-029A-230
16	16	100.0	8	4	US-09-282-029A-348
17	16	100.0	8	4	US-09-185-908-177
18	16	100.0	8	4	US-09-185-908-230
19	16	100.0	8	4	US-09-434-355A-177
20	16	100.0	8	4	US-09-434-355A-230
21	16	100.0	8	4	US-09-434-355A-348
22	16	100.0	9	4	US-09-359-304B-2
23	16	100.0	9	4	US-09-359-304B-5
24	16	100.0	9	4	US-09-359-304B-7
25	16	100.0	9	4	US-09-000-217-2
26	16	100.0	9	4	US-09-341-982-67
27	16	100.0	9	4	US-09-282-029A-180

28	16	100.0	9	4	US-09-282-029A-233	Sequence 233, App
29	16	100.0	9	4	US-09-282-029A-351	Sequence 351, App
30	16	100.0	9	4	US-09-185-908-180	Sequence 180, App
31	16	100.0	9	4	US-09-185-908-233	Sequence 233, App
32	16	100.0	9	4	US-09-434-355A-180	Sequence 180, App
33	16	100.0	9	4	US-09-434-355A-233	Sequence 233, App
34	16	100.0	9	4	US-09-434-355A-351	Sequence 351, App
35	16	100.0	10	1	US-08-277-007-1	Sequence 1, Appli
36	16	100.0	10	1	US-08-485-181-1	Sequence 1, Appli
37	16	100.0	10	2	US-08-964-338-1	Sequence 1, Appli
38	16	100.0	10	3	US-08-975-917-1	Sequence 1, Appli
39	16	100.0	11	4	US-09-817-310-5	Sequence 5, Appli
40	16	100.0	11	4	US-09-937-215-5	Sequence 5, Appli
41	16	100.0	11	4	US-10-355-724A-5	Sequence 5, Appli
42	16	100.0	11	5	PCT-US92-01433A-6	Sequence 6, Appli
43	16	100.0	12	1	US-08-434-255-15	Sequence 15, Appl
44	16	100.0	12	1	US-08-459-967-15	Sequence 15, Appl
45	16	100.0	12	1	US-08-460-327-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1  
US-08-197-792-25  
; Sequence 25, Application US/08197792  
; Patent No. 5525488  
; GENERAL INFORMATION:  
; APPLICANT: Anthony J. Mason  
; APPLICANT: Peter H. Seeburg  
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,792  
; FILING DATE: 16-FEB-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/958414  
; FILING DATE: 08-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744207  
; FILING DATE: 12-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/215466  
; FILING DATE: 05-JUL-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 06/906729  
; FILING DATE: 31-DEC-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 06/827710  
; FILING DATE: 07-FEB-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 06/783910  
; FILING DATE: 03-OCT-1985  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 297P2D4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881

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;
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; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-197-792-25

Query Match      100.0%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db       4 FID 6

RESULT 2
US-08-459-850-25
; Sequence 25, Application US/08459850
; Patent No. 5665568
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,850
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197792
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-459-850-25

Query Match      100.0%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db       4 FID 6

RESULT 3
US-08-459-214-25
; Sequence 25, Application US/08459214
; Patent No. 5716810
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,214
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197792
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-459-850-25
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;
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-459-850-25

Query Match      100.0%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db       4 FID 6

RESULT 3
US-08-459-214-25
; Sequence 25, Application US/08459214
; Patent No. 5716810
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,214
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197792
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
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; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-459-850-25
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; ; SEQUENCE CHARACTERISTICS:
;   LENGTH: 7 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
US-08-459-214-25

Query Match      100.0%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
   |||
Db 4 FID 6

RESULT 4
US-09-282-029A-174
; Sequence 174, Application US/09282029A
; Patent No. 6723700
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C1
; CURRENT FILING DATE: 1999-03-30
; CURRENT APPLICATION NUMBER: US/09/282,029A
; NUMBER OF SEQ ID NOS: 480
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 174
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-282-029A-174

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
   |||
Db 5 FID 7

RESULT 5
US-09-282-029A-227
; Sequence 227, Application US/09282029A
; Patent No. 6723700
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C1
; CURRENT FILING DATE: 1999-03-30
; CURRENT APPLICATION NUMBER: US/09/282,029A
; NUMBER OF SEQ ID NOS: 480
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 227
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide

US-09-282-029A-227

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
   |||
Db 5 FID 7

RESULT 6
US-09-282-029A-345
; Sequence 345, Application US/09282029A
; Patent No. 6723700
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C1
; CURRENT FILING DATE: 1999-03-30
; CURRENT APPLICATION NUMBER: US/09/282,029A
; NUMBER OF SEQ ID NOS: 480
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 345
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: claudin-6 cell adhesion recognition sequence
US-09-282-029A-345

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
   |||
Db 5 FID 7

RESULT 7
US-09-185-908-174
; Sequence 174, Application US/09185908A
; Patent No. 6756356
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT FILING DATE: 1998-11-03
; CURRENT APPLICATION NUMBER: US/09/185,908A
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 174
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-174

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 FID 3
Db      5 FID 7

RESULT 8
US-09-185-908-227
; Sequence 227, Application US/09185908A
; Patent No. 6756356
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-227

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      5 FID 7

RESULT 9
US-09-434-355A-174
; Sequence 174, Application US/09434355A
; Patent No. 6830894
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: James Mathew Symonds
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C2
; CURRENT APPLICATION NUMBER: US/09/434,355A
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 531
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; OTHER INFORMATION: sequences
; OTHER INFORMATION: Cyclic Peptide
US-09-434-355A-174

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      5 FID 7

RESULT 10
US-09-434-355A-227
; Sequence 227, Application US/09434355A
; Patent No. 6830894
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: James Mathew Symonds
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C2
; CURRENT APPLICATION NUMBER: US/09/434,355A
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 531
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
; OTHER INFORMATION: Cyclic Peptide
US-09-434-355A-227

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      5 FID 7

RESULT 11
US-09-434-355A-345
; Sequence 345, Application US/09434355A
; Patent No. 6830894
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: James Mathew Symonds
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C2
; CURRENT APPLICATION NUMBER: US/09/434,355A
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 531
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 345
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: claudin-6 cell adhesion recognition sequence
US-09-434-355A-345

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      5 FID 7

RESULT 12
US-09-042-071-52
; Sequence 52, Application US/09042071
; Patent No. 6294372
; GENERAL INFORMATION:

```

APPLICANT: Burian, Jan  
APPLICANT: Kay, William W.  
TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM  
TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING  
TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,071  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McWaters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 660081.407  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-042-071-52

Query Match 100.0%; Score 16; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
Db 2 FID 4

RESULT 13  
US-09-946-678-8  
Sequence 8, Application US/09946678  
Patent No. 6541236  
GENERAL INFORMATION:  
APPLICANT: ITO, Kotaro  
APPLICANT: UMITSUKI, Genryou  
APPLICANT: KOYAMA, Yasuji  
TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same  
FILE REFERENCE: 0283-0158p  
CURRENT APPLICATION NUMBER: US/09/946,678  
CURRENT FILING DATE: 2001-09-06  
PRIOR APPLICATION NUMBER: JP 2000-270371  
PRIOR FILING DATE: 2000-09-06  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Cryptococcus nodaensis  
US-09-946-678-8

Query Match 100.0%; Score 16; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3

Db 2 FID 4  
RESULT 14  
US-09-282-029A-177  
Sequence 177, Application US/09282029A  
Patent No. 6723700  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
TITLE OF INVENTION: FUNCTIONS  
FILE REFERENCE: 100086.409C1  
CURRENT APPLICATION NUMBER: US/09/282,029A  
CURRENT FILING DATE: 1999-03-30  
NUMBER OF SEQ ID NOS: 480  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 177  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Product of  
OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R  
FEATURE:  
OTHER INFORMATION: Cyclic Peptide  
US-09-282-029A-177

Query Match 100.0%; Score 16; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
Db 6 FID 8

RESULT 15  
US-09-282-029A-230  
Sequence 230, Application US/09282029A  
Patent No. 6723700  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
TITLE OF INVENTION: FUNCTIONS  
FILE REFERENCE: 100086.409C1  
CURRENT APPLICATION NUMBER: US/09/282,029A  
CURRENT FILING DATE: 1999-03-30  
NUMBER OF SEQ ID NOS: 480  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 230  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Product of  
OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences  
FEATURE:  
OTHER INFORMATION: Cyclic Peptide  
US-09-282-029A-230

Query Match 100.0%; Score 16; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3  
Db 6 FID 8

Search completed: April 18, 2005, 14:25:39  
Job time : 8.16279 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 16:06:45 ; Search time 43 Seconds  
(without alignments)  
6.713 Million cell updates/sec

Title: US-09-674-716B-13  
Perfect score: 16  
Sequence: 1 FID 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 23

Minimum DB seq length: 0  
Maximum DB seq length: 3

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	37.5	3	3 S68328	blood cell protein
2	3	18.8	3	3 A22565	R-phycoerythrin al
3	3	18.8	3	3 PQ0010	angiotensin-conver
4	3	18.8	3	3 A43391	TRH-like tripeptid
5	2	12.5	3	3 T13892	cytochrome-c oxida
6	2	12.5	3	3 A33802	thyrotropin-releas
7	1	6.2	3	3 S13894	histidinol dehydro
8	1	6.2	3	3 F37196	bradykinin-potenti
9	1	6.2	3	3 I50412	gene p20K protein
10	1	6.2	3	3 PT0578	T-cell receptor be
11	1	6.2	3	3 I78890	tyrosine protein k
12	1	6.2	3	3 B23751	spinal cord peptid
13	0	0.0	3	3 RHSHT	thyroliberin - she
14	0	0.0	3	3 A92971	thyroliberin - eas
15	0	0.0	3	3 RHTDFO	thyroliberin - Bom
16	0	0.0	3	3 E37196	bradykinin-potenti
17	0	0.0	3	3 PT0636	T-cell receptor be
18	0	0.0	3	3 PT0571	T-cell receptor be
19	0	0.0	3	3 PT0622	T-cell receptor be
20	0	0.0	3	3 GKHU	growth-modulating
21	0	0.0	3	3 RHPGT	thyroliberin - pig
22	0	0.0	3	3 A60898	bursin - chicken
23	0	0.0	3	3 A23751	spinal cord peptid

ALIGNMENTS

RESULT 1

S68328

blood cell protein A - Molgula manhattensis (fragment)

C;Species: Molgula manhattensis

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C;Accession: S68328

R;Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from t

A;Reference number: S68325; MUID:96132650; PMID:8554314

A;Accession: S68328

A;Molecule type: protein

A;Residues: 1-3 <TAY>

Query Match 37.5%; Score 6; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

DB 2 F 2

RESULT 2

A22565

R-Phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)

C;Species: Gastroclonium coulteri

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C;Accession: A22565

R;Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A;Reference number: A22565; MUID:85182601; PMID:3886644

A;Accession: A22565

A;Molecule type: protein

A;Residues: 1-3 <KLO>

Query Match 18.8%; Score 3; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 2.8e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

DB 2 Y 2

RESULT 3

PQ0010

angiotensin-converting enzyme inhibitor (FLP-3) - common fig

N;Alternate names: ficus latex peptide 3

C;Species: Ficus carica (common fig)

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C;Accession: PQ0010

R;Maruyama, S.; Miyoshi, S.; Tanaka, H.

Agric. Biol. Chem. 53, 2763-2767, 1989

A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A;Reference number: PQ0008

A;Accession: PQ0010

A;Molecule type: protein

A;Residues: 1-3 <MAR>

A;Experimental source: latex

C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 18.8%; Score 3; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 2.8e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2

DB 2 V 2

RESULT 4

A43391

TRH-like tripeptide - alfalfa  
 C:Species: Medicago sativa (alfalfa)  
 C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C:Accession: A43391  
 R:Lackey, D.B.  
 J. Biol. Chem. 267, 17508-17511, 1992  
 A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglutaminyl-L-histidyl-L-proline  
 A:Reference number: A43391; MUID:92388092; PMID:1517203  
 A:Accession: A43391  
 A:Molecule type: protein  
 A:Residues: 1-3 <LAC>  
 C:Keywords: amidated carboxyl end; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 18.8%; Score 3; DB 3; Length 3;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 2 Y 2

RESULT 5  
 T13892  
 cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (fragment)  
 C:Species: Mitochondrion Lampetra fluviatilis (river lamprey)  
 C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C:Accession: T13892  
 R:Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.  
 Mol. Biol. Evol. 14, 807-813, 1997  
 A:Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI  
 A:Reference number: Z17775; MUID:97398704; PMID:9254918  
 A:Accession: T13892  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3 <DEL>  
 A:Cross-references: EMBL:Y09528; NID:92340016; PIDN:CMA70721.1; PID:G4379123  
 C:Genetics:  
 A:Genome: mitochondrion  
 A:Note: COI  
 C:Keywords: mitochondrion; oxidoreductase

Query Match 12.5%; Score 2; DB 3; Length 3;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2  
 Db 3 L 3

RESULT 6  
 A33802  
 thyrotropin-releasing hormone-like peptide - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Mar-2004  
 C:Accession: A33802  
 R:Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.  
 J. Biol. Chem. 264, 7788-7791, 1989  
 A:Title: A novel peptide, pyroglutamylglutamylproline amide, in the rabbit prostate compound  
 A:Reference number: A33802; MUID:89255196; PMID:2498305  
 A:Accession: A33802  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-3 <COC>  
 C:Keywords: amidated carboxyl end; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 12.5%; Score 2; DB 3; Length 3;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 D 3  
 Db 2 E 2

RESULT 7  
 S13894  
 histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)  
 C:Species: Brassica oleracea (wild cabbage)  
 C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C:Accession: S13894  
 R:Nagai, A.; Scheidegger, A.  
 Arch. Biochem. Biophys. 284, 127-132, 1991  
 A:Title: Purification and characterization of histidinol dehydrogenase from cabbage.  
 A:Reference number: S13894; MUID:91112783; PMID:1989490  
 A:Accession: S13894  
 A:Molecule type: protein  
 A:Residues: 1-3 <NAG>  
 A:Experimental source: var. capitata  
 C:Keywords: dimer; NAD; oxidoreductase

Query Match 6.2%; Score 1; DB 3; Length 3;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2  
 Db 2 M 2

RESULT 8  
 F37196  
 bradykinin-potentiating peptide 6 - island jararaca  
 C:Species: Bothrops insularis (island jararaca)  
 C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C:Accession: F37196  
 R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
 J. Protein Chem. 9, 221-227, 1990  
 A:Title: Primary structure and biological activity of bradykinin potentiating peptides  
 A:Reference number: A37196; MUID:90351557; PMID:2386615  
 A:Accession: F37196  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-3 <CIN>  
 C:Keywords: pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 6.2%; Score 1; DB 3; Length 3;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 3 W 3

RESULT 9  
 I50412  
 gene p20K protein - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C:Accession: I50412  
 R:Mao, P.L.; Beauchemin, M.; Bedard, P.A.  
 J. Biol. Chem. 268, 8131-8139, 1993  
 A:Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken  
 A:Reference number: A46643; MUID:93216790; PMID:8463325  
 A:Accession: I50412  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3 <MAO>  
 A:Cross-references: GB:I02537; NID:9212616; PID:9212617

C;Genetics:  
A;Gene: p20K

Query Match 6.2%; Score 1; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2  
: 1 M 1  
Db

## RESULT 10

PT0578  
T-cell receptor beta chain V-D-J region (141-1BD) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0578  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0578  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <PEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 6.2%; Score 1; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2  
: 3 M 3  
Db

## RESULT 11

I78890  
tyrosine protein kinase - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: I78890  
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.  
Oncogene 9, 3437-3448, 1994  
A;Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protein kinase.  
A;Reference number: I58407; MUID:95060800; PMID:7970703  
A;Accession: I78890  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <RES>  
A;Cross-references: GB:I33339; NID:9609536; PIDN:AAA64432.1; PID:9609538  
C;Genetics:  
A;Gene: p52ntk

Query Match 6.2%; Score 1; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2  
: 1 M 1  
Db

## RESULT 12

B23751  
spinal cord peptide SCP-5 - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Mar-2004  
C;Accession: B23751  
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.  
Arch. Biochem. Biophys. 240, 178-183, 1985

A;Reference number: A23751; MUID:85250425; PMID:4015098  
A;Accession: B23751  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-3 <HS1>

Query Match 6.2%; Score 1; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2  
: 1 M 1  
Db

## RESULT 13

RHSHT  
thyroliberin - sheep  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004  
C;Accession: A93750; A01415  
R;Desiderio Jr., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.  
Org. Mass Spectrom. 5, 221-228, 1971  
A;Title: The elucidation of the primary structure of the hypothalamic thyroid stimulatory hormone.  
A;Reference number: A93750  
A;Accession: A93750  
A;Molecule type: protein  
A;Residues: 1-3 <DES>  
A;Cross-references: UNIPROT:P01151  
R;Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.  
Nature 226, 321-325, 1970  
A;Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.  
A;Reference number: A93161; MUID:70163386; PMID:4985794  
A;Contents: annotation  
A;Note: physicochemical characteristics and biological activities of the natural and synthetic peptides.  
C;Superfamily: thyroliberin  
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 D 3  
1 Q 1  
Db

## RESULT 14

A92971  
thyroliberin - eastern newt (tentative sequence)  
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004  
C;Accession: A92971; A01415  
R;Grimm-Jorgensen, Y.; McKelvy, J.F.  
J. Neurochem. 23, 471-478, 1974  
A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain.  
A;Reference number: A92971; MUID:75035605; PMID:4214528  
A;Accession: A92971  
A;Molecule type: protein  
A;Residues: 1-3 <GRI>  
A;Cross-references: UNIPROT:P01151  
A;Note: a peptide with the chromatographic and electrophoretic characteristics of thyrotropin releasing factor.

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 D 3  
Db 1 Q 1

## RESULT 15

RHTDIO

thyroliberin - Bombina orientalis

C:Species: Bombina orientalis

C&gt;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004

C/Accession: A90919; A01415

R:Yasuhara, T.; Nakajima, T.

Chem. Pharm. Bull. 23, 3301-3303, 1975

A&gt;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.

A/Reference number: A90919; PMID:76138399; PMID:815011

A/Accession: A90919

A/Molecule type: protein

A/Residues: 1-3 &lt;YAS&gt;

A/Cross-references: UNIPROT:P01151

C:Superfamily: thyroliberin

C/Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid

F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 D 3  
Db 1 Q 1

Search completed: April 18, 2005, 16:16:15  
Job time : 45 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:58:29 ; Search time 174 Seconds  
(without alignments)  
8.829 Million cell updates/sec

Title: US-09-674-716B-13  
Perfect score: 16  
Sequence: 1 FID 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0  
Maximum DB seq length: 3

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6	37.5	3	1 LUXE VIBFI	P24272 vibrio fisc
2	1	6.2	2	1 GWA SEPOF	P83570 sepiia offic
3	0	0.0	3	1 GRWM HUMAN	P01157 homo sapien
4	0	0.0	3	1 THYL_BOMOR	P62970 bombina ori
5	0	0.0	3	1 THYL_NOTVI	P62971 notophthalm
6	0	0.0	3	1 THYL_PIG	P62968 sus scrofa
7	0	0.0	3	1 THYL_SHEEP	P62969 ovis aries

#### ALIGNMENTS

RESULT 1  
LUXE VIBFI  
ID LUXE VIBFI STANDARD; PRT; 3 AA.  
AC P24272; 1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-protein synthetase) (Fragment).  
GN Name=luxe;  
OS Vibrio fischeri.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91072226; PubMed=2254256;  
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;  
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination

RT site for the lux operon.";  
RL J. Bacteriol. 172:6797-6802(1990).  
CC -!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It is a component of the fatty acid reductase complex responsible for converting tetradecanoic acid to the aldehyde which serves as substrate in the luciferase-catalyzed reaction.  
CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.  
CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.  
CC -!- SIMILARITY: Belongs to the luxE family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; M62812; -; NOT ANNOTATED\_CDS.  
KW Ligase; Luminescence.  
FT NON\_TER 1  
SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 D 3  
DB 3 D 3

#### RESULT 2

GWA SEPOF  
ID GWA SEPOF STANDARD; PRT; 2 AA.  
AC P83570;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Neuropeptide GWA.  
OS Sepia officinalis (Common cuttlefish).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OX Decapodiformes; Sepioidae; Sepiidae; Sepia.  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
RC TISSUE=Optic lobe;  
RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;  
RA Henry J., Favrel P., Boucaud-Camou E.;  
RT Isolation and identification of a novel Ala-Pro-Gly-Tyr-amide-related peptide inhibiting the motility of the mature oviduct in the cuttlefish, Sepia officinalis.";  
RL Peptides 18:1469-1474(1997).  
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity targeting the distal oviduct. Inhibits the motility of the oviduct by decreasing tonus, frequency and amplitude of contractions.  
CC -!- SUBCELLULAR LOCATION: Secreted  
CC -!- MASS SPECTROMETRY: MW=239.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 2  
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 2;  
Best Local Similarity 0.0%; Pred. No. 1.6e+06;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
DB 2 W 2

#### RESULT 3

## RESULTS

KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
 FT MOD\_RES 3 3 Proline amide.  
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;  
 Best Local Similarity 0.0%; Pred. No. 1.6e+06;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 D 3  
 Db 1 Q 1

RESULT 7  
 THYL SHEEP  
 ID THYL SHEEP STANDARD; PRT; 3 AA.  
 AC P62969; F01151;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (TSH-releasing factor) (Protirelin).  
 DE releasing factor) (TSH-releasing factor) (Protirelin).  
 GN Name=TRH;  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 OX [1]  
 RN  
 RP SEQUENCE.  
 RC TISSUE=Hypothalamus;  
 RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R., Ward D.N.;  
 RA "The elucidation of the primary structure of the hypothalamic thyroid stimulating hormone releasing factor of ovine origin by means of mass spectrometry.";  
 RT Org. Mass Spectrom. 5:221-228 (1971).  
 RN [2]  
 RP SYNTHESIS.  
 RX MEDLINE=70163386; PubMed=4985794;  
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W., Guillemin R.;  
 RA "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.";  
 RT Nature 226:321-325 (1970).  
 RL Nature 226:321-325 (1970).  
 CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/neuromodulator in the central and peripheral nervous systems.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 DR PIR: A93750; RSHST.  
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
 FT MOD\_RES 3 3 Proline amide.  
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;  
 Best Local Similarity 0.0%; Pred. No. 1.6e+06;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 D 3  
 Db 1 Q 1

Search completed: April 18, 2005, 16:15:24  
 Job time : 174 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	16	100.0	3	3	AAy32259	Light cha
2	11	68.8	3	2	AAR64556	RF-1 pept
3	11	68.8	3	2	ADP77860	Therapeut
4	10	62.5	3	2	AAR25193	IDA-pepti
5	10	62.5	3	6	ABR55054	MMP substr
6	9	56.2	3	2	AAY50605	Resin bou
7	9	56.2	3	2	AAY50604	Resin bou
8	9	56.2	3	5	ABg77789	Targettin
9	8	50.0	2	5	ABG63747	Human alb
10	8	50.0	2	7	ADC36684	Mutated v
11	8	50.0	2	8	ADL77012	Albumin f
12	8	50.0	3	2	AAR48960	NL4-3 tru
13	8	50.0	3	2	AAR82907	Non-RGD,
14	8	50.0	3	2	AAR25187	LDV-pepti
15	8	50.0	3	3	AAy49399	Morphine
16	8	50.0	3	3	AAB01568	Cell bind
17	8	50.0	3	4	ABN91892	Opioid pe
18	8	50.0	3	4	ABN91984	Fibronect
19	8	50.0	3	5	ABG93534	Human P-g
20	8	50.0	3	5	AAM48034	MDL pepti
21	8	50.0	3	5	ABG77875	Targettin
22	8	50.0	3	7	ADC36673	Mutated v
23	8	50.0	3	7	ADC36683	Mutated v
24	7	43.8	3	4	ABN91211	Neurocept
25	7	43.8	3	6	ABR44229	Linker pe

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents

XX  
 XX Sequence 3 AA;

Query Match 100.0%; Score 16; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 Db 1 FID 3

RESULT 2  
 AAR64556  
 ID AAR64556 standard; peptide; 3 AA.

XX  
 AC AAR64556;

XX 25-MAR-2003 (revised)

DT 01-SEP-1995 (first entry)

XX RF-1 peptide 1 from respiratory syncytial virus.

XX antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;  
 KW human immunodeficiency virus; transmembrane protein; gp41; alpha helix;  
 KW leucine zipper; DP-185; respiratory syncytial virus; RSV.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1  
 FT /note= "optionally has an amino, acetyl, 9-  
 FT fluorenylmethoxy-carbonyl, hydrophobic or macromolecular  
 FT carrier gp. attached"

FT Modified-site 3  
 FT /note= "optionally has a carboxyl, amido, hydrophobic or  
 FT macromolecular carrier gp. attached"

XX WO9428920-A1.

XX 22-DEC-1994.

XX 07-JUN-1994; 94WO-US005739.

XX 07-JUN-1993; 93US-00073028.

XX (UYDU-) UNIV DUKE.

XX Bolognesi DP, Matthews TJ, Wild CT, Barney SO, Lambert DM;  
 PI Petteway SR;

XX WPI; 1995-036105/05.

XX Computer search generated synthetic peptides - are inhibitors of HIV  
 PT transmission.

XX Claim 14; Page 137; 182pp; English.

XX AAR64556-589 are peptide derivatives of a 37 mer RF-1 peptide derived  
 CC from respiratory syncytial virus (RSV) (AAR64590) which have been  
 CC truncated at the carboxy terminus. The peptides are DP-178 like peptides.

CC DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI  
 CC transmembrane protein gp41. It forms a putative alpha helix at the C-  
 CC terminal end of the gp41 ectodomain, and complexes with DP-107  
 CC (corresponds to amino acids 558-595) which contains a leucine zipper  
 CC motif. The peptides complex via non-covalent protein-protein  
 CC interactions. The peptide derivatives were identified by a computer  
 CC assisted peptide sequence search. The antiviral activity of this peptide  
 CC is not stated in the specification. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

XX Sequence 3 AA;

Query Match 68.8%; Score 11; DB 2; Length 3;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FID 3  
 |||  
 Db 1 FVD 3

RESULT 3  
 ADF77860  
 ID ADF77860 standard; peptide; 3 AA.

XX  
 AC ADF77860;

XX 11-MAR-2004 (first entry)

DE Therapeutic peptide of the invention #SEQ ID 13.

XX Antinflammatory; hypotensive; sarcoidosis;

KW vasoactive intestinal peptide; VIP;

KW pituitary adenylate cyclase-activating polypeptide; PACAP; lung;

KW secondary pulmonary hypertension; blood pressure.

XX Homo sapiens.

XX WO2003103702-A1.

XX 18-DEC-2003.

XX 05-JUN-2003; 2003WO-CH0000357.

XX 10-JUN-2002; 2002EP-00012767.

XX (MOND-) MONDOBIOTECH LAB ANSTALT.

XX Bevec D;

XX WPI; 2004-081972/08./

XX Use of peptides having highly conserved amino acid sequence of vasoactive  
 PT intestinal peptides in the manufacture of medicament for the treatment of  
 PT disease correlated with sarcoidosis.

XX Claim 2; SEQ ID NO 13; 31pp; English.

XX The invention relates to the manufacture of a medicament for the  
 CC treatment of a disease or disorder correlated with sarcoidosis. The  
 CC medicament of the invention contains a peptide that is a vasoactive  
 CC intestinal peptide (VIP) or a pituitary adenylate cyclase-activating  
 CC polypeptide (PACAP). Peptides of the invention are useful for the  
 CC treatment of a disease or disorder correlated with sarcoidosis in the  
 CC human lung, and also secondary pulmonary hypertension. The peptides,  
 CC having highly conserved sequence of amino acids exhibit an improved  
 CC therapeutic efficacy than the prior art. The peptides reduce the  
 CC pulmonary arterial pressure, the diastolic blood pressure and the  
 CC systolic blood pressure. The current sequence represents a peptide of the  
 CC invention.

XX Sequence 3 AA;

Query Match 68.8%; Score 11; DB 8; Length 3;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FID 3  
 DB 1 FTD 3

RESULT 4  
 AAW25193  
 ID AAW25193 standard; peptide; 3 AA.  
 XX  
 AC AAW25193;  
 XX  
 DT 05-JAN-1998 (first entry)  
 XX  
 DE IDA-peptide capable of binding cell adhesion molecules.  
 XX  
 KW IDA; isoleucine; aspartic acid; alanine; cell adhesion molecule; binding;  
 KW bladder irrigation; tumour removal; endoscopic operation;  
 KW transurethral resection; cancer; neoplasia.  
 XX  
 OS Synthetic.  
 XX  
 PN DE19529909-A1.  
 XX  
 PD 20-FEB-1997.  
 XX  
 PF 15-AUG-1995; 95DE-01029909.  
 XX  
 PR 15-AUG-1995; 95DE-01029909.  
 XX  
 PA (PREP ) PRESENTIUS AG.  
 XX  
 PI Boehle A;  
 XX  
 DR WPI; 1997-133793/13.  
 XX  
 PT Endoscopic irrigation solns. - contg. peptide(s) that bind to cell  
 PT adhesion molecules.  
 XX  
 PS Claim 7; Page 8; 8pp; German.  
 XX  
 CC AAW25193-W25195 are peptides containing an IDA sequence or equivalent.  
 CC The peptides are capable of binding to cell adhesion molecules and are  
 CC used in aqueous irrigation solutions for use during and after endoscopic  
 CC operations. Preferred irrigation solutions are electrolyte-free and  
 CC contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing  
 CC the amino acid sequences: RGD, LDV, IDA, DGEA, GPRP, VTL, YIGSR, KQAGDV  
 CC and/or REDV (given in one letter amino acid code). The solutions are  
 CC especially used for irrigating the bladder during and after tumour  
 CC removal by transurethral resection. The peptides protect against  
 CC recurrence of tumours  
 XX  
 SQ Sequence 3 AA;

Query Match 62.5%; Score 10; DB 2; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3  
 DB 1 ID 2

RESULT 5  
 ABR55054  
 ID ABR55054 standard; peptide; 3 AA.  
 XX  
 AC ABR55054;  
 XX  
 DT 02-JUL-2003 (first entry)

Query Match 62.5%; Score 10; DB 2; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3  
 DB 1 ID 2

RESULT 6  
 AAY50605  
 ID AAY50605 standard; peptide; 3 AA.  
 XX  
 AC AAY50605;  
 XX  
 DT 09-FEB-2000 (first entry)  
 XX  
 DE Resin bound cyclic peptide 38.  
 XX  
 KW Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;  
 KW hypotensive; PTH receptor; treatment; hyper-calcaemia; hypo-calcaemia;  
 KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;  
 KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Arg(PMC)"  
 FT Misc-difference 3 /note= "This C-terminal amino acid is in the form of an  
 FT

XX MMP substrate cleavage related peptide SEQ ID NO:56.  
 DE Matrix metalloproteinase; MMP-2; MMP-9, MT1-MMP; substrate; cytostatic;  
 XX peptidomimetic; antiinflammatory; neuroprotective; gene therapy;  
 KW tumour angiogenesis; inflammatory disease; neurodegenerative disease.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003025125-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 13-SEP-2002; 2002WO-US029060.  
 XX  
 PR 14-SEP-2001; 2001US-00953592.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 SM Smith JW, Chen EI, Kridel SJ;  
 XX WPI; 2003-354595/33.  
 DR  
 XX  
 PT New isolated matrix metalloproteinase-2 (MMP-2), MMP-9, MT1-MMP selective  
 PT substrate polypeptide, useful for diagnosing and treating tumor  
 PT angiogenesis, inflammatory or neurodegenerative diseases.  
 XX  
 PS Disclosure; Page 67; 146pp; English.  
 XX  
 CC The present invention describes an isolated matrix metalloproteinase-2  
 CC (MMP-2), MMP-9 or MT1-MMP selective substrate polypeptide (I), or its  
 CC functional peptidomimetic. Also described is a method for preferentially  
 CC directing a moiety to a site of MMP-2, MMP-9 or MT1-MMP activity by  
 CC administering (I) to the subject. (I) have cytostatic, antiinflammatory  
 CC and neuroprotective activities, and can be used in gene therapy. The  
 CC polypeptides and methods from the present invention can be used for  
 CC diagnosing and treating tumour angiogenesis, inflammatory or  
 CC neurodegenerative diseases. ABR54999 to ABR55122 and ACC49718 to ACC49722  
 CC represent sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 3 AA;

```

FT Misc-difference 3 ester with benzyl alcohol"
FT FT /note= "Asp(Oallyl)"
XX PN
XX WO9952933-A1.
XX PD 21-OCT-1999.
XX PF 15-APR-1999; 99WO-US008435.
XX PR 15-APR-1998; 98US-0081897P.
XX PA (RHON ) RHONE-POULENC RORER PHARM INC.
XX PI Sledeski AW, Mancel JJ;
XX PI WPI; 1999-633822/54.
XX DR
XX PT Convergent synthesis of peptides for treating e.g. bone disorders.
XX PS Disclosure; Page 79; 85pp; English.
XX CC This invention describes a novel method for the preparation of peptides
XX CC (II) that contain both cyclic and linear peptide fragments comprises
XX CC sequential reaction of a resin-bound linear fragment with the cyclic
XX CC fragment in N-protected form and optionally other linear fragments. The
XX CC products of the invention have osteopathic and hypotensive activity. (II)
XX CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The
XX CC method is particularly used to prepare cyclic peptide analogs of
XX CC parathyroid hormone (PTH) or PTH-related peptides which are useful for
XX CC treating diseases that respond to treatment with agents that bind to PTH
XX CC receptors (with or without activation of adenylyl cyclase activity), e.g.
XX CC hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
XX CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also
XX CC for promoting repair of bone fractures. Separate synthesis of the cyclic
XX CC fragment allows convergent synthesis of resin-bound (II), with better
XX CC yields and higher throughput. The difficulties associated with
XX CC preparation of the bridged fragment are confined to a small peptide which
XX CC can be purified before reaction with the resin-bound component. AAY50568-
XX CC Y50614 represent the peptide fragments described in the method of the
XX CC invention
XX SQ Sequence 3 AA;

Query Match 56.2%; Score 9; DB 2; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
Db 2 VD 3

RESULT 7
AAY50604
ID AAY50604 standard; peptide; 3 AA.
XX AC AAY50604;
XX XX
XX DT 09-FEB-2000 (first entry)
XX XX Resin bound cyclic peptide 37.
XX DE
XX KW Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
XX KW hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;
XX KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
XX KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.
XX XX
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
FT Misc-difference 1 /note= "FMOC-Arg (PMC)"
FT FT

```

```

FT Misc-difference 3 /note= "This C-terminal amino acid is in the form of an
FT FT ester with benzyl alcohol"
FT FT Misc-difference 3 /note= "Asp(Oallyl)"
XX PN
XX WO9952933-A1.
XX PD 21-OCT-1999.
XX PF 15-APR-1999; 99WO-US008435.
XX PR 15-APR-1998; 98US-0081897P.
XX PA (RHON ) RHONE-POULENC RORER PHARM INC.
XX PI Sledeski AW, Mancel JJ;
XX PI WPI; 1999-633822/54.
XX DR
XX PT Convergent synthesis of peptides for treating e.g. bone disorders.
XX PS Disclosure; Page 78; 85pp; English.
XX CC This invention describes a novel method for the preparation of peptides
XX CC (II) that contain both cyclic and linear peptide fragments comprises
XX CC sequential reaction of a resin-bound linear fragment with the cyclic
XX CC fragment in N-protected form and optionally other linear fragments. The
XX CC products of the invention have osteopathic and hypotensive activity. (II)
XX CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The
XX CC method is particularly used to prepare cyclic peptide analogs of
XX CC parathyroid hormone (PTH) or PTH-related peptides which are useful for
XX CC treating diseases that respond to treatment with agents that bind to PTH
XX CC receptors (with or without activation of adenylyl cyclase activity), e.g.
XX CC hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
XX CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also
XX CC for promoting repair of bone fractures. Separate synthesis of the cyclic
XX CC fragment allows convergent synthesis of resin-bound (II), with better
XX CC yields and higher throughput. The difficulties associated with
XX CC preparation of the bridged fragment are confined to a small peptide which
XX CC can be purified before reaction with the resin-bound component. AAY50568-
XX CC Y50614 represent the peptide fragments described in the method of the
XX CC invention
XX SQ Sequence 3 AA;

Query Match 56.2%; Score 9; DB 2; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
Db 2 VD 3

RESULT 8
ABG77789
ID ABG77789 standard; peptide; 3 AA.
XX AC ABG77789;
XX XX
XX DT 05-NOV-2002 (first entry)
XX XX
XX DE Targetting peptide selective for human organ, tissue or cell type #322.
XX KW Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;
XX KW immunomodulator; antibacterial; antiviral; gene therapy; cancer;
XX KW arthritis; diabetes; inflammatory disease; atherosclerosis;
XX KW autoimmune disease; bacterial infection; viral infection;
XX KW cardiovascular disease; degenerative disease.
XX XX
XX OS Homo sapiens.
XX FT

```

PN WO200220723-A2.  
 XX 14-MAR-2002.  
 XX 07-SEP-2001; 2001WO-US028044.  
 XX 08-SEP-2000; 2000US-0231266P.  
 PR 17-JAN-2001; 2001US-00765101.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA  
 XX Arap W, Pasqualini R;  
 XX WPI; 2002-599247/64.  
 XX New targeting peptides identified by phage display, useful for treating a  
 PT disease state, e.g. cancer, diabetes, inflammatory disease  
 PT atherosclerosis, autoimmune disease, bacterial or viral infection or  
 PT cardiovascular disease.  
 XX Claim 16; Page 79; 269pp; English.  
 XX The invention describes an isolated peptide of 100 amino acids or less in  
 CC size. The peptide is useful for treating a disease state, e.g. cancer,  
 CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune  
 CC disease, bacterial infection, viral infection, cardiovascular disease or  
 CC degenerative disease. This sequence represents a human targeting peptide  
 CC selective for human organs, tissues or cell types  
 XX Sequence 3 AA;  
 SQ  
 Query Match 56.2%; Score 9; DB 5; Length 3;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ID 3  
 Db :  
 2 VD 3  
 RESULT 9  
 ABG63747  
 ID ABG63747 standard; protein; 2 AA.  
 XX AC  
 XX ABG63747;  
 DT 27-AUG-2002 (first entry)  
 XX DE  
 XX Human albumin fusion protein #422.  
 XX KW  
 KW Albumin fusion protein; therapeutic protein X; human albumin; HA;  
 KW human serum albumin; HSA; cancer; reproductive disorder;  
 KW digestive disorder; immune disorder; endocrine disorder;  
 KW haematopoietic disorder; neural disorder; connective disorder;  
 KW cyostatic; antifertility; antinflammatory; antilucer;  
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;  
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antiarthritic.  
 XX OS  
 OS Homo sapiens.  
 OS Synthetic.  
 XX PA  
 PN WO200177137-A1.  
 XX 18-OCT-2001.  
 XX 12-APR-2001; 2001WO-US011988.  
 XX 12-APR-2000; 2000US-0229358P.  
 PR 25-APR-2000; 2000US-0199384P.  
 PR 21-DEC-2000; 2000US-0256931P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA

XX Rosen CA, Haseltine WA;  
 XX WPI; 2002-010886/01.  
 XX New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein.  
 XX Claim 1; Page 820; 2102pp; English.  
 XX The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA, also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or disorder  
 CC that may be modulated by therapeutic protein X. The albumin extends the  
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo  
 CC activity. The protein is useful for treating and diagnosing disorders  
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's  
 CC disease, ulcerative colitis), immune disorders (e.g. acquired  
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),  
 CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,  
 CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,  
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).  
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention  
 XX Sequence 2 AA;  
 SQ  
 Query Match 50.0%; Score 8; DB 5; Length 2;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FI 2  
 Db :  
 1 FL 2  
 RESULT 10  
 ADC36684  
 ID ADC36684 standard; peptide; 2 AA.  
 XX AC  
 XX ADC36684;  
 XX DT 18-DEC-2003 (first entry)  
 XX DE  
 XX Mutated version JA-16 epitope peptide #20.  
 KW Growth Differentiation Factor-8; GDF-8; Antidiabetic; Osteopathic;  
 KW Immunomodulator; Anorectic; Neuroprotective; Inotropic;  
 KW muscular disorder; neuromuscular disorder; osteoporosis.  
 XX OS  
 OS Homo sapiens.  
 XX WO2003027248-A2.  
 XX 03-APR-2003.  
 PD 26-SEP-2002; 2002WO-US030452.  
 PF 26-SEP-2001; 2001US-0324528P.  
 XX (AMHP ) WYETH.  
 PA (DUNH/) DUNHAM W J.  
 XX Aghajanian J, Wolfman NM, Veldman GM, Davies MV, Whittemore L;  
 PI O'hara D, Bridges KG, Khurana TS, Bouxsein M;  
 XX WPI; 2003-421158/39.  
 XX New isolated anti-GDF-8 antibody, useful for treating, diagnosing and  
 PT preventing disorders associated with the GDF-8 protein, such as a type 2  
 PT diabetes, muscular dystrophy, muscle atrophy, cachexia, obesity and/or  
 PT osteoporosis.  
 XX Disclosure; SEQ ID NO 85; 150pp; English.  
 PS

XX The present invention relates to an isolated antibody that specifically  
 CC binds to a Growth Differentiation Factor-8 (GDF-8) protein and reduces  
 CC one or more biological activities associated with the GDF-8 protein. The  
 CC methods and compositions of the present invention are useful for the  
 CC treatment of disorders associated with the GDF-8 protein, such as a  
 CC muscular disorder, neuromuscular disorder, adipose tissue disorder, type  
 CC 2 diabetes or bone degenerative disorder, muscular dystrophy, muscle  
 CC atrophy, congestive obstructive pulmonary disease, muscle wasting  
 CC syndrome, sarcopenia, cachexia, obesity and/or osteoporosis. They can  
 CC also be used for the diagnosis and prevention of the same disorders. The  
 CC present sequence is a protein of the invention.  
 XX SQ Sequence 2 AA;  
 Query Match 50.0%; Score 8; DB 7; Length 2;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ID 3  
 Db 1 LD 2  
 RESULT 11  
 ADL77012  
 ID ADL77012 standard; peptide; 2 AA.  
 XX AC ADL77012;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 494.  
 XX KW albumin fusion protein; cytostatic; antianaemic; antiarthritic;  
 KW antiaesthetic; anti-HIV; immunosuppressive; antiinflammatory;  
 KW antiparasitic; antibacterial; osteopathic; dermatological; antitumor;  
 KW immunomodulator; antiarrhythmic; cardiac; nontropic; antilipemic;  
 KW nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;  
 KW antidiabetic; anabolic; hypertensive; vulnerable; gene therapy; cancer;  
 KW reproductive system disorder; therapeutic protein.  
 XX OS Unidentified.  
 XX EN US2004010134-A1.  
 XX PD 15-JAN-2004.  
 XX PF 12-APR-2001; 2001US-00833245.  
 XX PR 12-APR-2000; 2000US-0229358P.  
 XX PR 25-APR-2000; 2000US-0199384P.  
 XX PR 21-DEC-2000; 2000US-0256931P.  
 XX PA (ROSE/) ROSEN C A.  
 XX PA (HASE/) HASELTINE W A.  
 XX PI Rosen CA, Haseltine WA;  
 XX WI WPI; 2004-090519/09.  
 XX PT New albumin fusion proteins, useful for diagnosing, treating, preventing  
 PT or ameliorating diseases or disorders e.g. cancer, anemia, arthritis,  
 PT asthma, inflammatory bowel disease or Alzheimer's disease.  
 XX PS Disclosure; SEQ ID NO 494; 279pp; English.  
 XX CC The invention relates to a novel albumin fusion protein. The invention  
 CC further relates to: a composition comprising the albumin fusion protein  
 CC and a pharmaceutical carrier; a kit comprising the composition of the  
 CC albumin fusion protein formula; a method of treating a disease or  
 CC disorder in a patient comprising the step of administering the albumin  
 CC fusion protein; a method of treating a patient with a disease or disorder

CC that is modulated by Therapeutic protein: X, or its fragment or variant;  
 CC a method of extending the shelf life of Therapeutic protein: X, or its  
 CC fragment or variant; a nucleic acid molecule comprising a polynucleotide  
 CC sequence encoding the albumin fusion protein; a vector comprising the  
 CC nucleic acid molecule of the albumin fusion protein, and a host cell  
 CC comprising the nucleic acid molecule of the albumin fusion protein. The  
 CC albumin fusion protein and its compositions have the following  
 CC activities: cytostatic, antianaemic, antiarthritic, antiaesthetic, anti-  
 CC HIV, immunosuppressive, antiinflammatory, antiparasitic, antibacterial,  
 CC osteopathic, dermatological, antitumor, immunomodulator, antiarrhythmic,  
 CC cardiac, nontropic, antilipemic, nephrotropic, uropathic,  
 CC neuroprotective, antiparkinsonian, tranquilizer, antidiabetic, anabolic,  
 CC hypertensive, and vulnerable. The albumin fusion protein nucleic acid may  
 CC be used in gene therapy to treat disorders. The albumin fusion protein is  
 CC useful for diagnosing, treating, preventing or ameliorating diseases or  
 CC disorders comprising indication: Y. The diseases or disorders include:  
 CC cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), acute  
 CC immune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, AIDS,  
 CC lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,  
 CC autoimmune disease, inflammatory bowel disease, psoriasis or Lyme  
 CC disease), reproductive system disorders (e.g. prostatitis, inguinal  
 CC hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-  
 CC Leydig tumours), musculoskeletal diseases (e.g. giant cell tumours,  
 CC Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy  
 CC or cachexia), cardiovascular disease (e.g. rhabdomyomas, heart disease,  
 CC arrhythmia, cardiac arrest, heat valve disease, hypernatraemia or  
 CC hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome,  
 CC Down's syndrome, Patau syndrome, Turner's syndrome, Apert syndrome or Tay  
 CC -Sachs disease), excretory diseases (e.g. urinary incontinence, urinary  
 CC tract infections or renal disorders), neural or sensory disease (e.g.  
 CC Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis,  
 CC cerebellar ataxia, attention deficit disorder, autism or obsessive  
 CC compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or  
 CC occupational lung disease), endocrine diseases (e.g. diabetes, Addison's  
 CC disease or glomerulonephritis), digestive diseases (e.g. portal  
 CC hypertension, irritable bowel disease, gastric atrophy or pancreatitis)  
 CC or connective tissue or epithelial diseases (e.g. Crohn's disease,  
 CC scleroderma, wound healing or epidermolysis bullosa). This sequence  
 CC represents a therapeutic protein X relating to the albumin fusion protein  
 CC of the invention. The sequence listing data for this specification was  
 CC downloaded from the USPTO website.  
 XX SQ Sequence 2 AA;

Query Match 50.0%; Score 8; DB 8; Length 2;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FI 2  
 Db 1 FL 2

RESULT 12  
 AAR48960  
 ID AAR48960 standard; protein; 3 AA.

XX AAR48960;

XX 25-MAR-2003 (revised)

DT 12-SEP-1994 (first entry)

XX NL4-3 truncated GAG C-terminal peptide.

XX HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;  
 KW naturally occurring virus; NOV; translation; replication; infectivity;  
 KW hepatitis B; HIV-2; SIV; flip-over PCR.

XX Synthetic.

XX WO9403596-A1.

XX 17-FEB-1994.

XX PF 30-JUL-1993; 93WO-US007179.  
 XX XX 30-JUL-1992; 92US-00921104.  
 XX XX (UYHA-) UNIV HAWAII.  
 XX PI Hu W, Wang J;  
 XX DR WPI; 1994-065685/08.  
 XX DR N-PSDB; AAQ57688.  
 XX FT New antisense viruses and anti:sense-ribozyme viruses - used for treating  
 XX FT or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.  
 XX PS Disclosure; Page 108; 167pp; English.  
 XX XX  
 CC This sequence is encoded by a PCR fragment of NL4-3 and represents the C-  
 CC terminal peptide fragment of the truncated GAG protein. The DNA encoding  
 CC this fragment was ligated into ClaI/SalI digested pX and the  
 CC corresponding plasmid was used to produce the antisense virus of the  
 CC invention. Antisense or truncated RNAs expressed by these viruses bind to  
 CC the mRNAs expressed by the naturally occurring viruses (NOVs) and prevent  
 CC the mRNAs from being translated into proteins, thereby preventing the NOV  
 CC from replicating. The antisense viruses maintain the infectivity of the  
 CC NOVs, allowing antisense RNAs to reach the mRNAs of the natural viruses.  
 CC Antisense viruses such as these may be used for treating or preventing a  
 CC viral infection, particularly HIV-1, HIV-2 or SIV infection or hepatitis  
 CC B infection. (Updated on 25-MAR-2003 to correct PN field.)  
 XX XX  
 SQ Sequence 3 AA;  
 Query Match 50.0%; Score 8; DB 2; Length 3;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ID 3  
 DB 1 LD 2

XX PF 20-DEC-1995 (first entry)  
 XX XX Non-RGD, non-YISGR cancer metastasis inhibitory peptide #1.  
 XX DE Cancer metastasis; adhesive peptide; core sequence; dextran; cancer;  
 XX KW water soluble polysaccharide; metastasis; wound; immunogenicity.  
 XX XX Synthetic.  
 XX OS JP07089999-A.  
 XX PN 04-APR-1995.  
 XX PD 17-SEP-1993; 93JP-00254779.  
 XX PF 17-SEP-1993; 93JP-00254779.  
 XX PR 17-SEP-1993; 93JP-00254779.  
 XX XX (JAPG ) NIPPON ZEON KK.  
 XX PA WPI; 1995-167254/22.  
 XX DR Cancer metastasis inhibitive peptide derive. - useful for inhibition of  
 XX PT cancer metastasis, healing of wounds and regulation of immunogenicity.  
 XX PS Disclosure; Page 3; 6pp; Japanese.  
 XX XX

CC The peptides AAR70472-90 and AAR82907-24 are peptide derivatives which  
 CC inhibit cancer metastasis. They are composed of an adhesive peptide with  
 CC a core sequence selected from: RGD (AAR70472-85), YIGSR (AAR70486-90) or  
 CC other sequence (AAR82907-24), linked to a water soluble polysaccharide,  
 CC preferably a water soluble dextran, at the C-terminus. The peptides are  
 CC useful in inhibiting cancer metastasis, healing wounds and the regulation  
 CC of immunogenicity  
 XX XX  
 SQ Sequence 3 AA;  
 Query Match 50.0%; Score 8; DB 2; Length 3;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ID 3  
 DB 1 LD 2

XX PF 05-JAN-1998 (first entry)  
 XX XX LDV-peptide capable of binding cell adhesion molecules.  
 XX DE LDV; leucine; aspartic acid; valine; cell adhesion molecule; binding;  
 XX KW bladder irrigation; tumour removal; endoscopic operation;  
 XX KW transurethral resection; cancer; neoplasia.  
 XX OS Synthetic.  
 XX XX DE19529909-A1.  
 XX PN 20-FEB-1997.  
 XX PD 15-AUG-1995; 95DE-01029909.  
 XX PF 15-AUG-1995; 95DE-01029909.  
 XX PR (PREP ) PRESENTUS AG.  
 XX PA Boehle A;  
 XX PI WPI; 1997-133793/13.  
 XX DR Endoscopic irrigation solns. - contg. peptide(s) that bind to cell  
 XX PT adhesion molecules.  
 XX PS Claim 6; Page 8; 8pp; German.  
 XX XX AAW25187-W25192 are peptides containing an LDV sequence or equivalent.  
 CC The peptides are capable of binding to cell adhesion molecules and are  
 CC used in aqueous irrigation solutions for use during and after endoscopic  
 CC operations. Preferred irrigation solutions are electrolyte-free and  
 CC contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing  
 CC the amino acid sequences: RGD, LDV, IDA, DGEA, GPRP, VTL, YIGSR, KQAGDV  
 CC and/or REDV (given in one letter amino acid code). The solutions are  
 CC especially used for irrigating the bladder during and after tumour  
 CC removal by transurethral resection. The peptides protect against  
 CC recurrence of tumours  
 XX XX  
 SQ Sequence 3 AA;  
 Query Match 50.0%; Score 8; DB 2; Length 3;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ID 3  
 DB 1 LD 2

```

Db      1 LD 2

RESULT 15
AAY49399
ID      AAY49399 standard; peptide; 3 AA.
XX
AC      AAY49399;
XX
DT      13-MAR-2000 (first entry)
XX
DE      Morphine modulating neuropeptide as diagnostic marker.
XX
KW      Diagnostic marker; human disorder; opiate; autism spectral disorder;
KW      autism pervasive developmental disorder; Aspergers syndrome;
KW      attention deficient disorder; attention hyperactivity disorder;
KW      multiple sclerosis; Parkinson's disease; Alzheimer's dementia; morphine;
KW      neuropeptide.
XX
OS      Synthetic.
OS      Homo sapiens.
XX
PN      EP969015-A2.
XX
PD      05-JAN-2000.
XX
PF      15-JUN-1999; 99EP-00304636.
XX
PR      15-JUN-1998; 98US-0089237P.
PR      15-JUN-1998; 98US-0089238P.
PR      24-MAY-1999; 99US-00317702.
XX
PA      (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI      Shanahan MR, Venturini AJ, Daiss JL, Friedman AE;
XX      WPI; 2000-074781/07.
XX
PT      Diagnosing human disorders e.g. autism spectral disorders, multiple
PT      sclerosis, Parkinson's disease and Alzheimer's dementia.
XX
PS      Claim 8; Page 7; 44pp; English.
XX
CC      The invention provides diagnostic markers for a human disorder,
CC      comprising either opiate-like peptides or opiate-derived peptides. The
CC      novel peptides are used as diagnostic marker, in ex-vivo methods of
CC      diagnosing human disorders e.g. autism spectral disorders including
CC      autism pervasive developmental disorder, Aspergers syndrome, attention
CC      deficient disorder and attention hyperactivity disorder, and multiple
CC      sclerosis, Parkinson's disease and Alzheimer's dementia. Sequences
CC      AAY49371-413 represent peptide diagnostic markers for the human disorders
CC      specified above
XX
SQ      Sequence 3 AA;

Query Match      50.0%; Score 8; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FI 2
        | :
        1 FL 2
Db

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- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09D\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	81.2	3	17	US-10-823-888-1
2	11	68.8	3	15	US-10-416-822-13
3	10	62.5	3	15	US-10-243-613-56
4	9	56.2	3	9	US-09-853-918-6
5	9	56.2	3	11	US-09-920-306-6
6	9	56.2	3	11	US-09-920-306-64
7	9	56.2	3	15	US-10-363-208-27
8	8	50.0	2	11	US-09-833-245-494
9	8	50.0	2	14	US-10-253-532-85
10	8	50.0	3	9	US-09-922-261-7
11	8	50.0	3	9	US-09-982-172-54
12	8	50.0	3	14	US-10-253-532-74
13	8	50.0	3	14	US-10-253-532-84

14	8	50.0	3	15	US-10-408-166-372	Sequence 372, Appl
15	8	50.0	3	16	US-10-297-147A-6	Sequence 6, Appl
16	8	50.0	3	17	US-10-418-032-258	Sequence 258, Appl
17	7	43.8	2	14	US-10-187-339-6	Sequence 6, Appl
18	7	43.8	3	11	US-09-920-306-58	Sequence 58, Appl
19	6	37.5	2	9	US-09-867-847-33	Sequence 33, Appl
20	6	37.5	2	9	US-09-867-847-34	Sequence 34, Appl
21	6	37.5	2	9	US-09-867-847-35	Sequence 35, Appl
22	6	37.5	2	9	US-09-867-847-36	Sequence 36, Appl
23	6	37.5	2	9	US-09-867-847-37	Sequence 37, Appl
24	6	37.5	2	9	US-09-867-847-38	Sequence 38, Appl
25	6	37.5	2	9	US-09-867-847-39	Sequence 39, Appl
26	6	37.5	2	9	US-09-867-847-40	Sequence 40, Appl
27	6	37.5	2	9	US-09-867-847-41	Sequence 41, Appl
28	6	37.5	2	9	US-09-867-847-42	Sequence 42, Appl
29	6	37.5	2	9	US-09-867-847-43	Sequence 43, Appl
30	6	37.5	2	9	US-09-867-847-44	Sequence 44, Appl
31	6	37.5	2	9	US-09-982-172-8	Sequence 8, Appl
32	6	37.5	2	9	US-09-982-172-105	Sequence 105, Appl
33	6	37.5	2	11	US-09-833-245-1122	Sequence 1122, Ap
34	6	37.5	2	11	US-09-920-306-5	Sequence 5, Appl
35	6	37.5	2	14	US-10-206-699-296	Sequence 296, App
36	6	37.5	2	15	US-10-137-867-262	Sequence 262, App
37	6	37.5	2	15	US-10-371-472-3	Sequence 3, Appl
38	6	37.5	2	15	US-10-371-472-6	Sequence 6, Appl
39	6	37.5	2	15	US-10-371-472-13	Sequence 13, Appl
40	6	37.5	2	15	US-10-371-472-17	Sequence 17, Appl
41	6	37.5	2	15	US-10-371-472-20	Sequence 20, Appl
42	6	37.5	2	15	US-10-371-472-34	Sequence 34, Appl
43	6	37.5	2	15	US-10-371-472-37	Sequence 37, Appl
44	6	37.5	2	15	US-10-371-472-40	Sequence 40, Appl
45	6	37.5	2	16	US-10-109-048-461	Sequence 461, App

ALIGNMENTS

RESULT 1  
US-10-823-888-1  
; Sequence 1, Application US/10823888  
; Publication No. US20050032138A1  
; GENERAL INFORMATION:  
; APPLICANT: Lathrop, Julia T.  
; APPLICANT: Hammond, David J.  
; APPLICANT: Cervenakova, Larisa  
; APPLICANT: Gheorghiu, Liliana  
; APPLICANT: Yakovleva, Oksana  
; TITLE OF INVENTION: Method for Identifying Ligands Specific for Structural Isoforms  
; FILE REFERENCE: 51821-0121 (51821-299534)  
; CURRENT APPLICATION NUMBER: US/10/823,888  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US 60/462,658  
; PRIOR FILING DATE: 2003-04-14  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; TYPE: PRT  
; LENGTH: 3  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-823-888-1

Query Match 81.2%; Score 13; DB 17; Length 3;  
Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3  
Db 1 YID 3

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RESULT 2
US-10-416-822-13
; Sequence 13, Application US/10416822
; Publication No. US20040063631A1
; GENERAL INFORMATION:
; APPLICANT: Mondobiotech SA
; TITLE OF INVENTION: Use of biologically active peptides for the treatment of pulmonary
; TITLE OF INVENTION: arteriolar hypertension and related diseases
; FILE REFERENCE: PMB-0203 US
; CURRENT APPLICATION NUMBER: US/10/416,822
; CURRENT FILING DATE: 2003-05-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-416-822-13
Query Match      68.8%; Score 11; DB 15; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FID 3
Db      1 FTD 3

RESULT 3
US-10-243-613-56
; Sequence 56, Application US/10243613
; Publication No. US20040053823A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Jeffrey W.
; APPLICANT: Chen, Emily I.
; APPLICANT: Kridel, Steven J.
; TITLE OF INVENTION: Selective Substrates for Matrix
; TITLE OF INVENTION: Metalloproteinases
; FILE REFERENCE: P-LJ 5432
; CURRENT APPLICATION NUMBER: US/10/243,613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/953,592
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-243-613-56
Query Match      62.5%; Score 10; DB 15; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ID 3
Db      1 ID 2

RESULT 4
US-09-853-918-6
; Sequence 6, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
US-09-853-918-6
Query Match      56.2%; Score 9; DB 11; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FID 3
Db      1 FED 3

RESULT 5
US-09-920-306-6
; Sequence 6, Application US/09920306
; Publication No. US20040029808A1
; GENERAL INFORMATION:
; APPLICANT: Unilever PLC
; APPLICANT: Unilever NV
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for
; FILE REFERENCE: Peptide Mimotopes
; CURRENT APPLICATION NUMBER: US/09/920,306
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: EP00306613.1
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-920-306-6
Query Match      56.2%; Score 9; DB 11; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FID 3
Db      1 FED 3

RESULT 6
US-09-920-306-64
; Sequence 64, Application US/09920306
; Publication No. US20040029808A1
; GENERAL INFORMATION:
; APPLICANT: Unilever PLC
; APPLICANT: Unilever NV
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for
; FILE REFERENCE: Peptide Mimotopes
; CURRENT APPLICATION NUMBER: US/09/920,306
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: EP00306613.1
US-09-920-306-64
Query Match      56.2%; Score 9; DB 11; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FID 3
Db      1 FED 3

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; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; FILE REFERENCE: POLYPEPTIDES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-918-6
Query Match      56.2%; Score 9; DB 9; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ID 3
Db      2 VD 3

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RESULT 5
US-09-920-306-6
; Sequence 6, Application US/09920306
; Publication No. US20040029808A1
; GENERAL INFORMATION:
; APPLICANT: Unilever PLC
; APPLICANT: Unilever NV
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for
; FILE REFERENCE: Peptide Mimotopes
; CURRENT APPLICATION NUMBER: US/09/920,306
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: EP00306613.1
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-920-306-6
Query Match      56.2%; Score 9; DB 11; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FID 3
Db      1 FED 3

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RESULT 6
US-09-920-306-64
; Sequence 64, Application US/09920306
; Publication No. US20040029808A1
; GENERAL INFORMATION:
; APPLICANT: Unilever PLC
; APPLICANT: Unilever NV
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for
; FILE REFERENCE: Peptide Mimotopes
; CURRENT APPLICATION NUMBER: US/09/920,306
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: EP00306613.1
US-09-920-306-64
Query Match      56.2%; Score 9; DB 11; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FID 3
Db      1 FED 3

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; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 64  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-920-306-64

Query Match 56.2%; Score 9; DB 11; Length 3;  
Best Local Similarity 33.3%; Pred. No. 1.3e+06;  
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FID 3  
|  
Db 1 YFD 3

RESULT 7  
US-10-363-208-27  
; Sequence 27, Application US/10363208  
; Publication No. US20040048243A1  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting  
; FILE REFERENCE: 005774.P005PCT  
; CURRENT APPLICATION NUMBER: US/10/363,208  
; CURRENT FILING DATE: 2003-03-07  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(3)  
; OTHER INFORMATION: synthetic construct  
US-10-363-208-27

Query Match 56.2%; Score 9; DB 15; Length 3;  
Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FID 3  
|  
Db 1 FHD 3

RESULT 8  
US-09-833-245-494  
; Sequence 494, Application US/09833245  
; Publication No. US20040010134A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF546PCT  
; CURRENT APPLICATION NUMBER: US/09/833,245  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229, 358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256, 931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199, 384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 494  
; LENGTH: 2  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-833-245-494

Query Match 50.0%; Score 8; DB 11; Length 2;  
Best Local Similarity 50.0%; Pred. No. 1.3e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FI 2  
|  
Db 1 FL 2

RESULT 9  
US-10-253-532-85  
; Sequence 85, Application US/10253532  
; Publication No. US20030138422A1  
; GENERAL INFORMATION:  
; APPLICANT: Agnajanian, Jane  
; APPLICANT: Wolfman, Neil  
; APPLICANT: Veldman, Geetruida  
; APPLICANT: Davies, Monique  
; APPLICANT: Whittemore, Lisa Anne  
; APPLICANT: O'Hara, Denise  
; APPLICANT: Bridges, Kristie  
; APPLICANT: Khurana, Tejiv  
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor  
; FILE REFERENCE: 08702.00012-00000  
; CURRENT APPLICATION NUMBER: US/10/253,532  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: 60/324,528  
; PRIOR FILING DATE: 2001-09-26  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 85  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-253-532-85

Query Match 50.0%; Score 8; DB 14; Length 2;  
Best Local Similarity 50.0%; Pred. No. 1.3e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3  
|  
Db 1 LD 2

RESULT 10  
US-09-922-261-7  
; Sequence 7, Application US/09922261  
; Patent No. US2002011471A1  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Purnham, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; FILE REFERENCE: 10001-005-999  
; CURRENT APPLICATION NUMBER: US/09/922,261  
; CURRENT FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US/09/461,697  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 3  
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-922-261-7

Query Match      50.0%; Score 8; DB 9; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
       :|
Db      2 LD 3

RESULT 11
US-09-982-172-54
; Sequence 54, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 54
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-54

Query Match      50.0%; Score 8; DB 9; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FI 2
       :|
Db      1 FL 2

RESULT 12
US-10-253-532-74
; Sequence 74, Application US/10253532
; Publication No. US20030138422A1
; GENERAL INFORMATION:
; APPLICANT: Aghajanian, Jane
; APPLICANT: Wolfman, Neil
; APPLICANT: Veldman, Geetruida
; APPLICANT: Davies, Monique
; APPLICANT: Whittemore, Lisa Anne
; APPLICANT: O'Hara, Denise
; APPLICANT: Bridges, Kristie
; APPLICANT: Khurana, Tejiv
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
; FILE REFERENCE: 08702.00012-00000
; CURRENT APPLICATION NUMBER: US/10/253,532
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 60/324,528
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 74
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-532-74

Query Match      50.0%; Score 8; DB 14; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
       :|
Db      2 LD 3

RESULT 13
US-10-253-532-84
; Sequence 84, Application US/10253532
; Publication No. US20030138422A1
; GENERAL INFORMATION:
; APPLICANT: Aghajanian, Jane
; APPLICANT: Wolfman, Neil
; APPLICANT: Veldman, Geetruida
; APPLICANT: Davies, Monique
; APPLICANT: Whittemore, Lisa Anne
; APPLICANT: O'Hara, Denise
; APPLICANT: Bridges, Kristie
; APPLICANT: Khurana, Tejiv
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
; FILE REFERENCE: 08702.00012-00000
; CURRENT APPLICATION NUMBER: US/10/253,532
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 60/324,528
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 84
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-532-84

Query Match      50.0%; Score 8; DB 14; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
       :|
Db      2 LD 2

RESULT 14
US-10-408-166-372
; Sequence 372, Application US/10408166
; Publication No. US20040018516A1
; GENERAL INFORMATION:
; APPLICANT: Francischetti, Ivo M. B.
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; TITLE OF INVENTION: Ixodes SCAPULARIS TISSUE FACTOR PATHWAY
; TITLE OF INVENTION: INHIBITOR
; FILE REFERENCE: NIH99.001C1
; CURRENT APPLICATION NUMBER: US/10/408,166
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: PCT/US01/42472
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/240,575
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 475
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Ixodes scapularis
US-10-408-166-372

Query Match      50.0%; Score 8; DB 15; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
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Db 2 LD 3

RESULT 15  
US-10-297-147A-6  
; Sequence 6, Application US/10297147A  
; Publication No. US20040110285A1  
; GENERAL INFORMATION:  
; APPLICANT: Mnemoscience GMBH  
; TITLE OF INVENTION: SHAPE MEMORY THERMOPLASTICS AND POLYMER NETWORKS FOR TISSUE ENGINEERING  
; FILE REFERENCE: MNE 102  
; CURRENT APPLICATION NUMBER: US/10/297,147A  
; CURRENT FILING DATE: 2001-03-31  
; PRIOR APPLICATION NUMBER: US 60/208,285  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-297-147A-6

Query Match 50.0%; Score 8; DB 16; Length 3;  
Best Local Similarity 50.0%; Pred. No. 1.3e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3  
; |  
Db 1 LD 2

Search completed: April 18, 2005, 16:28:00  
Job time : 131 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 16:07:21 ; Search time 42 Seconds  
(without alignments)  
5.332 Million cell updates/sec

Title: US-09-674-716B-13  
Perfect score: 16  
Sequence: 1 FID 3

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1169

Minimum DB seq length: 0  
Maximum DB seq length: 3

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	62.5	3	3	US-09-086-421-2
2	9	56.2	2	3	US-09-264-709A-30
3	9	56.2	2	4	US-09-442-989-33
4	9	56.2	2	4	US-09-442-989-34
5	9	56.2	3	1	US-08-127-904-7
6	9	56.2	3	2	US-09-061-337-3
7	9	56.2	3	2	US-09-122-129-3
8	9	56.2	3	3	US-09-340-991-3
9	9	56.2	3	3	US-08-974-609-3
10	9	56.2	3	3	US-09-264-709A-26
11	9	56.2	3	4	US-09-549-098-3
12	9	56.2	3	4	US-09-442-989-35
13	9	56.2	3	4	US-09-442-989-36
14	9	56.2	3	5	PCT-US94-10475-7
15	8	50.0	3	1	US-08-081-539-117
16	8	50.0	3	1	US-08-466-647-117
17	8	50.0	3	1	US-08-411-389-20
18	8	50.0	3	1	US-08-634-060-36
19	8	50.0	3	1	US-08-338-282-11
20	8	50.0	3	2	US-08-934-222-12
21	8	50.0	3	2	US-08-933-402-12
22	8	50.0	3	2	US-09-207-621-12
23	8	50.0	3	2	US-08-532-818-12
24	8	50.0	3	3	US-09-231-797-12
25	8	50.0	3	3	US-09-086-421-1
26	8	50.0	3	3	US-08-934-224-12
27	8	50.0	3	3	US-08-933-843-12

28 8 50.0 3 3 US-08-934-223-12 Sequence 12, Appl  
29 8 50.0 3 3 US-09-413-492-12 Sequence 12, Appl  
30 8 50.0 3 3 US-09-461-697-7 Sequence 7, Appl  
31 7 43.8 2 4 US-09-434-837-6 Sequence 6, Appl  
32 7 43.8 3 1 US-08-118-135A-1 Sequence 1, Appl  
33 7 43.8 3 1 US-08-118-135A-8 Sequence 8, Appl  
34 7 43.8 3 1 US-08-118-135A-9 Sequence 9, Appl  
35 7 43.8 3 1 US-08-446-908-14 Sequence 14, Appl  
36 7 43.8 3 1 US-08-231-205A-14 Sequence 14, Appl  
37 7 43.8 3 1 US-08-153-848-17 Sequence 17, Appl  
38 7 43.8 3 2 US-08-642-045B-25 Sequence 25, Appl  
39 7 43.8 3 2 US-08-871-161-14 Sequence 14, Appl  
40 7 43.8 3 3 US-09-299-843A-17 Sequence 17, Appl  
41 7 43.8 3 3 US-09-088-337B-17 Sequence 17, Appl  
42 7 43.8 3 4 US-09-212-663-12 Sequence 12, Appl  
43 7 43.8 3 5 PCT-US93-11153-17 Sequence 17, Appl  
44 6 37.5 2 1 US-07-820-154A-15 Sequence 15, Appl  
45 6 37.5 2 1 US-07-820-154A-23 Sequence 23, Appl

#### ALIGNMENTS

RESULT 1  
US-09-086-421-2  
; Sequence 2, Application US/09086421A  
; Patent No. 6093696  
; GENERAL INFORMATION:  
; APPLICANT: Head, John C  
; APPLICANT: Archibald, Sarah C  
; APPLICANT: Warreilow, Graham J  
; TITLE OF INVENTION: Tyrosine Derivatives  
; FILE REFERENCE: CELLO058  
; CURRENT APPLICATION NUMBER: US/09/086,421A  
; CURRENT FILING DATE: 1998-05-29  
; EARLIER FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6093696al Sequence  
US-09-086-421-2

Query Match 62.5%; Score 10; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ID 3  
Db 1 ID 2

#### RESULT 2

US-09-264-709A-30  
; Sequence 30, Application US/09264709A  
; Patent No. 6320024  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, Eugene  
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and Improve the Quality of Life  
; FILE REFERENCE: 2124-310  
; CURRENT APPLICATION NUMBER: US/09/264,709A  
; CURRENT FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: 08/797,782  
; PRIOR FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 2

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: memory-modulating peptide
US-09-264-709A-30

Query Match          56.2%; Score 9; DB 3; Length 2;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FI 2
Db      1 FV 2

RESULT 3
US-09-442-989-33
; Sequence 33, Application US/09442989
; Patent No. 656993
; GENERAL INFORMATION:
; APPLICANT: Sledeski, Adam W.
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
; FILE REFERENCE: A3113B-US
; CURRENT APPLICATION NUMBER: US/09/442,989
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: 60/081,897
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (2)
; OTHER INFORMATION: Asp(Oallyl)
; NAME/KEY: PEPTIDE
; LOCATION: (1)
; OTHER INFORMATION: BOC-Val
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (2)
; OTHER INFORMATION: "This C-terminal amino acid is in the form of an
; OTHER INFORMATION: ester with benzyl alcohol."
US-09-442-989-33

Query Match          56.2%; Score 9; DB 4; Length 2;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
Db      1 VD 2

RESULT 4
US-09-442-989-34
; Sequence 34, Application US/09442989
; Patent No. 656993
; GENERAL INFORMATION:
; APPLICANT: Sledeski, Adam W.
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
; FILE REFERENCE: A3113B-US
; CURRENT APPLICATION NUMBER: US/09/442,989
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: 60/081,897
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (2)
; OTHER INFORMATION: Asp(Oallyl)
; NAME/KEY: PEPTIDE
; LOCATION: (1)
; OTHER INFORMATION: BOC-Val
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (2)
; OTHER INFORMATION: "This C-terminal amino acid is in the form of an
; OTHER INFORMATION: ester with benzyl alcohol."
US-09-442-989-34

Query Match          56.2%; Score 9; DB 4; Length 2;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
Db      1 VD 2

RESULT 5
US-08-127-904-7
; Sequence 7, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For Antagonizing
; TITLE OF INVENTION: Amnestic Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving the
; TITLE OF INVENTION: Quality of Life in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,904
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: Amino Acid
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RESULT 8  
US-09-340-991-3  
; Sequence 3, Application US/09340991  
; Patent No. 6066457  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Yuying  
; APPLICANT: Lenz, Martin

;; TITLE OF INVENTION: HIGH SPECIFICITY HOMOCYSTEINE ASSAYS FOR  
;; TITLE OF INVENTION: BIOLOGICAL SAMPLES  
;; NUMBER OF SEQUENCES: 19  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 2000 Pennsylvania Avenue, NW  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20006-1888  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/340,991  
;; FILING DATE: 24 July 1998  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/899,776  
;; FILING DATE: 24-JUL-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/918,214  
;; FILING DATE: 25-AUG-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/941,921  
;; FILING DATE: 01-OCT-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/974,609  
;; FILING DATE: 19-NOV-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 09/061,337  
;; FILING DATE: 17-APRIL-1998  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Donahue, E. Victor  
;; REGISTRATION NUMBER: 35,492  
;; REFERENCE/DOCKET NUMBER: 312762001322  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 887-1546  
;; TELEFAX: (202) 887-0763  
;; TELEX: 90-4030  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-09-340-991-3  
  
Query Match 56.2%; Score 9; DB 3; Length 3;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 ID 3  
Db 2 VD 3  
  
RESULT 9  
US-08-974-609-3  
; Sequence 3, Application US/08974609  
; Patent No. 6140102  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Yuying  
; APPLICANT: Lenz, Martin  
; TITLE OF INVENTION: HIGH SPECIFICITY HOMOCYSTEINASES AND  
; TITLE OF INVENTION: GENES THEREFOR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW  
; CITY: Washington

;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20006-1888  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/974,609  
;; FILING DATE: 24-OCT-1997  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/941,921  
;; FILING DATE: 01-OCT-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Donahue, E. Victor  
;; REGISTRATION NUMBER: 35,492  
;; REFERENCE/DOCKET NUMBER: 31276-20013.20  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 887-1500  
;; TELEFAX: (202) 822-0168  
;; TELEX: 90-4030  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-974-609-3  
  
Query Match 56.2%; Score 9; DB 3; Length 3;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 ID 3  
Db 2 VD 3  
  
RESULT 10  
US-09-264-709A-26  
; Sequence 26, Application US/09264709A  
; Patent No. 6320024  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, Eugene  
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and  
; TITLE OF INVENTION: Improve the Quality of Life  
; FILE REFERENCE: 2124-310  
; CURRENT APPLICATION NUMBER: US/09/264,709A  
; CURRENT FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: 08/797,782  
; PRIOR FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial  
; OTHER INFORMATION: Sequence:memory-modulating peptide  
;; US-09-264-709A-26  
  
Query Match 56.2%; Score 9; DB 3; Length 3;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 FI 2  
Db 2 FV 3

RESULT 11  
US-09-549-098-3  
; Sequence 3, Application US/09549098  
; Patent No. 6468762  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Yuying  
; APPLICANT: Lenz, Martin  
; TITLE OF INVENTION: HIGH SPECIFICITY HOMOCYSTEINE ASSAYS FOR  
; TITLE OF INVENTION: BIOLOGICAL SAMPLES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/549,098  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/340,991  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/918,214  
; FILING DATE: 25-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/941,921  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/974,609  
; FILING DATE: 19-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/061,337  
; FILING DATE: 17-APRIL-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Donahue, E. Victor  
; REGISTRATION NUMBER: 35,492  
; REFERENCE/DOCKET NUMBER: 312762001322  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1546  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-549-098-3

Query Match 56.2%; Score 9; DB 4; Length 3;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3  
;:  
Db 2 VD 3

RESULT 12  
US-09-442-989-35  
; Sequence 35, Application US/09442989  
; Patent No. 6569993  
; GENERAL INFORMATION:  
; APPLICANT: Sledeski, Adam W.  
; APPLICANT: Mencil, James J.

; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC  
; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: A3113B-US  
; CURRENT APPLICATION NUMBER: US/09/442,989  
; CURRENT FILING DATE: 1999-11-18  
; EARLIER APPLICATION NUMBER: 60/081,897  
; EARLIER FILING DATE: 1998-04-15  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)  
; OTHER INFORMATION: FMOC-Arg (PMC)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (3)  
; OTHER INFORMATION: Asp(Oallyl)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (3)  
; OTHER INFORMATION: "This C-terminal amino acid is in the form of an  
; OTHER INFORMATION: ester with benzyl alcohol."  
US-09-442-989-35

Query Match 56.2%; Score 9; DB 4; Length 3;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3  
;:  
Db 2 VD 3

RESULT 13  
US-09-442-989-36  
; Sequence 36, Application US/09442989  
; Patent No. 6569993  
; GENERAL INFORMATION:  
; APPLICANT: Sledeski, Adam W.  
; APPLICANT: Mencil, James J.  
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC  
; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: A3113B-US  
; CURRENT APPLICATION NUMBER: US/09/442,989  
; CURRENT FILING DATE: 1999-11-18  
; EARLIER APPLICATION NUMBER: 60/081,897  
; EARLIER FILING DATE: 1998-04-15  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)  
; OTHER INFORMATION: Arg (PMC)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (3)  
; OTHER INFORMATION: Asp(Oallyl)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (3)  
; OTHER INFORMATION: "This C-terminal amino acid is in the form of an  
; OTHER INFORMATION: ester with benzyl alcohol."  
US-09-442-989-36

Query Match 56.2%; Score 9; DB 4; Length 3;

Best Local Similarity 50.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0; Mismatches 0; Matches 1; Conservative 1;

QY 2 ID 3  
:|  
Db 2 VD 3

RESULT 14  
PCT-US94-10475-7  
; Sequence 7, Application PC/TUS9410475  
; GENERAL INFORMATION:  
; APPLICANT: Eugene Roberts  
; TITLE OF INVENTION: Method For  
; TITLE OF INVENTION: Antagonizing Amnestic  
; TITLE OF INVENTION: Effects of Amyloid n  
; TITLE OF INVENTION: Protein and Improving  
; TITLE OF INVENTION: the Quality of Life  
; TITLE OF INVENTION: in Individuals  
; TITLE OF INVENTION: With Alzheimer Disease  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: City of Hope  
; STREET: 1500 East Duarte Road  
; CITY: Duarte  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91010-0269  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3M Double Density 5 1/4"  
; MEDIUM TYPE: diskette  
; COMPUTER: Wang PC  
; OPERATING SYSTEM: MS DOS Version 3.20  
; SOFTWARE: Microsoft  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/10475  
; FILING DATE: 16 September 1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: U. S. Application  
; PRIOR APPLICATION DATA: Serial No.  
; PRIOR APPLICATION DATA: 08/127,904; filed  
; PRIOR APPLICATION DATA: 29 September 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Irons, Edward S.  
; REGISTRATION NUMBER: 16,541  
; REFERENCE/DOCKET NUMBER: None  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 626-3564 or 783-6030  
; TELEFAX: (202) 783-6031  
; TELEX: None  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3  
; TYPE: Amino Acid  
; STRANDEDNESS:  
; TOPOLOGY: Unknown  
PCT-US94-10475-7

Query Match 56.2%; Score 9; DB 5; Length 3;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FI 2  
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Db 1 FV 2

RESULT 15  
US-08-539-117  
; Sequence 117, Application US/08081539  
; Patent No. 5501982  
; GENERAL INFORMATION:  
; APPLICANT: Braford-Goldberg, Sarah R.

; APPLICANT: Easton, Alan M.  
; APPLICANT: Klein, Barbara K.  
; APPLICANT: McRearn, John P.  
; APPLICANT: Olin, Peter O.  
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine  
; TITLE OF INVENTION: Chimeric Hybrid Polypeptides  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate  
; ADDRESSEE: Patent Dept.  
; STREET: P. O. Box 5110  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60680  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/081,539  
; FILING DATE: 19930621  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanady, Mary J.  
; REGISTRATION NUMBER: 28623  
; REFERENCE/DOCKET NUMBER: 2724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (708)470-6501  
; TELEFAX: (708)470-6881  
; INFORMATION FOR SEQ ID NO: 117:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-081-539-117

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Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3  
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Search completed: April 18, 2005, 16:17:02  
Job time : 43 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 11:10:40 ; Search time 1545.75 Seconds  
(without alignments)  
10908.879 Million cell updates/sec

Title: US-09-674-716B-17  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
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- 5: gb\_ov.\*
- 6: gb\_pat.\*
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- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
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- 12: gb\_sy.\*
- 13: gb\_uni.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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2	348	100.0	348 6 BD232451 BD232451 Antibodie
3	348	100.0	348 6 AX010614 AX010614 Sequence
4	348	100.0	348 6 AX010645 AX010645 Sequence
5	292	83.9	740 6 AX076853 AX076853 Sequence
6	292	83.9	740 6 AX076855 AX076855 Sequence
7	277.6	79.8	410 9 HSIKGLV46 X72467 H.sapiens m
8	276	79.3	353 9 HSA272080 AJ272080 Homo sapi
9	276	79.3	360 9 HSTOP003 X93771 H.sapiens m
10	276	79.3	360 9 HSTOP016 X93776 H.sapiens m
11	276	79.3	360 9 HSTOP019 X93772 H.sapiens m
12	276	79.3	360 9 HSTOP220 X93805 H.sapiens m
13	276	79.3	360 9 HSTOP305 X93807 H.sapiens m
14	276	79.3	360 9 HSTOP307 X93807 H.sapiens m
15	276	79.3	377 9 HSIKGLV45 X72466 H.sapiens m
16	276	79.3	407 9 HSIKGLV31 X72452 H.sapiens m
17	274.4	78.9	360 9 HSTOP014 X93772 H.sapiens m
18	274.4	78.9	360 9 HSTOP027 X93778 H.sapiens m
19	274.4	78.9	360 9 HSTOP101 X93780 H.sapiens m

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23	274.4	78.9	360	9	HSTOP214	X93789 H.sapiens m
24	274.4	78.9	360	9	HSTOP217	X93790 H.sapiens m
25	274.4	78.9	360	9	HSTOP237	X93793 H.sapiens m
26	274.4	78.9	360	9	HSTOP243	X93796 H.sapiens m
27	274.4	78.9	360	9	HSTOP247	X93797 H.sapiens m
28	274.4	78.9	360	9	HSTOP250	X93799 H.sapiens m
29	274.4	78.9	360	9	HSTOP254	X93800 H.sapiens m
30	274.4	78.9	360	9	HSTOP301	X93802 H.sapiens m
31	274.4	78.9	360	9	HSTOP303	X93803 H.sapiens m
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35	274	78.7	720	6	E35208	E35208 Human monocl
36	273	78.4	720	6	E35205	E35205 Human monocl
37	272.8	78.4	360	9	HSTOP001	X93769 H.sapiens m
38	272.8	78.4	360	9	HSTOP015	X93773 H.sapiens m
39	272.8	78.4	360	9	HSTOP018	X93775 H.sapiens m
40	272.8	78.4	360	9	HSTOP028	X93779 H.sapiens m
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ALIGNMENTS

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BD232424 348 bp DNA linear PAT 17-JUL-2003  
LOCUS Antibodies against CD23, derivatives thereof and therapeutic  
DEFINITION utilization of the same.  
ACCESSION BD232424.1 GI:33042194  
VERSION JP 2002514421-A/8.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 348)  
AUTHORS Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and Shearin,J.  
TITLE Antibodies against CD23, derivatives thereof and therapeutic  
JOURNAL utilization of the same  
Patent: JP 2002514421-A 8 21-MAY-2002;  
GLAXO GROUP LTD  
COMMENT OS Artificial Sequence  
PN JP 2002514421-A/8  
PD 21-MAY-2002  
PF 07-MAY-1999 JP 2000548470  
PR 09-MAY-1998 GB 9809839.5  
PI JEAN YVES MARCEL PAUL BONNEFOY,SCOTT JAMES CROME,JONATHAN PI  
HENRY ELLIS,  
PI NICHOLAS TIMOTHY RAPSON,JEAN SHEARIN  
PC C12N15/02,A61K39/395,C07K16/28,C12N15/00  
CC Description of Artificial Sequence: Humanised anti-CD23 CC  
antibody light  
chain variable region  
CC Location/Qualifiers  
FH Key Location/Qualifiers  
FT CDS (1)..(348).

FEATURES  
source

ORIGIN

Query Match 100.0%; Score 348; DB 6; Length 348;  
Best Local Similarity 100.0%; Pred. No. 3.3e-103;  
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS BD232451 348 bp DNA linear PAT 17-JUL-2003
DEFINITION Antibodies against CD23, derivatives thereof and therapeutic
utilization of the same.
ACCESSION BD232451
VERSION JP 2002514421-A/35.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM
REFERENCE
AUTHORS Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and
Shearin,J.
TITLE Antibodies against CD23, derivatives thereof and therapeutic
utilization of the same
JOURNAL Patent: JP 2002514421-A 35 21-MAY-2002;
GLAXO GROUP LTD
COMMENT OS Artificial Sequence
PN JP 2002514421-A/35
PD 21-MAY-2002
PF 07-MAY-1999 JP 2000548470
PI 09-MAY-1998 GB 9809839.5
PI JEAN YVES MARCEL PAUL BONNEFOY, SCOTT JAMES CROWE, JONATHAN PI
HENRY ELLIS,
PI NICHOLAS TIMOTHY RAPSON, JEAN SHEARIN
PC C12N15/02,A61K39/395,C07K16/28,C12N15/00
CC Description of Artificial Sequence: Humanised anti-CD23 CC
antibody light
chain variable region
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Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 TCAGGGGTCCCTGACAGGTTCAAGTGTGAGTGGATCAGGCACAGATTTACACTGAAATC 240
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DB 108 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGTAGATATCCA 49
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DB 48 TTCACGTTCCGCGCAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 1

RESULT 3
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LOCUS AX010614 348 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 17 from Patent WO958679.
ACCESSION AX010614
VERSION AX010614.1 GI:9997425
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM
REFERENCE
AUTHORS Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL Patent: WO 958679-A 17 18-NOV-1999;
BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON
NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY
(GB); SHEARIN JEAN (US)
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Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 89.9%; Pred. No. 1e-84;
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Db 600 ATCTCTGTCGCTCGAGTAAAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 541
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Db 540 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATCAGATGTCACCACTTGC 481
QY 181 TCAGGGGTCCTGACAGGTTCACTGTCAGTGCAGTGCAGGACAGATTTTACACTGAAATC 240
Db 480 TCAGGGGTCCTGACAGGTTCACTGTCAGTGCAGTGCAGGACAGATTTTACACTGAAATC 421
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Db 420 AGCAGATGGAGCTGAGGATGTTGGGTTTATTCTGTCACAGCTGCTAGAGTATCCA 361
QY 301 TTCACGTTCCGCCAAGGACCAAGTGGAGATCAAAACGTCACGGTGGCT 348
Db 360 CGGACGTTCCGCCAAGGACCAAGTGGAGATCAAAACGTCACGGTGGCT 313

RESULT 7
HSIGKLV46 410 bp mRNA linear PRI 31-JAN-1994
LOCUS H.sapiens mRNA for rearranged Ig kappa light chain variable region
DEFINITION (II.46).
ACCESSION X72467
VERSION X72467.1 GI:441402
KEYWORDS C-region; immunoglobulin; J-segment; kappa light chain; V-region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 410)
AUTHORS Klein,R., Jaenichen,R. and Zachau,H.G.
TITLE Expressed human immunoglobulin kappa genes and their hypermutation
JOURNAL Eur. J. Immunol. 23 (12), 3248-3262 (1993)
MEDLINE 94080891
PUBMED 8258341
REFERENCE 2 (bases 1 to 410)
AUTHORS Zachau,H.G.
TITLE Direct Submission
JOURNAL Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische
Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2,
FRG

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RESULT 8
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DEFINITION region -Anti-F(ab')2 autoantibody (IGVL gene), isolate SN3.
ACCESSION AJ272080
VERSION AJ272080.1 GI:7024356
KEYWORDS anti-F(ab')2; autoantibody; IGVL gene; immunoglobulin; light chain;
variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Elagib,K.E., Borretzen,M., Vatn,I., Natvig,J.B. and Thompson,K.M.
TITLE Characterization and V(H) sequences of human monoclonal
anti-F(ab')2 autoantibodies from normals and Sjogren's syndrome
patients
JOURNAL Clin. Immunol. 98 (1), 62-69 (2001)
MEDLINE 20581399
PUBMED 11141328
REFERENCE 2 (bases 1 to 353)
AUTHORS Elagib,K.E.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2000) Elagib K.E., Laboratory for Rheumatology
Research, Institute of Immunology, Fr. Qvamsgate 1, N-172 Oslo,
NORWAY

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## ORIGIN

Query Match 79.3%; Score 276; DB 9; Length 353;  
Best Local Similarity 87.1%; Pred. No. 1.9e-79;  
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## RESULT 9

HSTOP003  
LOCUS H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;  
clone HSTOP003).  
DEFINITION

ACCESSION X93771.1 GI:3928404

KEYWORDS constant region; immunoglobulin; immunoglobulin kappa chain;  
immunoglobulin light chain; joining region; variable region.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 360)  
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
Barrington, T., Hough, L., Juul, L., Madsen, H.O., Ryder, L.P.,  
Heilmann, C. and Svejgaard, A.TITLE The progeny of a single virgin B cell predominates the human recall  
B cell response to the capsular polysaccharide of Haemophilus  
influenzae type b  
J. Immunol. 157 (9), 4016-4027 (1996)

JOURNAL 97047794

MEDLINE 8892635

PUBMED 2 (bases 1 to 360)

AUTHORS Barrington, T.

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## Source

Direct Submission  
Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory  
7631, Rigshospitalet, National University Hospital, Tagensvej 20,  
DK-2200 Copenhagen N, DENMARK  
On Nov 26, 1998 this sequence version replaced gi:1296757.  
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340..360  
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## ORIGIN

Query Match 79.3%; Score 276; DB 9; Length 360;  
Best Local Similarity 87.1%; Pred. No. 1.9e-79;  
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
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DB 1 GATATTGTGACTCAGTCTCCACTCTCCCTGCGCTCACCCCTGGAGAGCGGCTCC 60  
QY 61 ATCTCTGTCGCTGAGTAAAGTCTCTGTATAGGATGGAGACATATTGAATTGG 120  
DB 61 ATCTCTGTCGCTGAGTAAAGTCTCTGTATAGGATGGAGACATATTGAATTGG 120  
QY 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTGATGTCACCCGGGCA 180  
DB 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGGTTCTATCGGCC 180  
QY 181 TCAGGGTCTCTGACAGGTTTCAGTGGAGTGGATCAGGCACAGATTTTACATGAAATC 240  
DB 181 TCAGGGTCTCTGACAGGTTTCAGTGGAGTGGATCAGGCACAGATTTTACATGAAATC 240  
QY 241 AGCAGAGTGGAGTGGAGTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300  
DB 241 AGTAGAGTGGAGTGGAGTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300  
QY 301 TTCACGTTTCGCGCCAGGCAAGGTGGAGATCAACAGTACGGTGGCT 348  
DB 301 TTCACGTTTCGCGCCAGGCAAGGTGGAGATCAACAGTACGGTGGCT 348

## RESULT 10

## HSTOP016

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## AUTHORS

HSTOP016  
LOCUS H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;  
clone HSTOP016).  
DEFINITION  
ACCESSION X93774.1 GI:3928407  
VERSION X93774  
KEYWORDS constant region; immunoglobulin; immunoglobulin kappa chain;  
immunoglobulin light chain; joining region; variable region.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 360)  
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
Barrington, T., Hough, L., Juul, L., Madsen, H.O., Ryder, L.P.,  
Heilmann, C. and Svejgaard, A.  
TITLE The progeny of a single virgin B cell predominates the human recall  
B cell response to the capsular polysaccharide of Haemophilus



VERSION X93792.1 GI:3928425  
 KEYWORDS constant region; immunoglobulin; immunoglobulin kappa chain; immunoglobulin light chain; joining region; variable region.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 360)  
 AUTHORS Barington, T., Houghs, L., Juul, L., Madsen, H.O., Ryder, L.P., Heilmann, C. and Svejgaard, A.  
 TITLE The progeny of a single virgin B cell predominates the human recall B cell response to the capsular polysaccharide of Haemophilus influenzae type b  
 JOURNAL J. Immunol. 157 (9), 4016-4027 (1996)  
 MEDLINE 97047794  
 PUBMED 8892635  
 REFERENCE 2 (bases 1 to 360)  
 AUTHORS Barington, T.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory 7631, Rigshospitalet, National University Hospital, Tagensvej 20, DK-2200 Copenhagen N, DENMARK  
 COMMENT On Nov 26, 1998 this sequence version replaced gi:1296778.  
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 /db\_xref="taxon:9606"  
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 Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
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 DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGCGGCTCC 60  
 QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAGGATGGGAAGACATCTTGAATTGG 120  
 DB 61 ATCTCTGTGAGGCTTAGTCAGAGCCCTCCTGCATAGTAATGGCAACATCTATTTCGATTGG 120  
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 DB 121 TACCTGCAGAACGACGAGGAGTCTCCACAGCTCCTGATCTATTGTGATGTCACCCGGGCA 180  
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 DB 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAATTC 240  
 QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300  
 DB 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300  
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 DB 301 TTCACGTTCCGGCCCAAGGACCAAGTGGATCAAAAGTACGCTGGCT 348

RESULT 13  
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 DEFINITION  
 ACCESSION X93805.1 GI:3928439  
 VERSION  
 KEYWORDS constant region; immunoglobulin; immunoglobulin kappa chain; immunoglobulin light chain; joining region; variable region.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 360)  
 AUTHORS Barington, T., Houghs, L., Juul, L., Madsen, H.O., Ryder, L.P., Heilmann, C. and Svejgaard, A.  
 TITLE The progeny of a single virgin B cell predominates the human recall B cell response to the capsular polysaccharide of Haemophilus influenzae type b  
 JOURNAL J. Immunol. 157 (9), 4016-4027 (1996)  
 MEDLINE 97047794  
 PUBMED 8892635  
 REFERENCE 2 (bases 1 to 360)  
 AUTHORS Barington, T.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory 7631, Rigshospitalet, National University Hospital, Tagensvej 20, DK-2200 Copenhagen N, DENMARK  
 COMMENT On Nov 26, 1998 this sequence version replaced gi:1296791.  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /chromosome="2"  
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 /tissue\_type="peripheral blood"  
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 /gene="V-kappa-A3/A19 and J-kappa-3"  
 /product="immunoglobulin kappa light chain"  
 /note="variable region and joining region"  
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 /note="constant region"

ORIGIN  
 Query Match 79.3%; Score 276; DB 9; Length 360;  
 Best Local Similarity 87.1%; Pred. No. 1.9e-79;  
 Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGCGGCTCC 60  
 DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGCGGCTCC 60  
 QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAGGATGGGAAGACATCTTGAATTGG 120  
 DB 61 ATCTCTGTGAGGCTTAGTCAGAGCCCTCCTGCATAGTAATGGCAACATCTATTTCGATTGG 120  
 QY 121 TACCTGCAGAACGACGAGGAGTCTCCACAGCTCCTGATCTATTGTGATGTCACCCGGGCA 180  
 DB 121 TACCTGCAGAACGACGAGGAGTCTCCACAGCTCCTGATCTATTGTGATGTCACCCGGGCA 180  
 QY 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAATTC 240  
 DB 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAATTC 240  
 QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300  
 DB 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300



Qy 121 TACCTGAGAACGAGGAGCTCCACAGCTCCTGATCTATTGATGTCCACCCGGCA 180  
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Db 150 TACCTGAGAACGAGGAGCTCCACAGCTCCTGATCTATTGATGTCCACCCGGCC 209  
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Db 270 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCG 329  
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Qy 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 348  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 1365.64 Seconds  
(without alignments)  
9699.731 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 348

Sequence: 1 gatattgtgactcagtc.....agatcaacgtacgtggct 348

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_ges1.\*  
9: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.6	79.8	597	6	CD689298 EST5820 h
2	277.6	79.8	743	6	CD987308 AGENCOURT
3	277.6	79.8	990	4	BI838327 601083265
4	276	79.3	600	6	CD700169 EST16693
5	276	79.3	605	6	CD698049 EST14572
6	276	79.3	817	6	CD957285 AGENCOURT
7	274.6	78.9	475	6	CD699289 EST15812
8	274.4	78.9	498	6	CD699812 EST16336
9	274.4	78.9	583	6	CD684087 EST607 hu
10	274.4	78.9	791	6	CD955891 AGENCOURT
11	274.4	78.9	830	6	CD985612 AGENCOURT
12	272.8	78.4	454	2	AW406883 UI-HF-BL0
13	272.8	78.4	524	6	CD700306 EST16830
14	272.8	78.4	616	6	CD703137 EST19728
15	272.8	78.4	700	6	CD987545 AGENCOURT
16	272.8	78.4	771	6	CD956254 AGENCOURT
17	272.8	78.4	995	5	BQ712430 AGENCOURT
18	271.2	77.9	522	4	BM511309 iJ46B08.Y
19	271.2	77.9	731	6	CD985070 AGENCOURT
20	271.2	77.9	757	6	CD985283 AGENCOURT
21	271.2	77.9	773	6	CD959401 AGENCOURT
22	271.2	77.9	815	6	CD985592 AGENCOURT
23	269.6	77.5	569	6	CD705909 EST22436
24	269.6	77.5	734	6	CD957433 AGENCOURT

25	269.6	77.5	739	6	CB986287
26	269.6	77.5	743	6	CB956921
27	269.6	77.5	751	4	BG542438 602569513
28	268.6	77.2	554	6	CD696178 EST12701
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30	268	77.0	442	1	AA405415 zu56D02.f
31	268	77.0	488	2	AW405725 UI-HF-BL0
32	268	77.0	512	6	CD707724 EST24251
33	268	77.0	565	6	CD691296 EST7819 h
34	268	77.0	623	6	CD694404 EST10927
35	268	77.0	634	4	BM783161 K-EST0061
36	268	77.0	658	6	CB958484 AGENCOURT
37	268	77.0	719	6	CB958133 AGENCOURT
38	268	77.0	731	6	CB955606 AGENCOURT
39	268	77.0	743	6	CB957183 AGENCOURT
40	268	77.0	766	6	CB956983 AGENCOURT
41	268	77.0	839	6	CB986712 AGENCOURT
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43	266.4	76.6	456	2	AW404683 UI-HF-BL0
44	266.4	76.6	500	6	CD696096 EST12619
45	266.4	76.6	512	6	CD709518 EST26045

#### ALIGNMENTS

##### RESULT 1

LOCUS CD689298 597 bp mRNA linear EST 25-JUN-2003  
DEFINITION EST5820 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD689298  
VERSION CD689298.1 GI:32208911  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 597)  
AUTHORS Liu,X.-O., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center

Sun Yat-sen University  
651 DongFeng Road East, GuangZhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@zsus.edu.cn.

FEATURES  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="normal nasopharynx"  
/clone\_lib="human nasopharynx"  
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

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Query Match 79.8%; Score 277.6; DB 6; Length 597;  
Best Local Similarity 87.4%; Pred. No. 2.1e-72;  
Matches 304; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGTCACCCCTGAGAGCGGCTCC 60  
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Qy 61 ATCTCTCTGTCGCTCGAGTAGAGTCTCCTGTATAGGATGGGAAGACATCTTGAATTGG 120  
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Qy      301  TTCACGTTGGCCCAAGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 348
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Db      410  TACACGTTGGCCCAAGGACCAAGGTGGAAATCAACAGCACTGTGGCT 457
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RESULT 2
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LOCUS
DEFINITION
  AGENCOURT_13643139 NIH_MGC_184 Homo sapiens cDNA clone EST 01-MAY-2003
  IMAGE:30328074 5', mRNA sequence.
CB987308
ACCESSION
  CB987308.1 GI:30281828
VERSION
  EST.
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 743)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
  cDNA Library Preparation: CLONTECH Laboratories, Inc.
  DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: NDCM138 row: b column: 19
  High quality sequence stop: 557.
  Location/Qualifiers
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    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:30328074"
    /lab_host="DH10B (TI phage-resistant)"
    /clone_lib="NIH_MGC_184"
    /notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
    SfiI (ggccattggcc); Site_2: SfiI (ggcgctcgcc);
    Library is oligo-dT primed and directionally cloned. cDNA
    was prepared from a glandular pool of tissues from thyroid,
    parathyroid, adrenal, cortex and pineal gland. 5' and 3'
    adaptors were used in cloning as follows: 5' adaptor
    sequence: 5'-CACGGCCATTATGCGC-3' and 3' adaptor sequence:
    5'-ATTCTAGAGCCGAGCGGCGGATG-3' (30) BN-3' (where B = A,
    C, G and N = A, C, G, or T). Average insert size 1.38
    kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
    by PCR. This library was enriched for full-length clones
    and was constructed by Clontech Laboratories (Palo Alto,
    CA). Note: this is a NIH_MGC Library."

ORIGIN
  Query Match 79.8%; Score 277.6; DB 6; Length 743;
  Best Local Similarity 87.4%; Pred. No. 2.2e-72;
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Db      94  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGGTCCACCTCGGAGAGCGGCTCC 153
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Qy      61  ATCTCTGCTCGAGTAAAGAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
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      |||
Qy      121  TACCTGCAGAAAGCCAGGCGCAGTCTCCACAGCTCTGATCTATTTGATGTCCACCGGGCA 180
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Db      214  TACCTGCAGAAAGCCAGGCGCAGTCTCCACAGCTCTGATCTATTTGGTCTTAAATCGGGCC 273
      |||
Qy      181  TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
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Qy      241  AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGCTAGAGTATCCA 300
      |||
Db      334  AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGCTAGAGTATCCA 393
      |||
Qy      301  TTCAGTTTCGCCCAAGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 348
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Db      394  CTCACCTTTTCGCCGAGGAGGACCAAGGTGGAGATCAAAAGCACTGTGGCT 441
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  603083265F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222297 5',
  mRNA sequence.
ACCESSION
  BI838327
VERSION
  BI838327.1 GI:15949877
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 990)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Life Technologies, Inc.
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM11559 row: a column: 18
  High quality sequence stop: 740.
  Location/Qualifiers
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    /clone="IMAGE:5222297"
    /lab_host="DH10B"
    /clone_lib="NIH_MGC_120"
    /notes="Organ: pooled pancreas and spleen; Vector:
    pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
    source anonymous pool of spleen and pancreas from 28 yo
    male. Library is oligo-dT primed and directionally cloned
    (EcoRV site is destroyed upon cloning). Average insert
    size 1.5 kb, insert size range 1-2.5 kb. Library is
    normalized and enriched for full-length clones and was
    constructed by C. Gruber (Invitrogen) Research Genetics
    tracking code 025. Note: this is a NIH_MGC Library."

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Db      147  ATCTCTGTAGTCTAGTTCAGAGCTCTCTGATTAATTAACGATACAGTATTGGATTGG 206
Qy      121  TACCTGAGAACGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGATCCACCCCGGCA 180
Db      207  TACCTGAGAACGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGATCTTAATCGGGCC 266
Qy      181  TCAGGGCTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db      267  TCGGGGTCCCTGACAGGTTCAAGGTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 326
Qy      241  AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db      327  AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTACTGCGTGAGTCTTACAAACCCCG 386
Qy      301  TTCAGGTTCCGCCAAGGACCAAGGTGGAGATCAAACTACGTTACGTTGGCT 348
Db      387  CTCACCTTCGGCGAGGACCAAGGTGGAGATCAAACTACGTTGGCT 434

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RESULT 4  
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DEFINITION EST16693 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD700169  
VERSION CD700169.1 GI:32230142  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 600)  
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.

FEATURES  
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Best Local Similarity 87.1%; Pred. No. 6.5e-72;  
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Qy      121  TACCTGAGAACGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGATCCACCCCGGCA 180
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Qy      181  TCAGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
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Qy      241  AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db      353  AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTCTTACAACTCCT 412
Qy      301  TTCAGCTTCGGCCCAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 348
Db      413  CTCACCTTCGGCGAGGACCAAGGTGGAGATCAAACTACGTTGGCT 460

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RESULT 5  
LOCUS CD698049 605 bp mRNA linear EST 25-JUN-2003  
DEFINITION EST14572 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD698049  
VERSION CD698049.1 GI:32226103  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 605)  
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.

TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.

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Qy      1  GATATTGTGATGACTCAGTCTCCTGTAAGGATGGGAAGACATACCTTGAATTGG 120
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Qy      61  ATCTCTCTGCTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACCTTGAATTGG 120
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Qy      121  TACCTGAGAACGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGATCCACCCCGGCA 180
Db      232  TACCTGAGAACGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGTTCTACTCGGGCC 291
Qy      181  TCAGGGGTCCCTGACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db      292  TCGGGGTCCCTGACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 351
Qy      241  AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db      352  ACCAGAGTGGAGGCTGAGGATGTTGGGATTTATTACTGTCAACAGCTGGTAGAGTATCCA 411
Qy      301  TTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 348

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Db 412 CCCACTTTGGCGGAGGACCAGGTGGAGATCAACGACTGTGGCT 459
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AGENCOURT 13666811 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30354094 5', mRNA sequence.
CB957285
CB957285 1 GI:30213402
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 817)
TITLE NIH-MGC http://mhc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@emall.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM155 row: n column: 23
High quality sequence stop: 534.
Location/Qualifiers
1. .817
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/db_xref="taxon:9606"
/clone="IMAGE:30354094"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattatggcc); Site 2: SfiI (ggcgctggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATATGCCC-3', and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCAGATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES
source
Query Match 79.3%; Score 276; DB 6; Length 817;
Best Local Similarity 87.1%; Pred. No. 7e-72;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCGTGGAGAGCGGCTCC 60
Db 96 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCGTGGAGAGCGGCTCC 155
QY 61 ATCTCTGTGCTCGAGTAAAGTCTCTGTATAAGATGGGAGACATACCTTGAATTGG 120
Db 156 ATCTCTGCGAGGTCTAGTCAGAGCCTCTCATAGTCATGATACCACTATTGGATTGG 215
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGTGATGCCCGGGCA 180
Db 216 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGGGTTCTATCGGCC 275
QY 181 TCAGGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCGACAGATTTACATGAAAATC 240
Db 276 TCCGGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCGACAGATTTACGCTGAAAATC 335

RESULT 6
LOCUS CB957285
DEFINITION AGENCOURT 13666811 NIH_MGC_184 Homo sapiens cDNA clone
ACCESSION CB957285
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 817)
TITLE NIH-MGC http://mhc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@emall.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM155 row: n column: 23
High quality sequence stop: 534.
Location/Qualifiers
1. .817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30354094"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattatggcc); Site 2: SfiI (ggcgctggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATATGCCC-3', and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCAGATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES
source
Query Match 79.3%; Score 276; DB 6; Length 817;
Best Local Similarity 87.1%; Pred. No. 7e-72;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCGTGGAGAGCGGCTCC 60
Db 131 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCGTGGAGAGCGGCTCC 190
QY 61 ATCTCTGTGCTCGAGTAAAGTCTCTGTATAAGATGGGAGACATACCTTGAATTGG 120
Db 191 ATCTCTGCGAGGTCTAGTCAGAGCCTCTCATAGTCATGATACCACTATTGGATTGG 250
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGTGATGCCCGGGCA 180
Db 251 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGGGTTCTATCGGCC 310
QY 181 TCAGGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCGACAGATTTACATGAAAATC 240
Db 311 TCCGGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCGACAGATTTACATGAAAATC 370
QY 241 AGCAGATGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 371 AGCAGATGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 430
QY 301 TTCACTCTCGGCAAGGGACCAAGGTGGAGATCAAAACGTTACCGTGTG 345
Db 431 CCGACGTTCCGGCAAGGGACCAAGGTGGAGATCAAAACGTTACCGTGTG 475

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RESULT 8
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LOCUS             EST16336 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION         CD699812
VERSION           CD699812.1 GI:32229450
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS           Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
                  Zeng,Y.-X.
TITLE             Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL           Unpublished (2003)
COMMENT           Contact: Yixin Zeng
                  Cancer Center
                  Sun Yat-sen University
                  651 Dongfeng Road East, Guangzhou 510060, China
                  Tel: 86-1380-9770-743
                  Fax: 86-20-8775-4506
                  Email: yxzeng@gzsums.edu.cn.
FEATURES          Location/Qualifiers
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                  /note="ESTs generated from a normal nasopharynx cDNA
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Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGAGAGCGCGCTCC 60
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Qy 121 TACCTGAGAGCCAGCGGAGTCTCCACAGTCTCTGATCTATTGTATGTCACCCCGGCA 180
Db 233 TACCTGAGAGCCAGCGGAGTCTCCACAGTCTCTGATCTATTGTGGGTTCTAATCGGGCC 292
Qy 181 TCAGGGGTCCCTGCAGGTTTCAGTGGCAGTGGATCAAGATTTTACACTGAAATC 240
Db 293 TCCGGGGTCCCTGCAGGTTTCAGTGGCAGTGGATCAAGATTTTACACTGAAATC 352
Qy 241 AGCAGATGGAGGCTGAGGATGTTGGGGTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 353 AGTAGAGTGGAGGCTGAGGATGTTGGGGTTATTACTGTCTGCAATCTCTACAAATTCG 412
Qy 301 TTACGTTCCGGCCAGGACCAAGGTGGAGATCAAACTACGTTGGCT 348
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RESULT 9
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LOCUS             EST607 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION         CD684087
VERSION           CD684087.1 GI:32198747
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 583)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE             Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL           Unpublished (2003)
COMMENT           Contact: Yixin Zeng
                  Cancer Center
                  Sun Yat-sen University
                  651 Dongfeng Road East, Guangzhou 510060, China
                  Tel: 86-1380-9770-743
                  Fax: 86-20-8775-4506
                  Email: yxzeng@gzsums.edu.cn.
FEATURES          Location/Qualifiers
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                  /clone_lib="human nasopharynx"
                  /note="ESTs generated from a normal nasopharynx cDNA
                  library from southern Chinese"
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Query Match      78.9%; Score 274.4; DB 6; Length 583;
Best Local Similarity 86.8%; Pred. No. 1.9e-71;
Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGAGAGCGCGCTCC 60
Db 121 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGAGAGCGCGCTCA 180
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Db 181 ATCTCTGTCTCGCTCGATAGAGTCTCTGTATAGGATGGAGACATCTTGAATTGG 240
Qy 121 TACCTGAGAGCCAGCGGAGTCTCCACAGTCTCTGATCTATTGTATGTCACCCCGGCA 180
Db 241 TACCTGAGAGCCAGCGGAGTCTCCACAGTCTCTGATCTATTGTGGTTCTAATCGGGCC 300
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Db 301 TCCGGGGTCCCTGCAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 360
Qy 241 AGCAGATGGAGGCTCAGGATGTTGGGGTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 361 AGCAGATGGAGGCTCAGGATGTTGGGGTTATTACTGTATGCAAGTCTACAAATTCG 420
Qy 301 TTCACGTTCCGGCCAGGACCAAGGTGGAGATCAAACTACGTTGGCT 348
Db 421 TACACTTTCGGCCAGGACCAAGGTGGAGATCAAACTACGTTGGCT 468

RESULT 10
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LOCUS             AGENCOURT 13777308 NIH MGC 184 Homo sapiens cDNA clone
DEFINITION        IMAGE:30350668 5', mRNA sequence.
ACCESSION         CB955891
VERSION           CB955891.1 GI:30212009
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS           NIH-MGC http://mgi.nci.nih.gov/.
TITLE             National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL           Unpublished (1999)
COMMENT           Contact: Robert Strausberg, Ph.D.
                  Email: cgabbs@mail.nih.gov
                  Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
                  cDNA Library Preparation: CLONTECH Laboratories, Inc.
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cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: NDCM146 row: p column: 05  
High quality sequence stop: 520.

## FEATURES

Location/Qualifiers

1. .791

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30350668"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH MGC 184"

/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site\_1:  
SfiI (ggccattatggcc); Site 2: SfiI (ggccctcgccg);  
Library is oligo-dt primed and directionally cloned. cDNA  
was prepared from a glandular pool of tissues from thyroid,  
parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.38  
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH MGC Library."

## ORIGIN

Query Match 78.9%; Score 274.4; DB 6; Length 791;  
Best Local Similarity 86.8%; Pred. No. 2.1e-71;  
Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60  
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QY 61 ATCTCTGCTGCTCGAGTAGAGTCTCCTGTATAGGATGGGAGACATCTTGAATTGG 120  
DB 155 ATCTCTGCTGCTCGAGTAGAGTCTCCTGTATAGGATGGGAGACATCTTGAATTGG 214  
QY 121 TACTCTGAGAACGACGAGGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCGGGCA 180  
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QY 181 TCAGGGGTCTCCAGAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAAATC 240  
DB 275 TCCGGGGTCTCCAGAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAAATC 334  
QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 335 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 394  
QY 301 TTACGTTCCGGCCAAAGGACCAAGTGGAGATCAAAAGCTACCGTGGCT 348  
DB 395 TGGACGTTCCGGCCAAAGGACCAAGTGGAGATCAAAAGCTACCGTGGCT 442

RESULT 11  
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LOCUS  
DEFINITION  
AGENCOURT 13459280 NIH MGC\_184 Homo sapiens cDNA clone  
IMAGE:30326266 5', mRNA sequence.  
CB985612  
CB985612.1 GI:30280136  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 830)  
AUTHORS  
NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: NDCM133 row: g column: 11  
High quality sequence stop: 412.

## FEATURES

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1. 830

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30326266"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH MGC 184"

/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site\_1:  
SfiI (ggccattatggcc); Site 2: SfiI (ggccctcgccg);  
Library is oligo-dt primed and directionally cloned. cDNA  
was prepared from a glandular pool of tissues from thyroid,  
parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGGAGCGCCGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.38  
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH MGC Library."

## ORIGIN

Query Match 78.9%; Score 274.4; DB 6; Length 830;  
Best Local Similarity 86.8%; Pred. No. 2.1e-71;  
Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60  
DB 94 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 153  
QY 61 ATCTCTGCTGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAGACATCTTGAATTGG 120  
DB 154 ATCTCTGCTGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAGACATCTTGAATTGG 213  
QY 121 TACTCTGAGAACGACGAGGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCGGGCA 180  
DB 214 TACTCTGAGAACGACGAGGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCGGG 273  
QY 181 TCAGGGGTCTCCAGAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAAATC 240  
DB 274 TCCGGGGTCTCCAGAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAAATC 333  
QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 334 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 393  
QY 301 TTACGTTCCGGCCAAAGGACCAAGTGGAGATCAAAAGCTACCGTGGCT 348  
DB 394 AGGACGTTCCGGCCAAAGGACCAAGTGGAGATCAAAAGCTACCGTGGCT 441

RESULT 12  
AW406883  
LOCUS  
DEFINITION  
UI-HF-BL0-adg-h-03-0-UI.r1 NIH MGC\_37 Homo sapiens cDNA clone  
IMAGE:3061493 5', mRNA sequence.  
AW406883  
AW406883.1 GI:6925940  
KEYWORDS  
EST.

```
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES
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        Location/Qualifiers
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                /organism="Homo sapiens"
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                /db_xref="taxon:9606"
                /clone="IMAGE:3061493"
                /tissue_type="lymph"
                /cell_type="germinal center B cells"
                /cell_line="MGC85"
                /lab_host="DH10B (LTI)"
                /clone_lib="NIH_MGC_37"
                /notes="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN
Query Match 78.4%; Score 272.8; DB 2; Length 454;
Best Local Similarity 86.5%; Pred. No. 5.6e-71;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 1 GATATTGTGACTGACTGCTCCACTCTCCCTCCCGTCAACCCCTGGAGAGCGGCTCC 60
Db 16 GATATTGTGACTGACTGCTCCACTCTCCCTCCCGTCAACCCCTGGAGAGCGGCTCC 75
QY 61 ATCTCTGTCGTCGAGTAGAGTCTCTGTATAGGATGGGAGACATATCTTGAATTGG 120
Db 76 ATCTCTGTCGAGTCTAGTCAGAGCTCTCTGTATAGGATGGGAGACATATCTTGAATTGG 135
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGTATAGTGTCCACCCCGGCA 180
Db 136 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGTATAGTGTCCACCCCGGCA 195
QY 181 TCAGGGGTCTCCACAGGTTTCAGTGGAGTGGATCAGGCACAGATTTACACTGAAATC 240
Db 196 TCAGGGGTCTCCACAGGTTTCAGTGGAGTGGATCAGGCACAGATTTACACTGAAATC 255
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATCTGTCAACAGCTGGTAGATATCCA 300
Db 256 ACAAAGTGGAGCTGAGGATGTTGGGTTTATCTGTCAACAGCTGGTAGATATCCA 315
QY 301 TTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAAGTACCGTGGCT 348
Db 316 CAGACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAAGTACCGTGGCT 363
RESULT 13
LOCUS CD700306
DEFINITION EST15630 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD700306
VERSION CD700306.1 GI:32230410
KEYWORDS EST.
```

```
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsums.edu.cn.
FEATURES
    source
        Location/Qualifiers
            1..524
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="normal nasopharynx"
                /clone_lib="human nasopharynx"
                /notes="ESTs generated from a normal nasopharynx cDNA
                library from southern Chinese"
ORIGIN
Query Match 78.4%; Score 272.8; DB 6; Length 524;
Best Local Similarity 86.5%; Pred. No. 5.8e-71;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 1 GATATTGTGACTGACTGCTCCACTCTCCCTCCCGTCAACCCCTGGAGAGCGGCTCC 60
Db 116 GATATTGTGACTGACTGCTCCACTCTCCCTCCCGTCAACCCCTGGAGAGCGGCTCC 175
QY 61 ATCTCTGTCGTCGAGTAGAGTCTCTGTATAGGATGGGAGACATATCTTGAATTGG 120
Db 176 ATCTCTGTCGAGTCTAGTCAGAGCTCTCTGTATAGGATGGGAGACATATCTTGAATTGG 235
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGTATAGTGTCCACCCCGGCA 180
Db 236 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGTATAGTGTCCACCCCGGCA 295
QY 181 TCAGGGGTCTCCACAGGTTTCAGTGGAGTGGATCAGGCACAGATTTACACTGAAATC 240
Db 296 TCAGGGGTCTCCACAGGTTTCAGTGGAGTGGATCAGGCACAGATTTACACTGAAATC 355
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATCTGTCAACAGCTGGTAGATATCCA 300
Db 356 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATCTGTCAACAGCTGGTAGATATCCA 415
QY 301 TTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAAGTACCGTGGCT 348
Db 416 CTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAAGTACCGTGGCT 463
RESULT 14
LOCUS CD703137
DEFINITION EST19728 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD703137
VERSION CD703137.1 GI:32233831
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
```



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 195.759 Seconds  
(without alignments)  
10523.523 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 348  
Sequence: 1 gatattgtgatgactcagtc.....agatcaaacgtacgtggct 348

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_16Dec04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	348	100.0	348	AAZ34747	Aaz34747 Humanised
2	292	83.9	740	AAFG63377	Aaf63377 Anti-Ep-C
3	292	83.9	740	AAFG63373	Aaf63373 Humanised
4	277.6	79.8	720	AD28460	Ade28460 Human ant
5	276	79.3	772	AAZ24418	Aaz24418 Human bla
6	274.4	78.9	720	AD28404	Ade28404 Human ant
7	274	78.7	720	AAAI3927	Aaai3927 Human PTH
8	273	78.4	720	AAAI3924	Aaai3924 Human PTH
9	272.8	78.4	720	AAAI3925	Aaai3925 Human PTH
10	272.8	78.4	720	AD28468	Ade28468 Human ant
11	272.8	78.4	720	AD28464	Ade28464 Human ant
12	272.8	78.4	1081	ABSS1811	Abss1811 Human mdd
13	272.4	78.3	720	AAAI3928	Aaai3928 Human PTH
14	271.8	78.1	720	AAAI3920	Aaai3920 Human PTH
15	271.2	77.9	649	ABZ22313	Abz22313 S: pneumo
16	271.2	77.9	720	AD28396	Ade28396 Human ant
17	270.8	77.8	720	AAAI3926	Aaai3926 Human PTH
18	269.8	77.5	337	AD28436	Ade28436 Human ant
19	269.8	77.5	337	AD007296	Ado07296 Human A3-
20	269.6	77.5	720	AAAI3921	Aaai3921 Human PTH

ALIGNMENTS

RESULT 1

AAZ34747  
ID AAZ34747 standard; cDNA; 348 BP.  
XX  
AC AAZ34747;  
XX  
DT 15-FEB-2000 (first entry)  
XX  
DE Humanised anti-CD23 Mab C11 light chain variable region cDNA.  
XX  
KW CD23; FCER1I; IgE receptor; monoclonal antibody; C11; mouse; human;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
KW therapy; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO9598679-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-GB001434.  
XX  
PR 09-MAY-1998; 98GB-00009839.  
XX  
P (GLAX ) GLAXO GROUP LTD.  
XX  
PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
XX WPI; 2000-053101/04.  
XX P-PSDB; AAY32262.  
XX  
PT Cell receptor specific antibodies useful for treating e.g. arthritis,  
XX diabetes, multiple sclerosis and psoriasis.  
XX  
PS Claim 17; Fig 3; 81pp; English.



XX This DNA sequence encodes the light chain variable region (VL) of  
CC humanised anti-CD23 (FCER1I) monoclonal antibody C11, composed of a human  
CC framework (H5IGKV1I) and the light chain complementarity determining  
CC regions (see AY32254-56) of murine antibody C11. The DNA was constructed  
CC by splice overlap PCR. The invention provides altered antibodies, such as  
CC chimeric or humanised antibodies, which comprise sufficient of the amino  
CC acid sequences of the C11 light and heavy chain complementarity  
CC determining regions to render them capable of binding to the CD23 type II  
CC molecule expressed on haematopoietic cells. The antibodies are used to  
CC block soluble CD23 formation in human therapy, for the treatment of  
CC arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple  
CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic  
CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative  
CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
CC malignancies (claimed). They are also useful for studying interactions  
CC between CD23 and various ligands and determining the binding agents  
XX

XX Sequence 348 BP; 81 A; 87 C; 97 G; 83 T; 0 U; 0 Other;

Query Match 100.0%; Score 348; DB 3; Length 348;  
Best Local Similarity 100.0%; Pred. No. 9e-97;  
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCTCC 60  
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCTCC 60  
QY 61 ATCTCTCTGCTCGAGTAAGAGTCTCTCTATAGGATGGGAGACATCTTGAATTGG 120  
DB 61 ATCTCTCTGCTCGAGTAAGAGTCTCTCTATAGGATGGGAGACATCTTGAATTGG 120  
QY 121 TACCTGCAGAACGCCAGGAGTCTCCACAGCTCCTGATCTATTGTGATGCCACCGGGCA 180  
DB 121 TACCTGCAGAACGCCAGGAGTCTCCACAGCTCCTGATCTATTGTGATGCCACCGGGCA 180  
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 240  
DB 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 240  
QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
QY 301 TTCACGTTTCGGCCCAAGGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 348  
DB 301 TTCACGTTTCGGCCCAAGGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 348

RESULT 2  
AAF63377/C  
ID AAF63377 standard; DNA; 740 BP.

XX AAF63377;  
AC AAF63377;  
XX 10-MAY-2001 (first entry)  
XX Anti-Ep-CAM antibody related DNA sequence SEQ ID 3.  
XX Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;  
XX chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer; ds.  
XX Unidentified.  
XX WO200107082-A1.  
XX 01-FEB-2001.  
XX 23-JUL-1999; 99WO-EP005271.  
XX

PR 23-JUL-1999; 99WO-EP005271.  
XX (GLAX ) GLAXO GROUP LTD.  
XX Knick VC, Stimmel JB, Thurmond LM;  
XX WPI; 2001-182729/18.  
XX Combination for treating cancer (e.g. breast, gastric or prostate  
XX cancers), or in the manufacture of a medicament for anti-cancer therapy,  
XX comprises an anti-Ep-cyclic adenosine monophosphate antibody with a  
XX chemotherapeutic agent.  
XX Disclosure; Page 66; 103pp; English.  
XX This invention relates to a combination of an anti-Ep-CAM (cyclic  
XX adenosine monophosphate) antibody with a chemotherapeutic agent, that is  
XX capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)  
XX phase or the second growth phase (M) of cell enlargement (G2)/DNA  
XX replication. The antibody exhibits cytostatic activity and is useful in  
XX the manufacture of a medicament for use in anti-cancer therapy,  
XX characterised in that a chemotherapeutic agent, which is capable of  
XX arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-  
XX administered to a patient with an anti-Ep-CAM antibody. The combination  
XX is useful for treating cancer, particularly colorectal cancer, breast  
XX cancer, gastric cancer, prostate cancer or non-small-cell lung cancer.  
XX The present sequence represents DNA related to the anti-Ep-CAM antibody  
XX used in the combination of the invention

XX Sequence 740 BP; 165 A; 187 C; 201 G; 187 T; 0 U; 0 Other;

Query Match 83.9%; Score 292; DB 4; Length 740;  
Best Local Similarity 89.9%; Pred. No. 2e-79;  
Matches 313; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCTCC 60  
DB 660 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCTCC 601  
QY 61 ATCTCTCTGCTCGAGTAAGAGTCTCTCTATAGGATGGGAGACATCTTGAATTGG 120  
DB 600 ATCTCTCTGAGTCTAGTAAAGATCTCTGATAGTATGATGATCTTATTGTATTGG 541  
QY 121 TACCTGCAGAACGCCAGGAGTCTCCACAGCTCCTGATCTATTGTGATGCCACCGGGCA 180  
DB 540 TACCTGCAGAACGCCAGGAGTCTCCACAGCTCCTGATCTATCAGATGTCACACCTTCC 481  
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 240  
DB 480 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 421  
QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 420 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCTCAAACTAGAGATTCT 361  
QY 301 TTCACGTTTCGGCCCAAGGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 348  
DB 360 CGGACGTTTCGGCCCAAGGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 313

RESULT 3  
AAF63373  
ID AAF63373 standard; cDNA; 740 BP.

XX AAF63373;  
AC AAF63373;  
XX 10-MAY-2001 (first entry)  
XX Humanised 323/A3 (IgG1) antibody light chain cDNA sequence.  
XX Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;  
XX chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;  
XX light chain; ss.  
XX



XX Mus sp.  
OS Homo sapiens.  
XX WO200107082-A1.  
XX 01-FEB-2001.  
XX 23-JUL-1999; 99WO-EP005271.  
XX 23-JUL-1999; 99WO-EP005271.  
XX (GLAX ) GLAXO GROUP LTD.  
XX Knick VC, Stimmel JB, Thurmond LM;  
XX WPI; 2001-182729/18.  
XX P-PSDB; AAB72227.  
XX Combination for treating cancer (e.g. breast, gastric or prostate  
PT cancers), or in the manufacture of a medicament for anti-cancer therapy,  
PT comprises an anti-Ep-cyclic adenosine monophosphate antibody with a  
PT chemotherapeutic agent.  
XX Example 6; Fig 15; 103pp; English.  
XX This invention relates to a combination of an anti-Ep-CAM (cyclic  
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is  
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)  
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA  
CC replication. The antibody exhibits cytostatic activity and is useful in  
CC the manufacture of a medicament for use in anti-cancer therapy,  
CC characterised in that a chemotherapeutic agent, which is capable of  
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-  
CC administered to a patient with an anti-Ep-CAM antibody. The combination  
CC is useful for treating cancer, particularly colorectal cancer, breast  
CC cancer, gastric cancer, prostate cancer or non-small-cell lung cancer.  
CC The present sequence represents cDNA encoding the light chain of anti-Ep-  
CC CAM antibody known as humanised 323/A3 (IgG1) which can be used in the  
CC combination of the invention  
XX  
SQ Sequence 740 BP; 187 A; 201 C; 187 G; 165 T; 0 U; 0 Other;

Query Match 83.9%; Score 292; DB 4; Length 740;  
Best Local Similarity 89.9%; Pred. No. 2e-79;  
Matches 313; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGGTACCCCTGGAGAGCGGCTCC 60  
DB 81 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGGTACCCCTGGAGAGCGGCTCC 140  
QY 61 ATCTCTCTGCTCGAGTAGAGTCTCTGTATAGAGTGGGAAGACATCTTGAATTGG 120  
DB 141 ATCTCTCTGAGTCTAGTAGAATCTCTGTATAGTAAAGCATCTTATTGTTATGG 200  
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCCGGCA 180  
DB 201 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATCAGATGTCACACTTGGC 260  
QY 181 TCAGGGGTCCCTCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAATTC 240  
DB 261 TCAGGGGTCCCTCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAATTC 320  
QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTCTGTCAACAGCTGGTGTAGATATCCA 300  
DB 321 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTCTGTCTCAAAATCTAGATATCTT 380  
QY 301 TTCACGTTCCGCCCAAGGACCAAGGTGGAGATCAAAACGCTACGCTGGCT 348  
DB 381 CGGACGTTCCGCCCAAGGACCAAGGTGGAGATCAAAACGCTACGCTGGCT 428

RESULT 4

ADE28460

ID ADE28460 standard; cDNA; 720 BP.

XX AC ADE28460;

XX DT 29-JAN-2004 (first entry)

XX DE Human anti-CD40 antibody 23-28-1 variable region light chain cDNA.

XX KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;

XX KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;

XX KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;

XX KW human; variable region light chain; ss; gene; 23-28-1.

XX OS Homo sapiens.

XX PN WO2003040170-A2.

XX PD 15-MAY-2003.

XX PF 08-NOV-2002; 2002WO-US036107.

XX PR 09-NOV-2001; 2001US-0348980P.

XX PA (PFIZ ) PFIZER PROD INC.

XX PA (ABGE-) ABGENIX INC.

XX PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX XX WPI; 2003-441521/41.

XX XX P-PSDB; ADE28461.

XX PT New chimeric or human monoclonal antibody or its antigen-binding portion

XX PT that specifically binds to and activates human CD40, useful for enhancing

XX PT an immune response in a human, or treating cancer, HIV, neutropenia or

XX PT viral infections.

XX XX Claim 24; SEQ ID NO 67; 177pp; English.

XX PS The invention relates to a novel chimeric or human monoclonal antibody or

XX PS its antigen-binding portion that specifically binds to and activates

XX PS human CD40. The anti-CD40 antibody of the invention demonstrates

XX PS cytostatic, virucide, antibacterial, immunostimulant and anti-HIV

XX PS activities and may be useful for treating a hyperproliferative disorder

XX PS such as cancer, viral and bacterial infection or genetic, primary or

XX PS combined immunodeficiency conditions including neutropenia or HIV

XX PS infection. The anti-CD40 antibodies may also be useful for detecting CD40

XX PS in a biological sample in vitro or in vivo, as well as during gene

XX PS therapy procedures. The current sequence is that of the human anti-CD40

XX PS antibody variable region light chain cDNA of the invention.

XX SQ Sequence 720 BP; 173 A; 192 C; 189 G; 166 T; 0 U; 0 Other;

Query Match 79.8%; Score 277.6; DB 10; Length 720;

Best Local Similarity 87.4%; Pred. No. 5.4e-75;

Matches 304; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGGTACCCCTGGAGAGCGGCTCC 60

DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGGTACCCCTGGAGAGCGGCTCC 120

QY 61 ATCTCTCTGCTCGAGTAGAGTCTCTGTATAGAGTGGGAAGACATCTTGAATTGG 120

DB 121 ATCTCTCTGAGTCTAGTACAGAGTGTCTGTATAGTAAAGCATCTTATTGTTATGG 180

QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCCGGCA 180

DB 181 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTGGTTCTAATCGGGC 240

QY 181 TCAGGGGTCCCTCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAATTC 240

DB 241 TCCGGGGTCCCTCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAATTC 300

QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCACAGCTGTAGAGTATCCA 300  
 DB 301 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCACAGCTGTAGAGTATCCA 360  
 QY 301 TTCCAGCTTGGCCCAAGGACCAAGAGTGGAGATCAACAGTACGGTGGCT 348  
 DB 361 TTCCAGCTTGGCCCTGGGACCAAGTGGATATCAACAGTACGGTGGCT 408

RESULT 5  
 AAZ24418  
 ID AAZ24418 standard; cDNA; 772 BP.  
 XX  
 AC AAZ24418;  
 XX  
 DT 14-FEB-2000 (first entry)  
 XX  
 DE Human bladder tumour cDNA library derived EST 30.  
 XX  
 KW Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;  
 KW treatment; gene therapy; EST; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE19818619-A1.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 21-APR-1998; 98DE-01018619.  
 XX  
 PR 21-APR-1998; 98DE-01018619.  
 XX  
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
 XX  
 PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;  
 XX  
 XX WPI; 1999-612028/53.  
 DR  
 XX  
 PT New nucleic acid sequences expressed in bladder tumor tissue, and derived  
 PT polypeptides, for treatment of bladder tumor and identification of  
 PT therapeutic agents.  
 XX  
 PS Claim 3; Page 84; 132pp; German.  
 XX  
 CC This invention describes novel polypeptide fragments (I) and the  
 CC polynucleotides (II) that encode them that are highly expressed in a  
 CC human bladder tumour and which have cytostatic activity. (II) are used  
 CC for recombinant expression of (I) and to isolate complete genes. (I) are  
 CC used to identify agents suitable for treatment of bladder cancer, to  
 CC directly treat this form of cancer (including expression from gene  
 CC therapy vectors) or are used in a preparation for cancer treatment. (I)  
 CC is also used for the generation of specific antibodies. (II) are  
 CC identified by assembling ESTs (expressed sequence tags) from a particular  
 CC tissue type before comparison of expression patterns. This allows a  
 CC significantly longer fragment of the gene to be revealed, and therefore  
 CC reduces the number of failures associated with the fact that ESTs from  
 CC different libraries may represent different parts of the same unknown  
 CC gene, distorting the estimated frequency of occurrence in a particular  
 CC tissue. AAZ3260-243309 represent expressed sequence tag (EST) fragments  
 CC isolated from a human bladder tumour cDNA library which encode the  
 CC proteins represented in AAY66143-Y66198  
 XX  
 SQ Sequence 772 BP; 181 A; 210 C; 206 G; 175 T; 0 U; 0 Other;  
 Query Match 79.3%; Score 276; DB 2; Length 772;  
 Best Local Similarity 87.1%; Pred. No. 1.7e-74;  
 Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCC 60  
 DB 87 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCC 146  
 QY 61 ATCTCCTGCTCGCTCGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATACTTTGAATGG 120

DB 147 ATCTCCTGCTCGCTCTAGTCACAGCTCTCTGTCATAGTAATGATACCACTATTGGATTGG 206  
 QY 121 TACCTGCAAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGGGCA 180  
 DB 207 TACCTGCAAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTTGGGTTCTAATCGGGCC 266  
 QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCGAGTCAGTCAGGCACAGATTTTACACTGAAAATC 240  
 DB 267 TCCGGGGTCCCTGACAGGTTTCAGTGGCGAGTCAGTCAGGCACAGATTTTACACTGAAAATC 326  
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 DB 327 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAAGCTCTACAAACTCCT 386  
 QY 301 TTCAGTTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348  
 DB 387 CTCACCTTTCGGCGGAGGACCAAGTGGAGATCAACAGTACGGTGGCT 434

RESULT 6  
 ADE28404  
 ID ADE28404 standard; cDNA; 720 BP.  
 XX  
 AC ADE28404;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human anti-CD40 antibody 7-1-2 variable region light chain cDNA.  
 XX  
 KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
 KW human; variable region light chain; ss; gene; 7-1-2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003040170-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 08-NOV-2002; 2002WO-US036107.  
 XX  
 PR 09-NOV-2001; 2001US-0348980P.  
 XX  
 PA (PFIZ ) PFIZER PROD INC.  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
 XX  
 DR WPI; 2003-441521/41.  
 DR P-PSDB; ADE28405.  
 XX  
 PS Claim 24; SEQ ID NO 11; 177pp; English.  
 XX  
 CC The invention relates to a novel chimeric or human monoclonal antibody or  
 CC its antigen-binding portion that specifically binds to and activates  
 CC human CD40. The anti-CD40 antibody of the invention demonstrates  
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
 CC activities and may be useful for treating a hyperproliferative disorder  
 CC such as cancer, viral and bacterial infection or genetic, primary or  
 CC combined immunodeficiency conditions including neutropenia or HIV  
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
 CC in a biological sample in vitro or in vivo, as well as during gene  
 CC therapy procedures. The current sequence is that of the human anti-CD40  
 CC antibody variable region light chain cDNA of the invention.  
 XX  
 SQ Sequence 720 BP; 173 A; 195 C; 192 G; 160 T; 0 U; 0 Other;

Query Match 78.9%; Score 274.4; DB 10; Length 720;  
 Best Local Similarity 86.8%; Pred. No. 5.3e-74;  
 Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCCTCCACCTCGAGAGCGCGCTCC 60  
 DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCCTCCACCTCGAGAGCGCGCTCC 120

QY 61 ATCTCTCTGCTCGCTGAGTAAAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120  
 DB 121 ATCTCTCTGAGTCTAGTCAGAGCTCTGTATAGTATGATGATCACTTTTGGATTGG 180

QY 121 TACCTGCAAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTTGATGTCCACCCGGGCA 180  
 DB 181 TACCTGCAAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTTGGGTTCTAATCGGGCC 240

QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
 DB 241 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 360

QY 301 TTCACGTTTCGGCCAAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 348  
 DB 361 CGGACGTTTCGGCCAAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 408

## RESULT 7

AAA13927  
 ID AAA13927 standard; DNA; 720 BP.  
 XX  
 AC AAA13927;  
 XX  
 XX 02-AUG-2000 (first entry)  
 XX  
 DE Human PTHrP monoclonal antibody clone 3G4-3 DNA SEQ ID NO:17.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;  
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
 KW antiarthritic; cytostatic; antiinflammatory; ds.

OS Homo sapiens.

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-00304793.

XX 17-JUN-1998; 98JP-00188196.

XX 26-JUN-1998; 98JP-00196729.

XX (NISR) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

XX P-PSDB; AAY82617.

XX A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain.

XX Example 10; Page 50; 89pp; Japanese.

XX The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood

CC calcium content. The monoclonal antibody can be used in the treatment of  
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a human  
 CC PTHrP monoclonal antibody clone nucleotide sequence from the present  
 CC invention

XX SQ Sequence 720 BP; 174 A; 191 C; 188 G; 163 T; 0 U; 4 Other;

Query Match 78.7%; Score 274; DB 3; Length 720;  
 Best Local Similarity 86.5%; Pred. No. 7e-74;  
 Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCCTCCACCTCGAGAGCGCGCTCC 60  
 DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCCTCCACCTCGAGAGCGCGCTCC 120

QY 61 ATCTCTCTGCTCGCTGAGTAAAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120  
 DB 121 ATCTCTCTGAGTCTAGTCAGAGCTCTGTATAGTATGATGATCACTTTTGGATTGG 180

QY 121 TACCTGCAAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTTGATGTCCACCCGGGCA 180  
 DB 181 TACCTGCAAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTTGGGTTCTAATCGGGCC 240

QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
 DB 241 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
 DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 360

QY 301 TTCACGTTTCGGCCAAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 348  
 DB 361 TTCACGTTTCGGCCAAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 408

## RESULT 8

AAA13924  
 ID AAA13924 standard; DNA; 720 BP.

XX AAA13924;

XX 02-AUG-2000 (first entry)

XX Human PTHrP monoclonal antibody clone 2F8-10-3 DNA SEQ ID NO:11.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;  
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
 KW antiarthritic; cytostatic; antiinflammatory; ds.

OS Homo sapiens.

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-00304793.

XX 17-JUN-1998; 98JP-00188196.

XX 26-JUN-1998; 98JP-00196729.

XX (NISR) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

XX P-PSDB; AAY82614.

XX A human monoclonal antibody to parathyroid hormone related protein. -

PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain.  
 XX  
 PS  
 XX  
 XX  
 XX Example 10; Page 41-42; 88pp; Japanese.  
 CC The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment of  
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a human  
 CC PTHrP monoclonal antibody clone nucleotide sequence from the present  
 CC invention  
 XX  
 SQ Sequence 720 BP; 174 A; 190 C; 188 G; 163 T; 0 U; 5 Other;  
 Query Match 78.4%; Score 273; DB 3; Length 720;  
 Best Local Similarity 86.2%; Pred. No. 1.4e-73;  
 Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;  
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCAGAGCGGGCTCC 60  
 DB 61 GATATTGTGATGANTCAGTNTCCACTCTCCCTGCCCGTCCACTCTCCAGAGCGGGCTCC 120  
 QY 61 ATCTCTGTCTGCTGAGTAAAGTCTCTCTGATATAGGATGGGAGACATCTTGAATTGG 120  
 DB 121 ATCTCTGTCAGGTTCTAGTCAGACCTCTCTGATGTAATGGAACAACATTTTGGATTGG 180  
 QY 121 TACCTGAGAAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCCGGCA 180  
 DB 181 TACCTGAGAAAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGTGGTTCTAATCGGGCC 240  
 QY 181 TCAGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
 DB 241 TCCGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300  
 QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300  
 DB 301 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 360  
 QY 301 TTCACGTTTCGGCCAGGACCAAGTGGATGATCAAAAGTGGATCAAAAGTGGCT 348  
 DB 361 TTCACGTTTCGGCCAGGACCAAGTGGATGATCAAAAGTGGATCAAAAGTGGCT 408  
 RESULT 9  
 AAA13925  
 ID AAA13925 standard; DNA; 720 BP.  
 XX  
 AC AAA13925;  
 XX  
 XX 02-AUG-2000 (first entry)  
 XX  
 XX Human PTHrP monoclonal antibody clone 1C1-3 DNA SEQ ID NO:13.  
 DE  
 XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture, cachexia, tooth disease; periodontal disease; gingiva; sepsis;  
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
 KW antiarthritic; cytostatic; antiinflammatory; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX JP2000080100-A.  
 XX  
 XX 21-MAR-2000.  
 XX  
 XX 12-OCT-1998; 98JP-00304793.  
 PF

XX 17-JUN-1998; 98JP-00188196.  
 PR 26-JUN-1998; 98JP-00196729.  
 XX  
 XX (NISR) JAPAN TOBACCO INC.  
 PA  
 XX  
 XX WPI: 2000-286723/25.  
 DR P-PSDB; AY82615.  
 XX  
 PT A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain.  
 XX  
 XX Example 10; Page 44-45; 88pp; Japanese.  
 PS The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment of  
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a human  
 CC PTHrP monoclonal antibody clone nucleotide sequence from the present  
 CC invention  
 XX  
 SQ Sequence 720 BP; 172 A; 197 C; 190 G; 160 T; 0 U; 1 Other;  
 Query Match 78.4%; Score 272.8; DB 3; Length 720;  
 Best Local Similarity 86.5%; Pred. No. 1.6e-73;  
 Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCAGAGCGGGCTCC 60  
 DB 61 GATATTGTGATGACTCAGTCTCCCTGCCCGTCCAGAGCGGGCTCC 120  
 QY 61 ATCTCTGTCTGCTGAGTAAAGTCTCTCTGATATAGGATGGGAGACATCTTGAATTGG 120  
 DB 121 ATCTCTGTGAGTCTGAGTCCAGAGCTCTCTGATGTAATGGAATTAATCTTGAATTGG 180  
 QY 121 TACCTGTCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTGTCACCCCGGCA 180  
 DB 181 TACCTGTCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGTCTTCTAATCGGGCC 240  
 QY 181 TCAGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
 DB 241 TCCGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300  
 QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300  
 DB 301 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 360  
 QY 301 TTCACGTTTCGGCCAGGACCAAGTGGAGATCAAAAGTGGATCAAAAGTGGCT 348  
 DB 361 TTCACGTTTCGGCCAGGACCAAGTGGATGATCAAAAGTGGATCAAAAGTGGCT 408  
 RESULT 10  
 ADE28468  
 ID ADE28468 standard; cDNA; 720 BP.  
 XX  
 AC ADE28468;  
 XX  
 XX 29-JAN-2004 (first entry)  
 XX  
 XX Human anti-CD40 antibody 23-29-1 variable region light chain cDNA.  
 DE  
 DE anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
 KW

KW human; variable region light chain; ss; gene; 23-29-1.

XX Homo sapiens.

XX WO2003040170-A2.

XX PD 15-MAY-2003.

XX 08-NOV-2002; 2002WO-US036107.

XX 09-NOV-2001; 2001US-0348980P.

XX (PFIZ ) PFIZER PROD INC.

XX (ABGE-) ABGENIX INC.

XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX WPI; 2003-441521/41.

XX P-PSDB; ADE28469.

XX New chimeric or human monoclonal antibody or its antigen-binding portion  
PT that specifically binds to and activates human CD40, useful for enhancing  
PT an immune response in a human, or treating cancer, HIV, neutropenia or  
PT viral infections.

XX Claim 24; SEQ ID NO 75; 177pp; English.

XX The invention relates to a novel chimeric or human monoclonal antibody or  
CC its antigen-binding portion that specifically binds to and activates  
CC human CD40. The anti-CD40 antibody of the invention demonstrates  
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
CC activities and may be useful for treating a hyperproliferative disorder  
CC such as cancer, viral and bacterial infection or genetic, primary or  
CC combined immunodeficiency conditions including neutropenia or HIV  
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
CC in a biological sample in vitro or in vivo, as well as during gene  
CC therapy procedures. The current sequence is that of the human anti-CD40  
CC antibody variable region light chain cDNA of the invention.

XX Sequence 720 BP; 173 A; 196 C; 192 G; 157 T; 0 U; 2 Other;

Query Match 78.4%; Score 272.8; DB 10; Length 720;

Best Local Similarity 86.5%; Pred. No. 1.6e-73;

Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTACCCCTGGAGAGCGGCTCC 60

DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTACCCCTGGAGAGCGGCTCC 120

QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAGACATATTGAATTGG 120

DB 121 ATCTCTGTCAGGCTAGTCAGAGCTCTCTGCTGTAATGATACACTATTGGATTGG 180

QY 121 TACTGTGAGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGTATGTCACCCCGGCA 180

DB 181 TACTGTGAGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGTGGTTCTAATCGGGCC 240

QY 181 TCAGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

DB 241 TCCGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300

DB 301 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 360

QY 301 TTCAGTTCGGCCAGGGAACAAGGTGGAGATCAACAGTACGTTGGCT 348

DB 361 CGGACGTTCCGCCAAGGGAACAAGGTGGAAATCAACAGCACTGTGGCT 408

RESULT 11

ADE28464

ID ADE28464 standard; cDNA; 720 BP.

XX ADE28464;

XX 29-JAN-2004 (first entry)

XX Human anti-CD40 antibody 23-28-1 full length light chain cDNA.

XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; light chain; ss; gene; 23-28-1.

XX Homo sapiens.

XX WO2003040170-A2.

XX PD 15-MAY-2003.

XX 08-NOV-2002; 2002WO-US036107.

XX 09-NOV-2001; 2001US-0348980P.

XX (PFIZ ) PFIZER PROD INC.

XX (ABGE-) ABGENIX INC.

XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX WPI; 2003-441521/41.

XX P-PSDB; ADE28465.

XX New chimeric or human monoclonal antibody or its antigen-binding portion  
PT that specifically binds to and activates human CD40, useful for enhancing  
PT an immune response in a human, or treating cancer, HIV, neutropenia or  
PT viral infections.

XX Claim 24; SEQ ID NO 71; 177pp; English.

XX The invention relates to a novel chimeric or human monoclonal antibody or  
CC its antigen-binding portion that specifically binds to and activates  
CC human CD40. The anti-CD40 antibody of the invention demonstrates  
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
CC activities and may be useful for treating a hyperproliferative disorder  
CC such as cancer, viral and bacterial infection or genetic, primary or  
CC combined immunodeficiency conditions including neutropenia or HIV  
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
CC in a biological sample in vitro or in vivo, as well as during gene  
CC therapy procedures. The current sequence is that of the human anti-CD40  
CC antibody full length light chain cDNA of the invention.

XX Sequence 720 BP; 172 A; 195 C; 191 G; 161 T; 0 U; 1 Other;

Query Match 78.4%; Score 272.8; DB 10; Length 720;

Best Local Similarity 86.5%; Pred. No. 1.6e-73;

Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTACCCCTGGAGAGCGGCTCC 60

DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTACCCCTGGAGAGCGGCTCC 120

QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAGACATATTGAATTGG 120

DB 121 ATCTCTGTCAGGCTAGTCAGAGCTCTCCTGTATAGTAATGATATTAATCTGGATTGG 180

QY 121 TACTGTGAGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGTGATGTCACCCCGGCA 180

DB 181 TACTGTGAGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGTGATGTCACCCCGGCA 240

QY 181 TCAGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

DB 241 TCCGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300

|||||

Db 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAAACTCCT 360  
 QY 301 TTCACGTTTGGCCCAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348  
 Db 361 CGGACGTTTGGCCCAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 408

## RESULT 12

ABSS1811  
 ID ABSS1811 standard; cDNA; 1081 BP.

AC ABSS1811;  
 XX

DT 21-OCT-2002 (first entry)  
 XX

DE Human mddt cDNA Incyte ID No: LI:1171219.2:2001JAN12.  
 XX

KW Human; molecule for disease detection and treatment; MDDT; cancer;  
 KW cell proliferative disorder; arteriosclerosis; cirrhosis; asthma;  
 KW autoimmune disorder; inflammatory disorder; Crohn's disease;  
 KW multiple sclerosis; cytostatic; antiarteriosclerotic; antiinflammatory;  
 KW hepatotropic; immunosuppressive; antiasthmatic; gene therapy; gene; ss.  
 XX

OS Homo sapiens.  
 XX

PN WO200255738-A2.  
 XX

PD 18-JUL-2002.  
 XX

PF 09-JAN-2002; 2002WO-US0001008.  
 XX

PR 12-JAN-2001; 2001US-0261622P.  
 XX

PR 16-JAN-2001; 2001US-0261865P.  
 XX

PR 17-JAN-2001; 2001US-0262208P.  
 XX

PR 17-JAN-2001; 2001US-0262209P.  
 XX

PR 17-JAN-2001; 2001US-0262326P.  
 XX

PR 19-JAN-2001; 2001US-0263063P.  
 XX

PR 19-JAN-2001; 2001US-0263065P.  
 XX

PR 19-JAN-2001; 2001US-0263329P.  
 XX

XX (INCY-) INCYTE GENOMICS INC.  
 XX

XX Panzer SR, Lincoln SE, Altus CM, Dufour GE, Hillman JL, Jones AL;  
 PI Dam TC, Liu TP, Harris B, Flores V, Daffo A, Marwaha R, Chen AJ;  
 PI Chang SC, Gerstin EH, Peralta CH, David MH, Lewis SA;  
 XX

DR WPI; 2002-590679/63.  
 DR P-PSDB; ABG70338.

XX New disease detection and treatment molecule (MDDT) polynucleotides and  
 XX polypeptides, useful in diagnosing, studying, preventing or treating  
 PT diseases associated with MDDT expression, e.g. autoimmune or inflammatory  
 PT disorders.  
 XX

XX Claim 1; Page 105; 129pp; English.  
 XX

CC The present invention relates to the isolation of novel human molecules  
 CC for disease detection and treatment (MDDT), and the polynucleotide  
 CC sequences (mddt) encoding them. The MDDT polypeptides may be used to  
 CC screen for molecules that bind to, or are bound by the encoded  
 CC polypeptides, and to develop a transcript image of a tissue or cell type.  
 CC Probes comprising at least 20 nucleotides of the mddt polynucleotide may  
 CC be used to assess the toxicity of a test compound. The MDDT polypeptides  
 CC and mddt polynucleotides are useful in the diagnosis, study, prevention  
 CC and treatment of diseases associated with the expression of molecules for  
 CC disease detection and treatment. Such disorders include cell  
 CC proliferative disorders (e.g. arteriosclerosis, cirrhosis, or cancers),  
 CC and autoimmune/inflammatory disorders (e.g. asthma, Crohn's disease, or  
 CC multiple sclerosis). The mddt polynucleotides may also be used as  
 CC molecule markers, in microarrays, and in somatic or germline gene  
 CC therapy. ABSS1779-ABSS1814 encode the MDDT proteins of the invention  
 XX  
 XX Sequence 1081 BP; 255 A; 303 C; 276 G; 247 T; 0 U; 0 Other;

Query Match 78.4%; Score 272.8; DB 6; Length 1081;  
 Best Local Similarity 86.5%; Pred. No. 1.9e-73;  
 Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCTCC 60  
 Db 87 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCTCC 146  
 QY 61 AFTCTCTGTGCTCGAGTAAGAGTCTCTGTATTAAGGATGGAGACACATCTTGAATTGG 120  
 Db 147 ATCTCTCTGAGGTCTAGTCAGAGCCTCTCTGCATAGTAATGGAACAACATTTTGAATTGG 206  
 QY 121 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCCCTGATCTATTTCATGTCACCCCGGCA 180  
 Db 207 TTCTTGCAGAAGCCAGGCGAGCTCCACAGCTCCCTGATCTATTTCATGTCACCCCGGCA 266  
 QY 181 TCAGGGGTCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 240  
 Db 267 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 326  
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300  
 Db 327 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCATGCAAGTAGTACAAATACCT 386  
 QY 301 TTCACGTTTGGCCCAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348  
 Db 387 TCCACTTTCCGGCGGAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 434

## RESULT 13

AAAL3928  
 ID AAAL3928 standard; DNA; 720 BP.

AC AAAL3928;  
 XX

DT 02-AUG-2000 (first entry)  
 XX

DE Human PTHrP monoclonal antibody clone 4B4-6-21 DNA SEQ ID NO:19.  
 XX

KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingivitis; sepsis;  
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
 KW antiarthritic; cytostatic; antiinflammatory; ds.  
 XX

OS Homo sapiens.  
 XX

PN JP2000080100-A.  
 XX

PD 21-MAR-2000.  
 XX

XX 12-OCT-1998; 98JP-00304793.  
 XX

PR 17-JUN-1998; 98JP-00188196.  
 PR 26-JUN-1998; 98JP-00196729.

XX (NIBS) JAPAN TOBACCO INC.  
 XX

PA WPI; 2000-286723/25.  
 XX

DR P-PSDB; AAY82618.  
 XX

PT A human monoclonal antibody to parathyroid hormone related protein.  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain.  
 XX

XX Example 10; Page 53-54; 88pp; Japanese.  
 XX

CC The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood

CC calcium content. The monoclonal antibody can be used in the treatment of  
CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
CC diseases and gingivae, sepsis, systemic inflammatory response syndrome  
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
CC antiinflammatory activities. The present sequence represents a human  
CC pHRp monoclonal antibody clone nucleotide sequence from the present  
CC invention  
XX  
SQ Sequence 720 BP; 174 A; 191 C; 186 G; 162 T; 0 U; 7 Other;

Query Match	78.3%	Score 272.4	DB 3	Length 720
Best Local Similarity	86.2%	Pred. No. 2.2e-73		
Matches 300	Conservative 0	Mismatches 48	Indels 0	Gaps 0
Qy	1	GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGCGCTCC	60	
Db	61	GATATTGTGATGANTCAGTTCACATCTCTCCCTGCCCGTCACCCCTGGAGAGCGCGCTCC	120	
Qy	61	ATCTCCTGTGTGCTCGAGTAAAGAGTCTCTGTATTAAGGATGGAAAGACATACTTCGAATTGG	120	
Db	121	ATCTCCTCGAGGTCTAGTCAGAGCCTCTCGAATAGTAATGATACNACTATTTCGATTGG	180	
Qy	121	TACCTGCAGAAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATGTCCACCCGGGCA	180	
Db	181	TACCTGCAGAAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGGGTTCATTAATCGGSC	240	
Qy	181	TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	240	
Db	241	TCGGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	300	
Qy	241	AGCAGAGTGGAGGTGAGGAGTGTGGGGTGTATTTACTGTCAAAGCTGGTAGAGTATCCA	300	
Db	301	AGCAGAGTGGAGGTGAGGAGTGTGGGGTGTATTTACTGTCATGCACTGCAAACTCTACAACCTCA	360	
Qy	301	TTCACTGTTGGGCCAAGGGAACCAAGGTGGAGATCAAAAGTCAGGTGGCT	348	
Db	361	TTCACTTTTCGGCCCTGGGACCAAAAGTGGATCAAAAGAACTGTGGCT	408	

RESULT 14  
AAAI3920  
ID AAA13920 standard; DNA; 720 BP.  
XX  
XX  
AC  
AAAI3920;  
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DT  
02-AUG-2000 (first entry)  
XX  
DE  
Human PThrP monoclonal antibody clone 15H7-8-3 DNA SEQ ID NO:3.

Human; parathyroid hormone related protein; PTHrP; monoclonal antibody; hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain; fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis; systemic inflammatory response syndrome; SIRS; hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.

**Homo sapiens.**

JP2000080100-A.

21-MAR-2000

12-00T-1998: 98.TD-00304793

17-TTN-1000. 00TB-00100100

26-JUN-1998; 98JP-00196729.

(NISB) JAPAN TOBACCO INC.

WPI; 2000-286723/25.

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[illegible]

PT useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone  
PT including metastasis, and pain.

Example 10; Page 31-32; 88pp; Japanese.

The present invention describes a human monoclonal antibody to parathyroid hormone related protein (PTHrP). The monoclonal antibody or its fragments, following the stimulation of PTHrP has the following properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits the release of calcium from bone; or (c) inhibits elevation of blood calcium content. The monoclonal antibody can be used in the treatment of hypercalcaemia, rheumatoid arthritis, cancer of bone including metastasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingiva, sepsis, systemic inflammatory response syndrome (SIRS) and hypophosphataemia. It has antarthritic, cytostatic and anti-inflammatory activities. The present sequence represents a human PTHrP monoclonal antibody clone nucleotide sequence from the present invention

XX  
SQ Sequence 720 BP; 174 A; 191 C; 188 G; 164 T; 0 U; 3 Other;

Query Match	78.1%	Score 271.8;	DB 3;	Length 720;
Best Local Similarity	86.2%;	Pred. No. 3.3e-73;		
Matches 300;	Conservative	0;	Mismatches 48;	Indels 0;
Matches 300;	Conservative	0;	Mismatches 48;	Indels 0;

Qy	1	61	120
GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCA	60	GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCA	GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCA
CGCCCTGAGAGCGCGGCTCC		CGCCCTGAGAGCGCGGCTCC	CGCCCTGAGAGCGCGGCTCC

Qy 61 ATCTCTGTGCTCGAGTAAGAGTCTCCTGTATAGCATGGGAAGACATCTTGAATTGG 120

Db 121 ATTTCTGCGAGTTTGTGACAGCCCTCTGCATAGTAATGGAACAACATTTTGGATTGG 180

Qy	121	TACCTCAGAA	GCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGCA	180
Db <th>181</th> <th>TACCTCAGAA</th> <th>GCCAGGGCAGTCTCCACAGTTCCTGATCTATTTGGGTTCTAATCGGGCC</th> <th>240</th>	181	TACCTCAGAA	GCCAGGGCAGTCTCCACAGTTCCTGATCTATTTGGGTTCTAATCGGGCC	240

Qy	181	TCAGGGGTCCCTGACAGGTTTCAGTGGCAGAGATTCAGTGGAAATC	240
Db <th>241</th> <th>TCCGGGGTCCCTGACAGGTTTCAGTGGCAGAGATTCAGTGGAAATC</th> <th>300</th>	241	TCCGGGGTCCCTGACAGGTTTCAGTGGCAGAGATTCAGTGGAAATC	300

Qy	241	AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTA	CTGTCAA	CAGCTGGTGAGTATCCA	300
		AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTA <td>CTGTCAA <td>CAGCTGGTGAGTATCCA <td></td> </td></td>	CTGTCAA <td>CAGCTGGTGAGTATCCA <td></td> </td>	CAGCTGGTGAGTATCCA <td></td>	
Db	301 <td>AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTA <td>CTGTCAA <td>CAGCTCTACAAACTCCA <td>360</td> </td></td></td>	AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTA <td>CTGTCAA <td>CAGCTCTACAAACTCCA <td>360</td> </td></td>	CTGTCAA <td>CAGCTCTACAAACTCCA <td>360</td> </td>	CAGCTCTACAAACTCCA <td>360</td>	360
		AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTA <td>CTGTCAA <td>CAGCTCTACAAACTCCA</td> <td></td> </td>	CTGTCAA <td>CAGCTCTACAAACTCCA</td> <td></td>	CAGCTCTACAAACTCCA	

**Qy**

301 TTCAAGTTCGGCCAAGGGACCAAGGTGGAGATCAAACGTACGCTGCCT 348  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

**Dδ**

.361 TTCACTTTCGGCCCTGGGACCAAGTGGATATCAAACGAACCTGTGCCT 408

RESULT 15

ID ABZ22313 standard; DNA; 649 BP.

AC ABZ22313:

XX DT 20-MAR-2003 (first entry)

DE S pneumoniae pps-3 antibody at light chain dna sequence SEQ ID NO. 8

XX  
XIX Antinnoimmocccccc]. antihody: monoclonal antihody: infection. ppg-2.  
XX

Streptococcus pneumoniae; capsular polysaccharide; gene; ds.  
KW  
vv

OS Streptococcus pneumoniae.

XXX

XX  
XXXX  
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130681060-007007 / 7007-171-01

PK 18-MAY-2001; 200105-023149ZF:

```
XX (PIRO/) PIROFSKY L.
PA (ZHON/) ZHONG Z.
PA (CHAN/) CHANG Q.
XX
XX PI Pirofsky L, Zhong Z, Chang Q;
XX
XX WPI; 2003-120598/11.
XX
XX New antibody or its antigen-binding fragment that specifically binds the
PT capsular polysaccharide of Streptococcus pneumoniae serotype 3, useful
PT for treating, inhibiting or preventing S. pneumoniae infections.
XX
XX Claim 27; Fig 6C; 56pp; English.
XX
XX The present invention describes an antibody or its antigen-binding
CC fragment (I) that specifically binds the capsular polysaccharide of
CC Streptococcus pneumoniae serotype 3 (S. pneumoniae PPS-3), comprising a
CC heavy and/or light chain amino acid sequence. (I) has antibacterial
CC activity and can be used in vaccines. The anti-S. pneumoniae PPS-3
CC antibody or its antigen-binding fragment is useful for treating,
CC inhibiting or preventing S. pneumoniae infections or conditions or
CC disorders caused by the infection. Methods from the present invention can
CC be used for preventing or reducing the severity of conditions or
CC disorders caused by S. pneumoniae serotype 3 infection, or for increasing
CC the resistance of a subject to infection by S. pneumoniae serotype 3. The
CC present sequence represents a S. pneumoniae PPS-3 antibody light chain
CC DNA sequence from the present invention
XX
XX Sequence 649 BP; 167 A; 182 C; 160 G; 137 T; 0 U; 3 Other;
SQ
Query Match 77.9%; Score 271.2; DB 8; Length 649;
Best Local Similarity 86.2%; Pred. No. 4.9e-73;
Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGACCGGCTCC 60
DB 1 GATATTGAGCTCACTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGACCGGCTCC 60
QY 61 ATCTCCTGTGCTCGAGTAAAGTCTCCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
DB 61 ATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTGGATTGG 120
QY 121 TACCTGCAGAGCCAGGGCAGTCTCCACAGCTCCTCATCTATTGTATGTCACCCCGGCA 180
DB 121 TACCTGCAGAAAGCCAGGGCAGTCTCCACAGCTCCTCATCTATTGTGGTCTAATCGGGCC 180
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240
DB 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240
QY 241 AGCAGAGTGAGGCTCAGAGATGTTGGGGTTTATCTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGCAGAGTGAGGCTCAGAGATGTTGGGGTTTATCTGTCAACAGCTGGTAGAGTATCCA 300
QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 348
DB 301 CGGACGTTCCGCCAAGGACCAAGGTGGAAATCAAAAGCACTGTGGCT 348
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Search completed: April 18, 2005, 11:34:45  
Job time : 196.759 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
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(without alignments)  
2228.534 Million cell updates/sec

Title: US-09-674-716B-17  
Perfect score: 348  
Sequence: 1 gatattgtgatgactcagtc.....agatcaaacgtacgtggtgct 348

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
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11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
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13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.6	79.8	720	17	US-10-292-088-39
2	274.4	78.9	720	17	US-10-292-088-15
3	272.8	78.4	720	17	US-10-292-088-55
4	272.8	78.4	720	17	US-10-292-088-63
5	272.8	78.4	1081	17	US-10-466-164-33
6	271.2	77.9	649	19	US-10-714-079C-8
7	271.2	77.9	720	17	US-10-292-088-7
8	269.8	77.5	337	17	US-10-292-088-35
9	269.8	77.5	337	19	US-10-638-265-11
10	269.8	77.5	337	19	US-10-638-265-31
11	269.6	77.5	720	17	US-10-292-088-79
Sequence 39, Appl					
Sequence 15, Appl					
Sequence 55, Appl					
Sequence 63, Appl					
Sequence 33, Appl					
Sequence 8, Appl					
Sequence 7, Appl					
Sequence 35, Appl					
Sequence 11, Appl					
Sequence 31, Appl					
Sequence 79, Appl					

ALIGNMENTS

RESULT 1

US-10-292-088-39  
; Sequence 39, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-292-088-39

Query Match 79.8%; Score 277.6; DB 17; Length 720;  
Best Local Similarity 87.4%; Pred. No. 1.1e-84;  
Matches 304; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
QY 1 GATATTGTGATGACTCAGTCTCCACCTCTCCCTCGCGTCCACCCCTCGAGAGCGGCTCC 60  
Db 61 GATATTGTGATGACTCAGTCTCCACCTCTCCCTCGCGTCCACCCCTCGAGAGCGGCTCC 120  
QY 61 ATCTCTCTGCTCGAGTAAAGTCTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120

Db 121 ATCTCTCGAGGCTAGTCAGAGTGTCTGTATAGTAATGATACAACTATTTTGGATTGG 180  
Qy 121 TACCTCGAAGCCAGGAGTCTCCACAGCTCTGATCTATTGATGTCCACCGGGCA 180  
Db 181 TACCTCGAAGCCAGGAGTCTCCACAGCTCTGATCTATTGAGTTCTAATCGGGCC 240  
Qy 181 TCAGGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 241 TCCGGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300  
Qy 241 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 300  
Db 301 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 360  
Qy 301 TTCAAGTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348  
Db 361 TTCACTTTCCGGCCCTGGACCAAGTGGATATCAAAAGTACGGTGGCT 408

## RESULT 2

US-10-292-088-15  
; Sequence 15, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-292-088-15

Query Match 78.9%; Score 274.4; DB 17; Length 720;  
Best Local Similarity 86.8%; Pred. No. 1.4e-83;  
Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGGAGAGCGGCTCC 60  
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGGAGAGCGGCTCC 120  
Qy 61 ATCTCTGCTCGCTAGAGTAAAGTCTCTGTATAGTAATGATACAACTATTTTGGATTGG 120  
Db 121 ATCTCTGCTCGCTAGTTCAGAGCTCTGTATAGTAATGATACAACTATTTTGGATTGG 180  
Qy 121 TACCTCGAAGCCAGGAGTCTCCACAGCTCTGATCTATTGATGTCCACCGGGCA 180  
Db 181 TACCTCGAAGCCAGGAGTCTCCACAGCTCTGATCTATTGAGTTCTAATCGGGCC 240  
Qy 181 TCAGGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 241 TCCGGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300  
Qy 241 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 300  
Db 301 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 360  
Qy 301 TTCAAGTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348  
Db 361 CGGACGTTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 408

## RESULT 3

US-10-292-088-55  
; Sequence 55, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 55  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-292-088-55

Query Match 78.4%; Score 272.8; DB 17; Length 720;  
Best Local Similarity 86.5%; Pred. No. 5.1e-83;  
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGGAGAGCGGCTCC 60  
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGGAGAGCGGCTCC 120  
Qy 61 ATCTCTGCTCGCTAGAGTAAAGTCTCTGTATAGTAATGATACAACTATTGATTTGG 120  
Db 121 ATCTCTGCTCGCTAGTTCAGAGCTCTGTATAGTAATGATACAACTATTGATTTGG 180  
Qy 121 TACCTCGAAGCCAGGAGTCTCCACAGCTCTGATCTATTGATGTCCACCGGGCA 180  
Db 181 TACCTCGAAGCCAGGAGTCTCCACAGCTCTGATCTATTGAGTTCTAATCGGGCC 240  
Qy 181 TCAGGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
Db 241 TCCGGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300  
Qy 241 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 300  
Db 301 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 360  
Qy 301 TTCAAGTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348  
Db 361 CGGACGTTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 408

## RESULT 4

US-10-292-088-63  
; Sequence 63, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 63  
; LENGTH: 720  
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-292-088-63

Query Match      78.4%; Score 272.8; DB 17; Length 720;
Best Local Similarity 86.5%; Pred. No. 5.1e-83;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTACCCCTGGAGAGCGGCTCC 60
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTACCCCTGGAGAGCGGCTCC 120

Qy 61 ATCTCTGTCGTCGAGTAAGTCTCTCTGATTAAGGATGGAGACATACCTTGAATTGG 120
Db 121 ATCTCTGTCGAGGTCTAGTCAGAGCTCTCTGCTGTAATGGATACACTATTTGGATTGG 180

Qy 121 TACTCTGAGAAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCCGGCA 180
Db 181 TACTCTGAGAAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCTGCGGCC 240

Qy 181 TCAGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240
Db 241 TCGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 300

Qy 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 301 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 360

Qy 301 TTCACGTTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348
Db 361 CGGACGTTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 408
```

```
RESULT 5
US-10-466-164-33
; Sequence 33, Application US/10466164
; Publication No. US20040058365A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; PANZER, Scott R.;
; APPLICANT: LINCOLN, Stephen E.; ALTUS, Christina M.;
; APPLICANT: DUFOUR, Gerard E.; JACKSON, Jennifer L.;
; APPLICANT: JONES, Anissa L.; DAM, Tam C.;
; APPLICANT: LIU, Tommy F.; HARRIS, Bernard;
; APPLICANT: FLORES, Vincent Z.; DAPFO, Abel;
; APPLICANT: MARWAHA, Rakesh; CHEN, Alice J.;
; APPLICANT: CHANG, Simon C.; GERSTIN, Jr., Edward H.;
; APPLICANT: PERALTA, Careyna H.; DAVID, Marie H.;
; APPLICANT: LEWIS, Samantha A.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1215 PCT
; CURRENT APPLICATION NUMBER: US/10/466,164
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/US02/01008
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,865
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/263,065
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/263,329
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/262,209
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,326
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/263,063
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/261,622
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 1081
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20040058365A1 LI:1171219.2:2001JAN12
US-10-466-164-33

Query Match      78.4%; Score 272.8; DB 17; Length 1081;
Best Local Similarity 86.5%; Pred. No. 5.9e-83;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTACCCCTGGAGAGCGGCTCC 60
Db 87 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTACCCCTGGAGAGCGGCTCC 146

Qy 61 ATCTCTGTCGTCGAGTAAGTCTCTCTGTAAGGATGGGAAGACATACCTTGAATTGG 120
Db 147 ATCTCTGTCGAGGTCTAGTCAGAGCTCTCTGCAATAGTAATGGAAACAACATTTTGGATTGG 206

Qy 121 TACTCTGAGAAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCCGGCA 180
Db 207 TCTCTGAGAAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTTGGTCTAGTCTGGGCC 266

Qy 181 TCAGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240
Db 267 TCGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 326

Qy 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 327 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGTACAAATACCT 386

Qy 301 TTCACGTTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348
Db 387 TCCACTTTTCGGCGGAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 434
```

```
RESULT 6
US-10-714-079C-8
; Sequence 8, Application US/10714079C
; Publication No. US20050014931A1
; GENERAL INFORMATION:
; APPLICANT: PIROFSKI, LIISE-ANNE
; APPLICANT: ZHONG, ZHAOJING
; APPLICANT: CHANG, QING
; TITLE OF INVENTION: HUMAN ANTIPNEUMOCOCCAL ANTIBODIES FROM NON-HUMAN
; TITLE OF INVENTION: ANIMALS
; FILE REFERENCE: ABX-AE1 CON
; CURRENT APPLICATION NUMBER: US/10/714,079C
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: PCT/US02/18363
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/291,492
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (462)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (495)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (513)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-714-079C-8
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Query Match 77.9%; Score 271.2; DB 19; Length 649;  
Best Local Similarity 86.2%; Pred. No. 1.8e-82;  
Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60  
DB 1 GATATTGAGCTCACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60

QY 61 ATCTCTGTGCTGCGTGAAGTCTCCTGTATAGATGGGAAGACATACCTTGAATTGG 120  
DB 61 ATCTCTGTGAGTCTAGTCAGAGCTCTCCGTAGTAATAGGATACAACTATTGGATTGG 120

QY 121 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCCTCATCTATTGTATGTTCCACCGGGCA 180  
DB 121 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCCTCATCTATTGTGGTCTTAATCGGGC 180

QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
DB 181 TCCGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

QY 241 AGCAGAGTGAGCTGAGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300  
DB 241 AGCAGAGTGAGCTGAGATGTTGGGGTTTATTACTGTCAATGCAAGCTTACAAACTCCT 300

QY 301 TTCACGTTTCGGCCAAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 348  
DB 301 CGGAGTTTCGGCCAAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 348

## RESULT 7

US-10-292-088-7

; Sequence 7, Application US/10292088

; Publication No. US20030211100A1

; GENERAL INFORMATION:

; APPLICANT: BEDIAN, VAHE

; APPLICANT: GLADUE, RONALD P.

; APPLICANT: CORVALAN, JOSE

; APPLICANT: JIA, XIAO-CHI

; APPLICANT: FENG, XIAO

; TITLE OF INVENTION: ANTIBODIES TO CD40

; FILE REFERENCE: ABX-PF/3 US

; CURRENT APPLICATION NUMBER: US/10/292,088

; CURRENT FILING DATE: 2003-03-14

; PRIOR APPLICATION NUMBER: 60/348,980

; PRIOR FILING DATE: 2001-11-09

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 720

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-292-088-7

Query Match 77.9%; Score 271.2; DB 17; Length 720;  
Best Local Similarity 86.2%; Pred. No. 1.8e-82;  
Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60  
DB 61 GATATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 120

QY 61 ATCTCTGTGCTGCGTGAAGTCTCCTGTATAGATGGGAAGACATACCTTGAATTGG 120  
DB 121 ATCTCTGTGAGTCTAGTCAGAGCTCTTGTATAGTAATGATACAACTTTTGGATTGG 180

QY 121 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCCTCATCTATTGTATGTTCCACCGGGCA 180  
DB 181 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCCTCATCTATTGTGGTCTTAATCGGGC 240

QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
DB 241 TCCGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 301 AGCAGATTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAAGCTCTACAACTCCT 360

QY 301 TTCACGTTTCGGCCAAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 348  
DB 361 CGGAGTTTCGGCCAAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 408

## RESULT 8

US-10-292-088-35

; Sequence 35, Application US/10292088

; Publication No. US20030211100A1

; GENERAL INFORMATION:

; APPLICANT: BEDIAN, VAHE

; APPLICANT: GLADUE, RONALD P.

; APPLICANT: CORVALAN, JOSE

; APPLICANT: JIA, XIAO-CHI

; APPLICANT: FENG, XIAO

; TITLE OF INVENTION: ANTIBODIES TO CD40

; FILE REFERENCE: ABX-PF/3 US

; CURRENT APPLICATION NUMBER: US/10/292,088

; CURRENT FILING DATE: 2003-03-14

; PRIOR APPLICATION NUMBER: 60/348,980

; PRIOR FILING DATE: 2001-11-09

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 35

; LENGTH: 337

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-292-088-35

Query Match 77.5%; Score 269.8; DB 17; Length 337;  
Best Local Similarity 87.5%; Pred. No. 4.3e-82;  
Matches 295; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60  
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60

QY 61 ATCTCTGTGCTGCGTGAAGTCTCCTGTATAGATGGGAAGACATACCTTGAATTGG 120  
DB 61 ATCTCTGTGCTGCGTGAAGTCTCCTGTATAGATGGGAAGACATACCTTGAATTGG 120

QY 121 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCCTCATCTATTGTATGTTCCACCGGGCA 180  
DB 121 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCCTCATCTATTGTGGTCTTAATCGGGC 180

QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
DB 181 TCCGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAAGCTTTTACAACTCCA 300

QY 301 TTCACGTTTCGGCCAAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 337  
DB 301 TTCACGTTTCGGCCCTGGGACCAAGGTGGATATCAAACT 337

## RESULT 9

US-10-638-265-11

; Sequence 11, Application US/10638265

; Publication No. US20050031614A1

; GENERAL INFORMATION:

; APPLICANT: Roskos, Lorin

; APPLICANT: Foltz, Ian

; APPLICANT: King, Chadwick

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID

; TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF

; FILE REFERENCE: ABGENIX.092A

; CURRENT APPLICATION NUMBER: US/10/638,265  
; CURRENT FILING DATE: 2003-08-08  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 337  
; TYPE: DNA  
; ORGANISM: Homosapien  
US-10-638-265-11

Query Match 77.5%; Score 269.8; DB 19; Length 337;  
Best Local Similarity 87.5%; Pred. No. 4.3e-82;  
Matches 295; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCGTCCCTGAGAGCGCGCTCC 60  
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCGTCCCTGAGAGCGCGCTCC 60  
QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATATCTTGAATTGG 120  
DB 61 ATCTCTGTGAGTCTAGTCAGAGCTCTCTGTATAGTAATGATACAAATATTTGGATTGG 120  
QY 121 TACCTGAGAACCCAGGCGAGTCTCCACAGTCTCTGATCTATTGTGTCACCGCGGCA 180  
DB 121 TACCTGAGAACCCAGGCGAGTCTCCACAGTCTCTGATCTATTTTGGGTTCTTATCGGGCC 180  
QY 181 TCAGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
DB 181 TCAGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAAAC 337  
DB 301 TGGACGTTGGCCCAAGGACCAAGTGGAAATCAAAAC 337

## RESULT 10

US-10-638-265-31

; Sequence 31, Application US/10638265

; Publication No. US20050031614A1

; GENERAL INFORMATION:

; APPLICANT: Roskos, Lorin

; APPLICANT: Foltz, Ian

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID

; FILE REFERENCE: HORMONE (PTH) AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/10/638,265

; CURRENT FILING DATE: 2003-08-08

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 31

; LENGTH: 337

; TYPE: DNA

; ORGANISM: Homosapien

US-10-638-265-31

Query Match 77.5%; Score 269.8; DB 19; Length 337;  
Best Local Similarity 87.5%; Pred. No. 4.3e-82;  
Matches 295; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCGTCCCTGAGAGCGCGCTCC 60  
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCGTCCCTGAGAGCGCGCTCC 60  
QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATATCTTGAATTGG 120  
DB 61 ATCTCTGTGAGTCTAGTCAGAGCTCTCTGTATAGTAATGATACAAATATTTGGATTGG 120  
QY 121 TACCTGAGAACCCAGGCGAGTCTCCACAGTCTCTGATCTATTGTGTCACCGCGGCA 180

DB 121 TTCTCTGCAGAAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTTGGGTTCTAATCGGGCC 180  
QY 181 TCAGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
DB 181 TCAGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAAAC 337  
DB 301 TGGACGTTGGCCCAAGGACCAAGTGGAAATCAAAAC 337

RESULT 11  
US-10-292-088-79  
; Sequence 79, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 79  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-292-088-79

Query Match 77.5%; Score 269.6; DB 17; Length 720;  
Best Local Similarity 85.9%; Pred. No. 6.5e-82;  
Matches 299; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCGTCCCTGAGAGCGCGCTCC 60  
DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCGTCCCTGAGAGCGCGCTCC 120  
QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCTGTATAAGGATGGGAAGACATATCTTGAATTGG 120  
DB 121 ATCTCTGTGAGTCTAGTCAGAGCTCTCTGCGTGGTAATGGATCAACTATTTGGATTGG 180  
QY 121 TACCTGAGAACCCAGGCGAGTCTCCACAGTCTCTGATCTATTGTGTCACCGCGGCA 180  
DB 181 TACCTGAGAACCCAGGCGAGTCTCCACAGTCTCTGATCTATTTTGGGTTCTAATCGGGCC 240  
QY 181 TCAGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
DB 241 TCAGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300  
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAAAC 337  
DB 361 CGGACGTTCTCGGCCAGGACCAAGTGGAAATCAAAAC 408

## RESULT 12

US-10-292-088-101

; Sequence 101, Application US/10292088

; Publication No. US20030211100A1

```

; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-101

Query Match      77.5%; Score 269.6; DB 17; Length 720;
Best Local Similarity 85.9%; Pred. No. 6.5e-82;
Matches 299; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY      1  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCAACCCCTGGAGAGCGGCTCC 60
DB      1  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCAACCCCTGGAGAGCGGCTCC 60

QY      61  ATCTCTCTGCTCGCTCGAGTAAGAGTCTCTCTGTATTAAGTAGGGAGACACATATCTTGAATTGG 120
DB      61  ATCTCTCTGAGTCTTAGTCAGAGCCCTCTCGATAGTAAATGATACAAATATTTGGATTGG 120

QY      121  TACCTGCAAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGATGTCCACCCGGGCA 180
DB      121  TTCTCTGCAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGGTCTTATTCGGGCC 180

QY      181  TCAGGGGTCCCTGCACAGGTTCACTGTCAGTGGATGATCAGGCACAGATTTTACACTGAAAAATC 240
DB      181  TCCGGGGTCCCTGCACAGGTTCACTGTCAGTGGATGATCAGGCACAGATTTTACACTGAAAAATC 240

QY      241  AGCAGAGTGGAGGCTGAGGATTTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB      241  AGCAGAGTGGAGGCTGAGGATTTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300

QY      301  TTCAGCTTGGGCAAGGACCAAGGTGGAGATCAAAAC 337
DB      301  TGGACGTTTGGGCCAAGGACCAAGGTGGAAATCAAAAC 337

RESULT 14
US-10-638-265-67
; Sequence 67, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; FILE REFERENCE: ABGENIX.092A
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homosapien
US-10-638-265-67

Query Match      77.1%; Score 268.2; DB 19; Length 337;
Best Local Similarity 87.2%; Pred. No. 1.5e-81;
Matches 294; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY      1  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCAACCCCTGGAGAGCGGCTCC 60
DB      1  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCAACCCCTGGAGAGCGGCTCC 60

QY      61  ATCTCTCTGCTCGCTCGAGTAAGAGTCTCTCTGTATTAAGTAGGGAGACACATATCTTGAATTGG 120
DB      61  ATCTCTCTGAGTCTTAGTCAGAGCCCTCTCGATAGTAAATGATACAAATATTTGGATTGG 120

QY      121  TACCTGCAAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGATGTCCACCCGGGCA 180
DB      121  TACCTGCAAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGGTCTTATTCGGGCC 180

QY      181  TCAGGGGTCCCTGCACAGGTTCACTGTCAGTGGATGATCAGGCACAGATTTTACACTGAAAAATC 240
DB      181  TCCGGGGTCCCTGCACAGGTTCACTGTCAGTGGATGATCAGGCACAGATTTTACACTGAAAAATC 240

QY      241  AGCAGAGTGGAGGCTGAGGATTTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB      241  AGCAGAGTGGAGGCTGAGGATTTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300

QY      301  TTCAGCTTGGGCAAGGACCAAGGTGGAGATCAAAAC 337
DB      301  TGGACGTTTGGGCCAAGGACCAAGGTGGAAATCAAAAC 337

RESULT 13
US-10-638-265-7
; Sequence 7, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; FILE REFERENCE: ABGENIX.092A
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homosapien
US-10-638-265-7

Query Match      77.1%; Score 268.2; DB 19; Length 337;
Best Local Similarity 87.2%; Pred. No. 1.5e-81;
Matches 294; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY      1  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCAACCCCTGGAGAGCGGCTCC 60
DB      1  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCAACCCCTGGAGAGCGGCTCC 60

QY      61  ATCTCTCTGCTCGCTCGAGTAAGAGTCTCTCTGTATTAAGTAGGGAGACACATATCTTGAATTGG 120
DB      61  ATCTCTCTGAGTCTTAGTCAGAGCCCTCTCGATAGTAAATGATACAAATATTTGGATTGG 120

QY      121  TACCTGCAAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGATGTCCACCCGGGCA 180
DB      121  TACCTGCAAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGGTCTTATTCGGGCC 180

QY      181  TCAGGGGTCCCTGCACAGGTTCACTGTCAGTGGATGATCAGGCACAGATTTTACACTGAAAAATC 240
DB      181  TCCGGGGTCCCTGCACAGGTTCACTGTCAGTGGATGATCAGGCACAGATTTTACACTGAAAAATC 240

QY      241  AGCAGAGTGGAGGCTGAGGATTTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB      241  AGCAGAGTGGAGGCTGAGGATTTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300

QY      301  TTCAGCTTGGGCAAGGACCAAGGTGGAGATCAAAAC 337
DB      301  TGGACGTTTGGGCCAAGGACCAAGGTGGAAATCAAAAC 337
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Db 301 TGGAGTTTCGCCCAAGGACCAAGGTGGAATCAAAAC 337

## RESULT 15

US-10-292-088-31  
; Sequence 31, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-292-088-31

Query Match 77.0%; Score 268; DB 17; Length 720;  
Best Local Similarity 85.6%; Pred. No. 2.3e-81;  
Matches 298; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCCTCACCCCTGGAGAGCGGCTCC 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCCTCACCCCTGGAGAGCGGCTCC 120  
Qy 61 ATCTCTGTGCTCGAGTAGAGTCTCCTGTATAGGATGGGAAGACATATCTGAATTGG 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 ATCTCTGTGAGGTCTAGTCAGAGCTCTACATACTAATGATACAACTATTTTCGATTGG 180  
Qy 121 TACCTGCAGAGCCAGGCGCAGTCTCCACAGCTCCTGATCTATTGTGATGCCACCCGGGCA 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 TACCTGCAGAGCCAGGCGCAGTCTCCACAACTCCTGATCTATTTCGGGTTCTAATTCGGGCC 240  
Qy 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 300  
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTCAAACTCCG 360  
Qy 301 TTCACGTTTCGCCCAAGGACCAAGTGGAGATCAAACTACGTTACGGTGGCT 348  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
361 TACAGTTTGGCCAGGGGACCAAGCTGGAGATCAAACTGAGGCTGTGGCT 408

Search completed: April 19, 2005, 00:13:29  
Job time : 948.356 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 67.129 Seconds  
(without alignments)  
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Title: US-09-674-716B-17  
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfilesi.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	261.2	75.1	339	1	US-08-082-623-2
2	256.8	73.8	968	4	US-10-000-489-7
3	252.8	72.6	336	3	US-09-000-088-1
4	252	72.4	336	3	US-09-240-274-99
5	249.4	71.7	339	1	US-08-264-093-9
6	244	70.1	420	3	US-09-214-095D-111
7	244	70.1	464	1	US-08-438-123-15
8	243.6	70.0	339	2	US-08-672-345C-88
9	243.6	69.1	339	3	US-09-214-095D-99
10	240.4	69.1	368	2	US-08-672-345C-86
11	240.4	69.1	368	3	US-09-214-095D-107
12	239.2	68.7	368	2	US-08-672-345C-90
13	239.2	68.7	368	3	US-09-214-095D-103
14	239.2	68.7	666	4	US-09-479-614-25
15	239.2	68.7	666	4	US-09-479-614-27
16	239.2	68.7	726	4	US-09-479-614-23
17	239.2	68.7	726	4	US-09-479-614-24
18	239.2	68.7	954	4	US-09-479-614-19
19	239.2	68.7	954	4	US-09-479-614-21
20	238.8	68.6	339	3	US-09-406-532-13
21	231.6	66.6	375	1	US-08-482-882-65
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24	231.6	66.6	375	2	US-08-473-503-65
25	231.6	66.6	375	2	US-08-483-932-65
26	231.6	66.6	375	2	US-08-720-420A-65
27	231.6	66.6	375	3	US-08-714-017-65

28	231.6	66.6	375	3	US-08-475-680-65
29	228.8	65.7	336	3	US-08-483-749A-3
30	228.6	65.7	344	4	US-09-840-459-98
31	228.6	65.7	344	4	US-09-840-459-105
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33	228.6	65.7	344	4	US-09-497-625A-105
34	227.6	65.4	419	4	US-09-472-087-52
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36	226	64.9	399	1	US-08-253-877C-9
37	226	64.9	399	2	US-08-452-164A-9
38	226	64.9	399	3	US-08-603-024-3
39	226	64.9	399	4	US-08-450-809-2
40	225.2	64.7	882	1	US-08-392-419-3
41	224.8	64.6	720	3	US-08-487-550-5
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44	222.2	63.9	1095	3	US-08-875-811-52
45	222.2	63.9	1098	3	US-08-875-811-54

ALIGNMENTS

RESULT 1  
US-08-082-623-2  
; Sequence 2, Application US/08082623  
; Patent No. 5750106  
; GENERAL INFORMATION:  
; APPLICANT: Ostberg, Lars G.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO  
; TITLE OF INVENTION: CYTOMEGALOVIRUS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082, 623  
; FILING DATE: 25-JUN-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/010,228  
; FILING DATE: 28-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-055-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 339 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..339  
; OTHER INFORMATION: /standard\_name= "Nucleotide  
; OTHER INFORMATION: Sequence of the V-1 region of SDZ MSL 109"  
; Patent No. 5750106

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US-08-082-623-2
Query Match      75.1%; Score 261.2; DB 1; Length 339;
Best Local Similarity 85.8%; Pred. No. 6.7e-77;
Matches 290; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
   |||||
Db 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
   |||||

QY 61 ATCTCTCGCTCGAGTAAAGTCTCTCTGTAAGAGTGGGAAGACATACCTTGAATTGG 120
   |||||
Db 61 ATCTCTCGAGTCTAGTCAGAGCTCTCTGATCTAATGATGATCAACTATTGGATTGG 120
   |||||

QY 121 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCACCCGGGCA 180
   |||||
Db 121 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTGATCTAATGATGTCACCCGGGCA 180
   |||||

QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTCAGGCACAGATTTTACACTGAAATC 240
   |||||
Db 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTCAGGCACAGATTTTACACTGAAATC 240
   |||||

QY 241 AGCAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
   |||||
Db 241 AGCAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
   |||||

QY 301 TTCACGTTGGCCAGGACCAAGGTGGAGATCAAAACG 338
   |||||
Db 301 CGGACGTTGGCCAGGACCAAGGTGGAGATCAAAACG 338
   |||||

RESULT 2
US-10-000-489-7
; Sequence 7, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.056.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; NAME/KEY: CDS
; LOCATION: 32..748
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; NAME/KEY: polyA_signal
; LOCATION: 928..933
; NAME/KEY: polyA_site
; LOCATION: 953..968
; US-10-000-489-7

US-09-000-088-1
Query Match      73.8%; Score 256.8; DB 4; Length 968;
Best Local Similarity 83.6%; Pred. No. 3.1e-75;
Matches 291; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
   |||||
Db 92 GATATTGTGATGACTCAGTCTCCACTCTCTCTGCCGTCACCCCTGGAGAGCGCGCTCC 151
   |||||

QY 61 ATCTCTCTGCTCGAGTAAAGTCTCTGTAAGAGTGGGAAGACATACCTTGAATTGG 120
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Db 152 ATCTCTCTGAGTCTAGTCAGAGCTCTCTGATGTTCAAGGGTCCAACTATTGGATTGG 211
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QY 121 TACCTGCAAGACCAAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGGGCA 180
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Db 212 TACCAACAGAGACCAAGGCGAGTCTCCCAACTCTCTGATATATTGGGTTCTAATCGGGCC 271
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QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
   |||||
Db 272 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 331
   |||||

QY 241 AGCAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
   |||||
Db 332 AGTAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 391
   |||||

QY 301 TTCACGTTGGCCAGGACCAAGGTGGAGATCAAAACG 348
   |||||
Db 392 TTCACGTTGGCCAGGACCAAGGTGGAGATCAAAACG 439
   |||||

RESULT 3
US-09-000-088-1
; Sequence 1, Application US/09000088
; Patent No. 6146629
; GENERAL INFORMATION:
; APPLICANT: DAGAN, Shlomo
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST HEPATITIS B VIRUS
; TITLE OF INVENTION: SURFACE ANTIGEN (HBVSAg)
; FILE REFERENCE: DAGAN=1
; CURRENT APPLICATION NUMBER: US/09/000,088
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: PCT/IL97/00183
; EARLIER FILING DATE: 1997-06-10
; EARLIER APPLICATION NUMBER: IL96/118626
; EARLIER FILING DATE: 1996-06-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 336
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(336)
; US-09-000-088-1

Query Match      72.6%; Score 252.8; DB 3; Length 336;
Best Local Similarity 84.5%; Pred. No. 4.2e-74;
Matches 284; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
   |||||
Db 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
   |||||

QY 61 ATCTCTCTGCTCGAGTAAAGTCTCTGTAAGAGTGGGAAGACATACCTTGAATTGG 120
   |||||
Db 61 ATCTCTCTGAGTCTAGTCAGAGCTCTCTGATGATGTCGAAACACATATTGGATTGG 120
   |||||

QY 121 TACCTGCAAGACCAAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGGGCA 180
   |||||
Db 121 TACCTGCAAGACCAAGGCGAGTCTCCACAGCTCTCTGATCTATTGTTGGTTCTAATCGGGCC 180
   |||||

QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
   |||||
```

Db 181 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGAGTATACACTGAAATC 240  
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGAGCTGGTAGAGTATCCA 300  
Db 241 AGTAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGAGCTTACAACTCCT 300  
Qy 301 TTCAGGTTCCGGCCAGGAGCAGAGGTTGGAGATCAAA 336  
Db 301 CGGACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA 336

RESULT 4

US-09-240-274-99  
; Sequence 99, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; EARLIER FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 99  
; LENGTH: 336  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain G01  
US-09-240-274-99

Query Match 72.4%; Score 252; DB 3; Length 336;  
Best Local Similarity 84.9%; Pred. No. 7.7e-74;  
Matches 282; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
Qy 7 GTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCCATCTCC 66  
Db 4 GAGTCACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCCATCTCC 63  
Qy 67 TGTGCTCGAGTAAAGTCTCTGTATAGGATGGGAAGACATCTTGAATTCGTACCTG 126  
Db 64 TGCAAGTCTAGTCAGAGCTCTCTGATAGTGGATTCACATTTTGGATTTGGTACCTG 123  
Qy 127 CAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCGGGATCAGGG 186  
Db 124 CAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTATGGTTCTAATCGGGCTCCGGG 183  
Qy 187 GTCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATCAGCAGA 246  
Db 184 GTCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATCAGCAGA 243  
Qy 247 GTGAGGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCAATTCAG 306  
Db 244 GTGAGGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTTACAAATTCCTCTCACT 303  
Qy 307 TTCGGCCCAAGGACCAAGGTTGGAGATCAAAACG 338  
Db 304 TTCGGCGGAGGACCAAGGTTGGAGATCAAAACG 335

RESULT 5

US-08-264-093-9  
; Sequence 9, Application US/08264093  
; Patent No. 5639863  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. Dan  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO  
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE

; TITLE OF INVENTION: ANTIGEN  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ridout & Maybee  
; STREET: 2300 Richmond-Adelaide Centre  
; STREET: 101 Richmond Street West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 2J7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: MS-DOS 6.00  
; SOFTWARE: ASCII Editor  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/264,093  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA: No. 5639863 applicable  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lake, James R.  
; REGISTRATION NUMBER: 31081  
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 868-1482  
; TELEFAX: (416) 362-0823  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 339 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
US-08-264-093-9

Query Match 71.7%; Score 249.4; DB 1; Length 339;  
Best Local Similarity 85.5%; Pred. No. 5.7e-73;  
Matches 290; Conservative 0; Mismatches 46; Indels 3; Gaps 1;  
Qy 1 GATATTGTGATGATCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCC 60  
Db 1 GATATTGTGATGATCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCC 60  
Qy 61 ATCTCTCTGCTCGAGTAAAGTCTCTCTGTATA---AGGATGGGAAGACATCTTGAAT 117  
Db 61 ATCTCTCTGAGTCTAGTCAGAGCTCTTGGATAGTATGATGGAACACCTATTGGAC 120  
Qy 118 TGGTACCTGCAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCGG 177  
Db 121 TGGTACCTGCAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATACGCTTCTCTATCG 180  
Qy 178 GCATCAGGGGTCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAA 237  
Db 181 GCCTCTGGAGTCCCAAGACAGAGTTCAGTGGCGTGGGTGAGGATTTTACACTGAAA 240  
Qy 238 ATCAGCAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTAT 297  
Db 241 ATCAGCAGGTTGAGGCTCAGGATGTTGGAGTTTATTCTGATGCAACAGTATAGAGTTT 300  
Qy 298 CCAATTCACGTTCCGGCCAGGACCAAGGTTGGAGATCAAA 336  
Db 301 CTTTTCACCTTCGGCGGAGGACCAAGGTTGGAGATCAAA 339

RESULT 6

US-09-214-095D-111  
; Sequence 111, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D

;; CURRENT FILING DATE: 1999-07-19  
;; NUMBER OF SEQ ID NOS: 121  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 111  
;; LENGTH: 420  
;; TYPE: DNA  
;; ORGANISM: Murine  
;; FEATURE:  
;; NAME/KEY: V segment  
;; LOCATION: (1)..(403)  
;; OTHER INFORMATION: n at any position represents any nucleotide including c,g,t,a,u  
US-09-214-095D-111

Query Match 70.1%; Score 244; DB 3; Length 420;  
Best Local Similarity 81.3%; Pred. No. 3.9e-71;  
Matches 283; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCCCTGGAGAGCGGCGCTCC 60  
DB 53 GATATGGTGTGATGACGAGGATGAACCTCTCCAACTCCTGTCACTTCTGGAGAATCAGTTTCC 112  
QY 61 ATCTCTGTGCTCGAGTGAAGTCTCCTGTATAGGATGGGAAGACATCTTGAATTGG 120  
DB 113 ATCTCTGTGAGTCTAGTAGGAGTCTCCTATATAGGATGGGAAGACATCTTGAATTGG 172  
QY 121 TACCTCGAAGCGGAGTCTCCACAGCTCTCTATTTGATGTCCACCCCGGCA 180  
DB 173 TTCTCGAGAGCAGGAGCACTCTCACTCTGATCTTTGATGTCCACCCCGTGA 232  
QY 181 TCAGGGTCTCGTACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACCTGAAATC 240  
DB 233 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGAACAGATTTACCTGGAATC 292  
QY 241 ACAGAGTGAGGCTCAGATGTTGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300  
DB 293 AGTAGAGTGAAGCTCAGGATGTGGGTGTATCTGTCAACACTTTGTAGACTATCCA 352  
QY 301 TTCACGTTGGCCTCAAGGACCAAGTGGAGATCAAACTGACGTTGGCT 348  
DB 353 TTCACGTTGGCTCGGGGACAAAGTTGGAGATAAACGGGTTGATGCT 400

RESULT 7  
US-08-438-123-15  
; Sequence 15, Application US/08438123  
; Patent No. 5552293  
; GENERAL INFORMATION:  
; APPLICANT: Lindholm et al  
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lowe, Price, LeBlanc & Becker  
; STREET: Suite 300, 99 Canal Center Plaza  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: DOS Text File  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/438,123  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/906,350  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: J.G. Mullins  
; REGISTRATION NUMBER: 33073  
; REFERENCE/DOCKET NUMBER: 149-011

;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703 684 1111  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 464 base pairs  
;; TYPE: Nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-438-123-15

Query Match 70.1%; Score 244; DB 1; Length 464;  
Best Local Similarity 81.3%; Pred. No. 4.1e-71;  
Matches 283; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCCCTGGAGAGCGGCGCTCC 60  
DB 102 GATATTGTGATGACTCAGGCTGACCCCTCTGTACCTGTCTCTCTGGAGAGTCAATATCC 161  
QY 61 ATCTCTGTGCTCGAGTGAAGAGTCTCCTGTATAGGATGGGAAGACATATACTTGAATTGG 120  
DB 162 ATCTCTGTGAGTCTAGTGAAGAGTCTCTGTATAGTATATGCAACACTTACTTGAATTGG 221  
QY 121 TACCTGCAAGAGCCAGGCGAGTCTCCACAGCTCTCTGTATTTGATGTCCACCCGGCA 180  
DB 222 TTCTCTGCAAGAGCCAGGCGAGTCTCTCAGCTCTCTGTATATCGGATGTCCAACTTGTCT 281  
QY 181 TCAGGGTCTCTGACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240  
DB 282 TCAGGAGTCTCAGACAGGTTCAAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 341  
QY 241 AGCAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
DB 342 AGTAGAGTGGAGGCTGAGGATGTTGGGTGTTTATTACTGTCTGCAACACTAGAGTATCG 401  
QY 301 TTCACGTTGGCCTCAAGGACCAAGTGGAGTCAAACTGACGTTGGCT 348  
DB 402 TTCACGTTGGCTCTGGGACCAAGTGGAGTGGGCTGAAACGGGCTGATGCT 449

RESULT 8  
US-08-672-345C-88  
; Sequence 88, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 339 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-672-345C-86

Query Match 70.0%; Score 243.6; DB 2; Length 339;  
Best Local Similarity 82.5%; Pred. No. 4.8e-71;  
Matches 279; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCTGAGAGCGCGCTCC 60  
DB 1 GATATTGTGATGACCCAGGATGAATCTCCAACTCTGTCACTTCTGGAGATCAGTTTC 60  
QY 61 ATCTCTCTGCTCGCTCAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 120  
DB 61 ATCTCTCTGAGTCTAGTAGAGTCTCTATATAGGATGGGAAGACATACCTTGAATTGG 120  
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGTGATGTCCACCCGGCA 180  
DB 121 TTTCTGCAGAGACCAGGACGATCTCTCAACTCTGATCTATTGTGATGTCCACCCGTTCA 180  
QY 181 TCAGGGTCTCTGACAGGTTCACTGAGTGGGAGTGGATCAGGCACAGATTTCACCTGAAATC 240  
DB 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGAAACAGATTTCACCTGGAATC 240  
QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTATTACTGTCAACAGCTGTAGAGTATCCA 300  
DB 241 AGTAGAGTGAAGCTGAGGATGGGTGTGATTACTGTCAACACTTTGTAGACTATCCA 300  
QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACG 338  
DB 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAGATAAAACG 338

RESULT 9  
US-09-214-095D-99  
; Sequence 99, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: Patent in version 3.0.  
; SEQ ID NO 99  
; LENGTH: 339  
; TYPE: DNA  
; ORGANISM: Murine  
US-09-214-095D-99

Query Match 70.0%; Score 243.6; DB 3; Length 339;  
Best Local Similarity 82.5%; Pred. No. 4.8e-71;  
Matches 279; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCTGAGAGCGCGCTCC 60  
DB 1 GATATTGTGATGACCCAGGATGAATCTCCAACTCTGTCACTTCTGGAGATCAGTTTC 60  
QY 61 ATCTCTCTGCTCGCTCAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 120  
DB 61 ATCTCTGCAAGTCTAGTAGAGTCTCTATATAGGATGGGAAGACATACCTTGAATTGG 120  
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGTGATGTCCACCCGGCA 180  
DB 121 TTTCTGCAGAGACCAGGACGATCTCTCAACTCTGATCTATTGTGATGTCCACCCGTTCA 180  
QY 181 TCAGGGTCTCTGACAGGTTCACTGAGTGGATCAGGCACAGATTTCACCTGAAATC 240  
DB 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGAAACAGATTTCACCTGGAATC 240

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTATTACTGTCAACAGCTGTAGAGTATCCA 300  
DB 241 AGTAGAGTGAAGCTGAGGATGTTGGGTGTGATTACTGTCAACACTTTGTAGACTATCCA 300  
QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACG 338  
DB 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAGATAAAACG 338

RESULT 10  
US-08-672-345C-86  
; Sequence 86, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 368 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-672-345C-86

Query Match 69.1%; Score 240.4; DB 2; Length 368;  
Best Local Similarity 82.0%; Pred. No. 5.9e-70;  
Matches 277; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCTGAGAGCGCGCTCC 60  
DB 1 GATATTGTGATGACGCAAGACGACTCTCCAATCTGTCTACTCTGAGAAATCAGTTTC 60  
QY 61 ATCTCTCTGCTCGCTCAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 120  
DB 61 ATCTCTGCAAGTCTAGTAAGAGTCTCTATATAGGATGGGAAGACATACCTTGAATTGG 120  
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTGATGTCCACCCGGCA 180  
DB 121 TTTCTGCAGAGACCAGGCAATCTCTCACTCTCTGATCTATTGTGATGTCCACCCGTTCA 180  
QY 181 TCAGGGTCTCTGACAGGTTCACTGAGTGGATCAGGCACAGATTTCACCTGAAATC 240  
DB 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGAAACAGATTTCACCTGGAATC 240  
QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTATTACTGTCAACAGCTGTAGAGTATCCA 300  
DB 241 AGTAGAGTGAAGCTGAGGATGTTGGGTGTGATTACTGTCAACACTTTGTAGAGTATCCA 300

QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAACG 338  
DB 301 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAGACG 338

## RESULT 11

US-09-214-095D-107

; Sequence 107, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 107

; LENGTH: 368

; TYPE: DNA

; ORGANISM: Murine

US-09-214-095D-107

Query Match 69.1%; Score 240.4; DB 3; Length 368;

Best Local Similarity 82.0%; Pred. No. 5.9e-70; Indels 0; Gaps 0;

Matches 277; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCGCTCC 60

DB 1 GATATGGTATGAGCAAGCAAGCAACTCTCAATCTCTGTCATCTTCGAGGAATCAGTTTCC 60

QY 61 ATCTCTGCTCGTCAAGTAAAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120

DB 61 ATCTCTGCAAGTCTAGTAAAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120

QY 121 TACCTCAGAACGACGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGGGCA 180

DB 121 TTTCTGAGAGACGAGACAACTCTCTACCTCTCTGATCTATTGATGTCACCCGGGCA 180

QY 181 TCAGGGGTCCCTGACAGGTTCAAGTGGGATGAGGATCAGGACAGATTTACACTGAAATC 240

DB 181 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGGTGAGGACAGATTTACACTGAAATC 240

QY 241 ACAGAGTGGAGCTCAGATGTTGGGGTTATTACTGTCAACAGCTGGTAGATATCCA 300

DB 241 AGTAGAGTGAAGCTCAGGATGTTGGGTGCGGTATTACTGTCAACAATTTGTAGATATCCA 300

QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAACG 338

DB 301 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAGACG 338

## RESULT 12

US-08-672-345C-90

; Sequence 90, Application US/08672345C

; Patent No. 5948658

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald, W.

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/672,345C

; FILING DATE: 24-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/51400

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 90:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 368 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-672-345C-90

Query Match 68.7%; Score 239.2; DB 2; Length 368;

Best Local Similarity 80.5%; Pred. No. 1.5e-69;

Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCGCTCC 60

DB 1 GATATGGTATGAGCAAGCAAGCAACTCTCAATCTCTGTCATCTTCGAGGAATCAGTTTCC 60

QY 61 ATCTCTGCTCGTCAAGTAAAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120

DB 61 ATCTCTGCAAGTCTAGTAAAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120

QY 121 TACCTCAGAACGACGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGGGCA 180

DB 121 TTTCTGAGAGACGAGACAACTCTCTACCTCTCTGATCTATTGATGTCACCCGGGCA 180

QY 181 TCAGGGGTCCCTGACAGGTTCAAGTGGGATGAGGATCAGGACAGATTTACACTGAAATC 240

DB 181 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGGTGAGGACAGATTTACACTGAAATC 240

QY 241 ACAGAGTGGAGCTCAGATGTTGGGGTTATTACTGTCAACAGCTGGTAGATATCCA 300

DB 241 AGTAGAGTGAAGCTCAGGATGTTGGGTGCGGTATTACTGTCAACAATTTGTAGATATCCA 300

QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAACG 348

DB 301 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAGACG 348

## RESULT 13

US-09-214-095D-103

; Sequence 103, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 103

; LENGTH: 368

; TYPE: DNA

; ORGANISM: MURINE

US-09-214-095D-103

Query Match 68.7%; Score 239.2; DB 3; Length 368;

Best Local Similarity 80.5%; Pred. No. 1.5e-69;

Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCGCTCC 60

Db 1 GATATGTGTAGTACGCAAGATGAATCTCTCAATCTCTCTCACTTTCTGGAGAATCAGTTTCC 60  
Qy 61 ATCTCTCTGCTCGCTAGTAAGATGCTCTCTGTATAAGGATGGGAAGACATATCTTGAATTGG 120  
Db 61 ATCTCTGCAAGTCTAGTAGAGTCTCTATATAGGATGGGAAGACATATCTTGAATTGG 120  
Qy 121 TACTCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180  
Db 121 TTTCTGCAGAGACCAGGACGATCTCTCACTCTCTGATCTATTGATGTCCACCCGGTCA 180  
Qy 181 TCAGGGTCTCTGACAGCTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240  
Db 181 TCAGGAGTCTCAGACCCGGTTAGTGGCAGTGGGTCAGGAACAGATTTTCACTCTGAAATC 240  
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
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Qy 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAACTACGGTGGCT 348  
Db 301 TTCACGTTCCGGCTCGGGGACAAAATTGGAGATAAAACGGGCTGATGCT 348

## RESULT 14

US-09-479-614-25

; Sequence 25, Application US/09479614

; Patent No. 6573372

; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine

; APPLICANT: Weber, Eric

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

; FILE REFERENCE: P-1047

; CURRENT APPLICATION NUMBER: US/09/479,614

; CURRENT FILING DATE: 2000-01-07

; EARLIER APPLICATION NUMBER: 60/115,033

; EARLIER FILING DATE: 1999-01-07

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 25

; LENGTH: 666

; TYPE: DNA

; ORGANISM: Felis catus

US-09-479-614-25

Query Match 68.7%; Score 239.2; DB 4; Length 666;  
Best Local Similarity 80.5%; Pred. No. 1.9e-69;  
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 1 GATATGTGTAGTACGCTCAGTCTCCACTCTCCCTGCCGCTCAGGAGCCGGCTCC 60  
Db 1 GATATGTGTAGTACGAGACCCCTCTGCTCTGCTCAGCTCAGGAGCCAGCTCA 60  
Qy 61 ATCTCTGCTCGCTAGTAAGATGCTCTCTGTATAAGGATGGGAAGACATATCTTGAATTGG 120  
Db 61 ATCTCTGCAAGTCTAGTAGAGTCTCTATATAGGATGGGAAGACATATCTTGAATTGG 120  
Qy 121 TACTCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180  
Db 121 TACTCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180  
Qy 181 TCAGGGTCTCTGACAGCTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240  
Db 181 TCTGGGGTCCGAGACAGTTCAGTGGCAGTGGGTCAGGACAGATTTTCACTCTGAGATC 240  
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
Db 241 AGCAGGGTGGAGGCTGACGAGCTCGGTGTTTATTACTCGGCTCAAGGTTTACAGCATCT 300  
Qy 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAACTACGGTGGCT 348  
Db 301 CTCACTTTCGGCCCGAGCTACCAAGCTGGAGATCAAAACGGAGTATGCT 348

## RESULT 15

US-09-479-614-27/c

; Sequence 27, Application US/09479614

; Patent No. 6573372

; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine

; APPLICANT: Weber, Eric

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

; FILE REFERENCE: P-1047

; CURRENT APPLICATION NUMBER: US/09/479,614

; CURRENT FILING DATE: 2000-01-07

; EARLIER APPLICATION NUMBER: 60/115,033

; EARLIER FILING DATE: 1999-01-07

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 27

; LENGTH: 666

; TYPE: DNA

; ORGANISM: Felis catus

US-09-479-614-27

Query Match 68.7%; Score 239.2; DB 4; Length 666;  
Best Local Similarity 80.5%; Pred. No. 1.9e-69;  
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 1 GATATGTGTAGTACGCTCAGTCTCCACTCTCCCTGCCGCTCAGGAGCCGGCTCC 60  
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Qy 121 TACTCTCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180  
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Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300  
Db 426 AGCAGGGTGGAGGCTGACGAGCTCGGTGTTTATTACTCGGCTCAAGGTTTACAGCATCT 367  
Qy 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAACTACGGTGGCT 348  
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Job time : 68.129 secs

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 5929.82 Seconds  
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Title: US-09-674-716B-18

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
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11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335	100.0	1335	6	BD232425 Antibodie
2	1335	100.0	1335	6	BD232452 Antibodie
3	1335	100.0	1335	6	AX010615 Sequence
4	1335	100.0	1335	6	AX010646 Sequence
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6	1160.8	87.0	1639	9	AK130434 Homo sapi
7	1160.6	86.9	1685	9	BC05820 Homo sapi
8	1158	86.7	1645	9	CQ850293 Sequence
9	1158	86.7	1645	9	AK127409 Homo sapi
10	1156	86.6	1679	9	BC018747 Homo sapi
11	1154.6	86.5	1392	6	CQ774324 Sequence
12	1154.6	86.5	1392	6	CQ790351 Sequence
13	1154.6	86.5	1392	6	CQ812157 Sequence
14	1154.6	86.5	1392	6	CQ816433 Sequence
15	1154.6	86.5	1392	6	AX594307 Sequence
16	1154.6	86.5	1392	6	AX616608 Sequence
17	1154.6	86.5	1392	6	AX616908 Sequence
18	1154.6	86.5	9568	6	AX616611 Sequence
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21	1149.2	86.1	1442	6	BD266675 Human mon
22	1147.8	86.0	1634	9	BC072419 Homo sapi
23	1147.2	85.9	1437	6	AR108865 Sequence
24	1147.2	85.9	1437	6	AR265199 Sequence
25	1147.2	85.9	1437	6	AR488221 Sequence
26	1147.2	85.9	1437	6	BD063037 Identific
27	1146.6	85.9	1630	9	BC024289 Homo sapi
28	1146.6	85.8	1659	9	BC014667 Homo sapi
29	1145.6	85.8	1694	9	BC640620 Homo sapi
30	1145	85.8	1694	9	HS080665 Sequence
31	1143.4	85.6	1416	6	CQ758863 Sequence
32	1142.8	85.6	6281	6	CQ758861 Sequence
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#### ALIGNMENTS

RESULT 1	BD232425	1335 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD232425	Antibodies against CD23, derivatives thereof and therapeutic			
DEFINITION	BD232425	utilization of the same.			
ACCESSION	BD232425	GI:33042195			
VERSION	BD232425	1			
KEYWORDS	JP 2002514421-A/9.				
SOURCE	JP 2002514421-A/9.				
ORGANISM	JP 2002514421-A/9.				
REFERENCE	1 (bases 1 to 1335)				
AUTHORS	Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and Shearin,J.				
TITLE	Antibodies against CD23, derivatives thereof and therapeutic				
JOURNAL	utilization of the same				
COMMENT	Patent: JP 2002514421-A 9 21-MAY-2002; GLAXO GROUP LTD				
	OS Artificial Sequence				
	PN JP 2002514421-A/9				
	PD 21-MAY-2002				
	PF 07-MAY-1999 JP 2000548470				
	PR 09-MAY-1998 GB 9809839.5				
	PI JEAN YVES MARCEL PAUL BONNEFOY,SCOTT JAMES CROWE,JONATHAN PI HENRY ELLIS,				
	PI NICHOLAS TIMOTHY RAPSON,JEAN SHEARIN				
	PC C12N15/02,A61K39/395,C07K16/28,C12N15/00				
	CC Description of Artificial Sequence: Humanised anti-CD23 CC antibody heavy chain variable region.				
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	FT CDS				
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ORIGIN					
	Query Match	100.0%;	Score 1335;	DB 6;	Length 1335;
	Best Local Similarity	100.0%;	Pred. No. 4.2e-264;		
	Matches 1335;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;

QY 1 GAGGTGCACTGGTGAAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
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 QY 61 TCCTGTGCACTAGCGGATTCATTTTCAGTGGCTACTGGATCTCCTGGTCCGCGAGGCT 120  
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 QY 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240  
 Db 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240  
 QY 241 CTGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCGTGTATTACTGTACAGAT 300  
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 QY 361 TCGGTCTTCCCTCGGACCTCTCTCAAGAGACACTCTGGGGGACAGGGCCCTGGGC 420  
 Db 361 TCGGTCTTCCCTCGGACCTCTCTCAAGAGACACTCTGGGGGACAGGGCCCTGGGC 420  
 QY 421 TGCTGTGCAAGACTACTTCCCGAACCGTGCAGCGTGTGCGGAACCTCAGCGGCCCTG 480  
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 QY 901 AGCGTCTCTACCGTCCCTGACCAAGGACTGGCTGAATGCGAAGGAGTACAAAGTCAAGGTC 960  
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 RESULT 2  
 BD232452/c  
 LOCUS  
 DEFINITION BD232452 1335 bp DNA linear PAT 17-JUL-2003  
 Antibodies against CD23, derivatives thereof and therapeutic  
 utilization of the same.  
 ACCESSION BD232452  
 VERSION BD232452.1 GI:33042222  
 KEYWORDS JP 2002514421-A/36.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 1335)  
 AUTHORS Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and Shearin,J.  
 TITLE Antibodies against CD23, derivatives thereof and therapeutic utilization of the same  
 JOURNAL Patent: JP 2002514421-A 36 21-MAY-2002;  
 COMMENT GLAXO GROUP LTD  
 OS Artificial Sequence  
 PN JP 2002514421-A/36  
 PD 21-MAY-2002  
 PF 07-MAY-1999 JP 2000548470  
 PR 05-MAY-1998 GB 9809839.5  
 PI JEAN YVES MARCEL PAUL BONNEFOY,SCOTT JAMES CROWE,JONATHAN PI HENRY ELLIS,  
 PI NICHOLAS TIMOTHY RAPSON,JEAN SHEARIN  
 PC Cl2N15/02,A61K39/395,C07K16/28,Cl2N15/00  
 CC Description of Artificial Sequence: Humanised anti-CD23 CC antibody heavy chain variable region  
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 Best Local Similarity 100.0%; Pred. No. 4.2e-264;  
 Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGTGCACTGGTGAAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
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QY 181 CATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240  
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LOCUS  
DEFINITION  
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ORGANISM  
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REFERENCE  
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AUTHORS  
Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.  
TITLE  
Antibodies to cd23, derivatives thereof, and their therapeutic uses.  
JOURNAL  
Patent: WO 958679-A 18 NOV-1999;  
Bonnefoy Jean Yves Marcel Paul (FR); Crowe Scott James (GB); Rapson  
Nicholas Timothy (GB); Glaxo Group Ltd (GB); Ellis Jonathan Henry  
(GB); Shearin Jean (US)  
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 NEDO human cDNA sequencing project  
 Unpublished  
 2 (bases 1 to 1626)

# AUTHORS TITLE JOURNAL

Sugano, S. and Suzuki, Y.  
 Direct Submission  
 Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,  
 University of Tokyo, Laboratory of Genome Structure, Human Genome  
 Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
 (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,  
 Fax: 81-3-5449-5416)

## COMMENT

NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
 Research Association for Biotechnology (RAB); cDNA library  
 construction and 5'-end one pass sequencing: Institute of Medical  
 Science, University of Tokyo, Laboratory of Genome Structure, Human  
 Genome Center; 3'-end one pass sequencing: RAB; clone selection for  
 full insert sequencing: RAB and Helix Research Institute.

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ACCESSION AK130434
VERSION AK130434.1 GI:34527234
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1639)
Sugano,S. and Suzuki,Y.
Direct Submission
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: flicdn@ing.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
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QY 1 GAGGTGCGAGCTGCTGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
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## RESULT 7

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REFERENCE 1 (bases 1 to 1685)  
AUTHORS Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,  
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Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1685)  
Strausberg, R.  
Direct Submission  
Submitted (26-JAN-2004) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapsb-r@mail.nih.gov](mailto:cgapsb-r@mail.nih.gov)  
Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,  
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth  
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,  
Kim Macdonald, Anara Maason, Mike R. Mayo, Josh Moran, Ryan Morin,  
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,  
Farvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,  
Duane Smalish, Jeff Stott, Miranda Tsai, George Yang, Jacquie  
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Clone distribution: MGC clone distribution information can be found  
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Series: IRAC Plate: 141 Row: b Column: 18  
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## RESULT 8

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ACCESSION CQ850293
VERSION   CQ850293.1 GI:51508505
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SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1  
AUTHORS Isegai, T., Yamamoto, J., Nishikawa, T., Isono, Y., Sugiyama, T.,  
Otsuki, T., Wakamatsu, A., Ishii, S., Nagai, K. and Irie, R.  
TITLE Full-length human cDNA  
JOURNAL Patent: EP 1447413-A 762 18-AUG-2004;  
Research Association for Biotechnology (JP)  
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ACCESSION AK127409  
VERSION AK127409.1 GI:34534304  
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ORGANISM Homo sapiens  
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AUTHORS Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,  
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,  
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and Isegai, T.  
TITLE NEDO human cDNA sequencing project  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1645)  
AUTHORS Isegai, T. and Yamamoto, J.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2003) Takao Isegai, FLJ Project (HRI Team); 2-6-7  
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan  
COMMENT (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
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## RESULT 10

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 VERSION BC018747.1 GI:175111791  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1679)  
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
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 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
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Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257  
12477932  
2 (bases 1 to 1679)  
Strausberg, R.  
Direct Submission  
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: Louis Staudt  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: TRAL Plate: 40 Row: i Column: 16  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein.

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TITLE      Compositions and methods for treating cancer using maytansinoid
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JOURNAL    Patent: EP 1391213-A 7 25-FEB-2004;
Boehringer Ingelheim International GmbH (DE)
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AUTHORS Adolf, G., Baum, A. and Heider, K.H.  
TITLE Compositions and methods for treating cancer using cytotoxic cd44 antibody immunoconjugates and chemotherapeutic agents  
JOURNAL Patent: WO 2004018000-A 7 04-MAR-2004;  
BOEHRINGER INGELHEIM ZENTRALE GMBH (DE)

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VERSION CQ812157.1 GI:47601386  
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SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS

TITLE Compositions and methods for treating cancer using cytotoxic CD4antibody immunoconjugates and radiotherapy  
JOURNAL Patent: EP 1417974-A 7 12-MAY-2004;  
Boehringer Ingelheim International GmbH (DE)  
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ORIGIN

Query Match 86.5%; Score 1154.6; DB 6; Length 1392;  
Best Local Similarity 92.5%; Pred. No. 5.1e-227;  
Matches 1240; Conservative 0; Mismatches 89; Indels 12; Gaps 2;  
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
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QY 61 TCCTGTGCAGCTAGCGGATTCACCTTTTCAGTGGCTACTTGGATGTCCTGGGTCCGCCAGGCT 120  
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DB 178 CCGGGGAAGGGCTGGAGTGGGTCTCAACCATTAG-----TAGTGGTGGTAGTTACACC 231  
QY 181 CATTATTCGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCMAAATCTAGA 240  
DB 232 TACTATCTAGACAGTATAAAGGCGCATTCACCATCTCCAGAGACAATGCCAAGAACTCC 291  
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DB 1372 TCCCTGTCTCCGGTAAATGA 1392  
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LOCUS Sequence 7 from Patent WO2004041307. linear PAT 03-JUN-2004  
DEFINITION CQ816433  
ACCESSION CQ816433  
VERSION CQ816433.1 GI:48144765  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Adolf, G., Baumann, M. and Heider, K.H.  
TITLE Compositions and methods for treating cancer using cytotoxic cd4antibody immunoconjugates and radiotherapy  
JOURNAL Patent: WO 2004041307-A 7 21-MAY-2004;  
Boehringer Ingelheim International GmbH (DE)  
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ORIGIN

Query Match 86.5%; Score 1154.6; DB 6; Length 1392;  
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Matches 1240; Conservative 0; Mismatches 89; Indels 12; Gaps 2;  
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Db 592 CTCAGCAGCGTGTGACCGTGCCTCTCAGCAGCTTGGGCAACCCAGACCTACATCTGCAAC 651  
Qy 595 GTGAATCACAAGCCCGGCAACCAAGGTGACAAAGTGAAGTGGAGCCCAATCTTGTGAC 654  
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Qy 835 GTGAGGTGCATATGCAAGCAAAAGCCGCGGAGGACGACGACGACGACGACGACGACGAC 894  
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Db 1072 CAGCCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAGAC 1131  
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Qy 1195 GGCTCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAAAC 1254  
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Db 1372 TCCTGTGCTCCGGTAAATGA 1392

RESULT 15  
AX594307  
LOCUS AX594307 1392 bp DNA linear PAT 14-FEB-2003  
DEFINITION Sequence 7 from Patent EP1258255.  
ACCESSION AX594307  
VERSION AX594307.1 GI:28396232  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Adolf, G., Heider, K.H., Patzelt, B. and Sproll, M.  
TITLE Conjugates of an antibody to cd44 and a maytansinoid  
JOURNAL Patent: EP 1258255-A 7 20-NOV-2002;  
Boehringer Ingelheim International GmbH (DE)  
FEATURES  
Location/Qualifiers  
source  
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ORIGIN  
Query Match 86.5%; Score 1154.6; DB 6; Length 1392;  
Best Local Similarity 92.5%; Pred. No. 5.1e-227;  
Matches 1240; Conservative 0; Mismatches 89; Indels 12; Gaps 2;  
Qy 1 GAGGTGAGCTGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
Db 58 GAAGTGCAGCTGTGGAGTCTGGGGAGGCTTAGTGAAGCTGGAGGCTCCCTAAGACTC 117  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 5238.89 Seconds

(without alignments)  
9699.731 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335

Sequence: 1 gaggtgcagctgtgtgagtc.....ccctgtctccggtaaatga t335

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gses1:\*

9: gb\_gses2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	985.4	73.8	1022	3	CR611254 full-leng
2	985.4	73.8	1048	3	CR595172 full-leng
3	985.4	73.8	1090	3	CR612308 full-leng
4	985.4	73.8	1091	3	CR604961 full-leng
5	985.4	73.8	1093	3	CR616804 full-leng
6	985.4	73.8	1098	3	CR626477 full-leng
7	985.4	73.8	1100	3	CR612813 full-leng
8	985.4	73.8	1102	3	CR601777 full-leng
9	985.4	73.8	1102	3	CR625051 full-leng
10	985.4	73.8	1103	3	CR595194 full-leng
11	985.4	73.8	1104	3	CR591904 full-leng
12	985.4	73.8	1106	3	CR613460 full-leng
13	985.4	73.8	1106	3	CR620071 full-leng
14	985.4	73.8	1107	3	CR598548 full-leng
15	985.4	73.8	1109	3	CR614200 full-leng
16	985.4	73.8	1109	3	CR619687 full-leng
17	985.4	73.8	1111	3	CR606782 full-leng
18	985.4	73.8	1114	3	CR593349 full-leng
19	985.4	73.8	1114	3	CR618075 full-leng
20	985.4	73.8	1118	3	CR613511 full-leng
21	985.4	73.8	1120	3	CR619868 full-leng
22	985.4	73.8	1124	3	CR611468 full-leng
23	985.4	73.8	1136	3	CR598462 full-leng
24	985.4	73.8	1142	3	CR598316 full-leng

25	985.4	73.8	1179	3	CR607277 full-leng
26	985.4	73.8	1287	3	CR611016 full-leng
27	985.4	73.8	1289	3	CR594000 full-leng
28	982.2	73.6	1734	3	CR749861 Homo sapi
29	932.4	69.8	1087	5	CR377695 BX377695
30	927.8	69.5	1090	5	CR414495 BX414495
31	898.8	67.3	1020	5	CR62878 AGENCOURT
32	896	67.1	1043	5	CR337477 BX337477
33	891.6	66.8	1094	5	CR381020 BX381020
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42	883.8	66.2	1086	3	CR603347 full-leng
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#### ALIGNMENTS

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LOCUS CR611254 1022 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CS0DE007YJ17 of Placenta of Homo sapiens (human).  
ACCESSION CR611254  
VERSION CR611254.1 GI:50492061  
KEYWORDS HTC; CNSIT\_CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1022)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue  
REFERENCE 2 (bases 1 to 1022)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

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Query Match 73.8%; Score 985.4; DB 3; Length 1022;  
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QY 701 CACCGTCACTCTCTCTCTTCCCGCCAAACCCCAAGGACACCTCTCATGATCTCCCGGACC 760
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QY 761 CTGAGGTCACTGCTGCTGCTGAGCTGAGCGTGCACCAAGACCTGAGGTCAAGTCAACT 820
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RESULT 2

CR595172

LOCUS

DEFINITION

full-length cDNA clone CS9D1040YA16 of Placenta Cot 25-normalized

of Homo sapiens (human).

ACCESSION

CR595172

VERSION

CR595172.1 GI:50475979

CR595172 1048 bp mRNA linear HTC 21-JUL-2004

full-length cDNA clone CS9D1040YA16 of Placenta Cot 25-normalized

of Homo sapiens (human).

CR595172

CR595172.1 GI:50475979

# KEYWORDS

HTC; CNSLT cDNA.  
Homo sapiens (human)

# ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

# REFERENCE

1 (bases 1 to 1048)  
Li W.B., Gruber C., Jessee J. and Polayes D.

# AUTHORS

Full-length cDNA libraries and normalization  
Unpublished

# JOURNAL

Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue

# REFERENCE

2 (bases 1 to 1048)  
Genoscope.  
Direct Submission

# AUTHORS

Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

# JOURNAL

- Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

# COMMENT

Location/Qualifiers  
1. .1048

# FEATURES

Location/Qualifiers  
1. .1048

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-Query Match 73.8%; Score 985.4; DB 3; Length 1048;  
Best Local Similarity 99.4%; Pred. No. 1.1e-244;  
Matches 989; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 401 GGGGACACAGCGGCTCGGCTGCTTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGT 460  
Db 85 GGGGACACAGCGGCTCGGCTGCTTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGT 144

QY 461 CGTGAAGTCAAGCGGCTCGGCTGCTTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGT 520  
Db 145 CGTGAAGTCAAGCGGCTCGGCTGCTTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGT 204

QY 521 CAGGACTCTACT 580  
Db 205 CAGGACTCTACT 264

QY 581 CTTACATCTGCAACCTGTAATCAAGCCCGACCAACCAAGGTGGACAAAGTGGAGC 640  
Db 265 CTTACATCTGCAACCTGTAATCAAGCCCGACCAACCAAGGTGGACAAAGTGGAGC 324

QY 641 CCAATCTGTGACAAAACCTGACATGCCCGGCTGCGGACCTGCACTGAACTCCGCGGGG 700  
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Db 385 GACCGTCACT 444

QY 761 CTGAGGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 820  
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QY 821 GGTACGTGACGCGGTGGAGGTGCATATGCCAAGACAAAGCCCGGGAGGAGCAGTACA 880  
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RESULT 4	CR604961	1091 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CS0DI009YJ10 of Placenta Cot 25-normalized				
DEFINITION	of Homo sapiens (human)				
ACCESSION	CR604961				
VERSION	CR604961.1	GI:50485768			
KEYWORDS	HTC; CNSLT cdNA				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1091)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Paraday Avenue				
REFERENCE	2 (bases 1 to 1091)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr				
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime				
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library				
	was normalized. Library was constructed by Life Technologies, a				
	division of Invitrogen.				
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Matches	989; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
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Qy	401 GGGGCACAGCGGCGCTGGGTGCTGGTCAAGACTACTTCCCGAAACCGGTGACGGTGT 460				
Db	72 GGGGCACAGAGCGCTGGGTGCTGGTCAAGACTACTTCCCGAAACCGGTGACGGTGT 131				
Qy	461 CGTGGAACTCAGCGCCCTGACACGAGCGGTGCACACCTTCCTCGGCTGTCTACAGTCT 520				
Db	132 CGTGGAACTCAGCGGCGCTGACACGAGCGGTGCACACCTTCCTCGGCTGTCTACAGTCT 191				
Qy	521 CAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTTCACAGAGCTTGGGACCCAGA 580				
Db	192 CAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTTCACAGAGCTTGGGACCCAGA 251				
Qy	581 CCTATCTCTCAGCTGAATCAACGCCAGCAACCAAGGTGGACGAAGAGTGGAGC 640				
Db	252 CCTATCTCTCAGCTGAATCAACGCCAGCAACCAAGGTGGACGAAGAGTGGAGC 311				
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Qy	701 CACGTCAGTCTTCTCTCCCTCCCAAAACCCAGACACCTCTATGATCTCCCGGACCC 760				
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DB |||||  
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DB |||||  
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DB |||||  
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ACCESSION CR626477  
VERSION CR626477.1 GI:50507284  
KEYWORDS HTC; CNSLT_cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.  
Full-length cDNA libraries and normalization.  
Unpublished  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1098)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE. (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
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Best Local Similarity 99.4%; Pred. No. 1.1e-244;  
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DB 12 CAGCCTCCACCAAGGGCCATCGCTTCCCTGGCACCTCTCTCCCAAGAGCACTCTG 71  
QY 401 GGGGCACAGCGGCCCTGGCTGCTCAAGGACTACTTCCCGAAGCCGCTGACGGTGT 460  
DB 72 GGGGCACAGCGGCCCTGGCTGCTCAAGGACTACTTCCCGAAGCCGCTGACGGTGT 131  
QY 461 CGTGGAACTCAGGCGCCCTGACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCCT 520  
DB 132 CGTGGAACTCAGGCGCCCTGACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCCT 191  
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DB 252 CCTACATCTGCAAGCTGAATCACAAGCCAGCAACCAAGGTGGACAAGAAAGTGGAGC 311  
QY 641 CCAAACTTTGTGACAAACTCACAATGCGCGTCCAGCACTGAACTCGCGGGGG 700  
DB |||||
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## RESULT 7

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 KEYWORDS HTC; CNSLT cDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1100)  
 AUTHORS Li, W. B., Gruber, C., Jesse, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue  
 REFERENCE 2 (bases 1 to 1100)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
 COMMENT - Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

## FEATURES

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REFERENCE 2 (bases 1 to 1102)  
 Genoscope.  
 AUTHORS Direct Submission  
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
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 DB 12 CAGCCTCCACCAAGGCGCCATCGGTCTTCCCTGGCACCCTCTCTCAAGAGCACCTCTG 71

QY 401 GGGGACAGGGCCCTGGGTCTCTGCTCAAGACTACTTCCCGAACCGGTGACGGTGT 460  
 DB 72 GGGGACAGGGCCCTGGGTCTCTGCTCAAGACTACTTCCCGAACCGGTGACGGTGT 131

QY 461 CGTGGAACTCAGGCGCCCTGACAGCGGGGTGCACACCTTCCCGGTGCTCTACAGTCT 520  
 DB 132 CGTGGAACTCAGGCGCCCTGACAGCGGGGTGCACACCTTCCCGGTGCTCTACAGTCT 191

QY 521 CAGGACTCTACTCTCTCAGCAGCGGTGTGACCTGCGCTTCCCGGTGCTCTACAGTCT 580  
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QY 701 CACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCTCATGATCTCCCGGACCC 760  
 DB 372 CACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCTCATGATCTCCCGGACCC 431

QY 761 CTGAGTCAATCGGTGGTGGAGCGTAGCCAGCAACCAAGAGCCTTGAGTCAAGTCAACT 820  
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 DB 732 AGCTGACCAAGAACCAAGGTGACCTGCTGGTCAAAAGGCTTCTATCCAGCGACA 791

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RESULT 10  
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 ACCESSION CR595194  
 VERSION CR595194.1 GI:50476001  
 KEYWORDS HTC; CNSLT\_CDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1103)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue  
 REFERENCE 2 (bases 1 to 1103)  
 Genoscope.  
 AUTHORS Direct Submission  
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.

FEATURES Location/Qualifiers  
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 Best Local Similarity 99.4%; Pred. No. 1.le-244;  
 Matches 989; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 401 GGGGACAGGGCCCTGGGTCTCTGCTCAAGACTACTTCCCGAACCGGTGACGGTGT 460  
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Qy 521 CAGGACTCTACTCCTCAGCAGCGTGGTACCGTCCCTCAGCAGACTTGGGCAACCCAGA 580
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Db 308 CCAATCTTGTGCAAAACTCACAATGCGCCACCGTCCCGCAGCACTGAACTCCCGGGG 367
Qy 701 CACCGTCAGTCTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 760
Db 368 GACCGTCAGTCTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 427
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of Homo sapiens (human).
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VERSION CR591904.1 GI:50472711
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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# REFERENCE

1 (bases 1 to 1104)  
Li, W.B., Gruber, C., Jesses, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1104)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail: seque@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)

# REFERENCE

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of invitrogen.  
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Best Local Similarity 99.4%; Pred. No. 1.1e-244;  
Matches 989; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 341 CAGCCTCCACCAAGGGCCCATCGGTCTTCCCTGGCACCCTCTCCAAAGACCTCTG 400  
Db 12 CAGCCTCCACCAAGGGCCCATCGGTCTTCCCTGGCACCCTCTCCAAAGACCTCTG 71  
Qy 401 GGGGCAAGCGGCGCTGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGTGT 460  
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Qy 461 CGTGGAACTCAGCGGCGCTGACCAAGCGGCGTGCACACTTCCCGGCTGTCTACAGTCT 520  
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[illegible]

## ORIGIN

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COMMENT
FEATURES
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ORIGIN
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of Homo sapiens (human).
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CR614200.1 GI:50495007
HTC; CNSLT_cDNA.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1109)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1109)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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QY 461 CGTGGAACTCAGCGCCCTGACCGCGGTGCACACCTTCCCGGTGCTCTTACAGTCT 520
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QY 521 CAGGACTCTACTCTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGA 580
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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10523.523 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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26	1149.2	86.1	1442	5	AAC84208	Aac84208 Plasmid G
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28	1147.2	85.9	1437	2	AAV35487	Aav35487 Macaque p
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#### ALIGNMENTS

##### RESULT 1

AAZ34748

ID AAZ34748 standard; CDNA; 1335 BP.

XX AAZ34748;

XX AAZ34748;

DT 15-FEB-2000 (first entry)

XX Humanised anti-CD23 MAb C11 heavy chain cDNA.

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 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 therapy; ds.

XX Homo sapiens.

OS Synthetic.

XX WO958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX ) GLAXO GROUP LTD.

XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX P-PSDB; AAV32263.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,

XX diabetes, multiple sclerosis and psoriasis.

XX Claim 17; Fig 4; 81pp; English.

XX This DNA sequence encodes the heavy chain of humanised anti-CD23 (IgE  
 CC receptor, FCER1) monoclonal antibody C11, composed of a human framework  
 CC (H5IGKV1) and the heavy chain complementarity determining regions (see  
 CC AAY32256-58) of murine antibody C11. The invention provides altered  
 CC antibodies, such as chimeric or humanised antibodies, which comprise  
 CC sufficient of the amino acid sequences of the C11 light and heavy chain  
 CC complementarity determining regions to render them capable of binding to  
 CC the CD23 type II molecule expressed on haematopoietic cells. The  
 CC antibodies are used to block soluble CD23 formation in human therapy, for  
 CC the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis,  
 CC multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria,  
 CC nephrotic syndrome, glomerulonephritis, inflammatory bowel disease,  
 CC ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies,  
 CC allergic asthma, intrinsic asthma, acute asthmatic exacerbation,  
 CC rhinitis, eczema, graft-versus-host disease, COPD, insulinitis, bronchitis  
 CC (particularly chronic bronchitis) or diabetes (particularly type 1  
 CC diabetes), and B-cell malignancies (claimed). They are also useful for  
 CC studying interactions between CD23 and various ligands and determining  
 CC the binding agents

XX SQ Sequence 1335 BP; 321 A; 414 C; 360 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 1335; DB 3; Length 1335;  
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QY 241 CTGTATCTGCAATGAACAGCCCTGAAACCGAGGACACAGCCGTGTATTACTGTACAGAT 300  
 DB 241 CTGTATCTGCAATGAACAGCCCTGAAACCGAGGACACAGCCGTGTATTACTGTACAGAT 300

QY 301 TTCATAGACTGGGGCCAGGGAACTAGTCACTAGTCACTCTCCTCAGCCTCCACCAAGGCCCA 360  
 DB 301 TTCATAGACTGGGGCCAGGGAACTAGTCACTAGTCACTCTCCTCAGCCTCCACCAAGGCCCA 360

QY 361 TCGGTCTTCCCTCCCTGGCACCTCTCTCAAGAGACCTCTGGGGGACAGGGCCCTGGGC 420  
 DB 361 TCGGTCTTCCCTCCCTGGCACCTCTCTCAAGAGACCTCTGGGGGACAGGGCCCTGGGC 420

QY 421 TGCTGTGCAAGACTACTTCCCGAACCCGTGACCGTGTGCGGAACTCAGCGGCCCTG 480  
 DB 421 TGCTGTGCAAGACTACTTCCCGAACCCGTGACCGTGTGCGGAACTCAGCGGCCCTG 480

QY 481 ACCAGCGGCGTGACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGC 540  
 DB 481 ACCAGCGGCGTGACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGC 540

QY 541 AGCGTGTGACCGTCCCTCAGGAGTCTGGGACCCAGACCTACATCTGCAACGTGAAT 600  
 DB 541 AGCGTGTGACCGTCCCTCAGGAGTCTGGGACCCAGACCTACATCTGCAACGTGAAT 600

QY 601 CACAAGCCAGCAACACCAAGGTGGAACAAGAAAGTGGAGCCCAAACTCTGTGACAAAAC 660  
 DB 601 CACAAGCCAGCAACACCAAGGTGGAACAAGAAAGTGGAGCCCAAACTCTGTGACAAAAC 660

QY 661 CACACATGCCCACCGTCCCGACGACTTGAATCTCGCGGGGACACCGTCAGTCTTCTCTTC 720  
 DB 661 CACACATGCCCACCGTCCCGACGACTTGAATCTCGCGGGGACACCGTCAGTCTTCTCTTC 720

DB 661 CACACATGCCCACCGTCCCGACGACTTGAATCTCGCGGGGACACCGTCAGTCTTCTCTTC 720  
 QY 721 CCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTG 780  
 DB 721 CCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTG 780  
 QY 781 GTGGACGTGAGCCACGACAGACCTCAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 840  
 DB 781 GTGGACGTGAGCCACGACAGACCTCAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 840  
 QY 841 GTGCATAATGCCAAGCAAAAGCCGCGGAGGAGTACAAAGCAACGTCACGTGTGGTC 900  
 DB 841 GTGCATAATGCCAAGCAAAAGCCGCGGAGGAGTACAAAGCAACGTCACGTGTGGTC 900  
 QY 901 AGCGTCTCACCCTCTCTGCAACAGACCTGCGTGAATGCGAAGGATCAAGTGCAGGTC 960  
 DB 901 AGCGTCTCACCCTCTCTGCAACAGACCTGCGTGAATGCGAAGGATCAAGTGCAGGTC 960  
 QY 961 TCCAAACAAAGCCCTCCAGCCCTCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCC 1020  
 DB 961 TCCAAACAAAGCCCTCCAGCCCTCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCC 1020  
 QY 1021 CGAGAACCAAGGTGTACACCTGCCCCATCCCGGATGAGTGCACCAAGAACCGAGTC 1080  
 DB 1021 CGAGAACCAAGGTGTACACCTGCCCCATCCCGGATGAGTGCACCAAGAACCGAGTC 1080  
 QY 1081 AGCCTGACCTGCTGCTCAAGGGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGC 1140  
 DB 1081 AGCCTGACCTGCTGCTCAAGGGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGC 1140  
 QY 1141 AATGGGACGCGGAGAAACAACTTCAAGACACCGCTCCCGTCTGAGCTCCGACGGCTCC 1200  
 DB 1141 AATGGGACGCGGAGAAACAACTTCAAGACACCGCTCCCGTCTGAGCTCCGACGGCTCC 1200  
 QY 1201 TTCTTCTCTTACAGCAAGTCTACCGTGGACAAAGAGCAGGTGGCAGAGGGGAACTCTTC 1260  
 DB 1201 TTCTTCTCTTACAGCAAGTCTACCGTGGACAAAGAGCAGGTGGCAGAGGGGAACTCTTC 1260  
 QY 1261 TCATGCTCCGTGATGATGAGGCTCTGCAACCACTACACGACAGAGAGCCTCTCCCTG 1320  
 DB 1261 TCATGCTCCGTGATGATGAGGCTCTGCAACCACTACACGACAGAGAGCCTCTCCCTG 1320  
 QY 1321 TCTCCGGGTAAATGA 1335  
 DB 1321 TCTCCGGGTAAATGA 1335

RESULT 2  
 ACC47231  
 ID ACC47231 standard; cDNA; 1386 BP.  
 XX ACC47231;  
 AC ACC47231;  
 XX  
 DT 18-AUG-2003 (first entry)  
 XX  
 DE Hu266 N56S heavy chain encoding cDNA.  
 XX  
 KW Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;  
 XX immunostimulant; gene; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..1386  
 FT /\*tag= a  
 FT /product= "heavy chain"  
 XX  
 PN WO2003016466-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US021322.  
 XX



PR 17-AUG-2001; 2001US-0313224P.  
XX (ELIL ) LILLY & CO ELI.  
XX Jia AV, Tsurushita N, Vasquez MJ;  
XX WPI; 2003-278557/27.  
XX P-PSDB; ABR39847.  
XX  
XX New antibodies comprising a heavy chain and a light chain complementarity  
XX determining regions from antibody 266, for treating and preventing  
XX conditions associated with the A beta peptide, e.g. Alzheimer's disease  
XX or Down syndrome.  
XX  
XX Disclosure; Fig 6; 82pp; English.  
XX  
XX The invention relates to an anti-Abeta (amyloid-beta peptide) antibody  
XX 266. The antibodies are useful for treating and preventing conditions  
XX associated with the A beta peptide, such as Alzheimer's disease, Down  
XX syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in  
XX humans; for determining whether a human subject will respond to treatment  
XX using humanized antibodies against A beta; for treating, preventing and  
XX reversing cognitive decline in clinical or pre-clinical Alzheimer's  
XX disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting  
XX formation of amyloid plaques of the effects of toxic soluble A beta  
XX species in humans. Treatment of the patients with antibody will inhibit  
XX or prevent cognitive decline typically associated with disease  
XX progression and reverses it. The present sequence represents a humanised  
XX anti-Abeta antibody 266 N56S heavy chain encoding cDNA  
XX  
XX Sequence 1386 BP; 321 A; 435 C; 368 G; 262 T; 0 U; 0 Other;  
XX  
XX Query Match 87.6%; Score 1169; DB 8; Length 1386;  
XX Best Local Similarity 92.8%; Pred. No. 8e-234;  
XX Matches 1239; Conservative 0; Mismatches 90; Indels 6; Gaps 1;  
XX  
Qy 1 GAGGTGAGTGTGGAGTGTGGGGAGGCTTGGTAAAGCCGGGGGCTCCCTTAGACTC 60  
Db 58 GAAGTGCAGTGTGGAGTGTGGGGAGGTTTGTAGTGAGGCTGGAGGGTCCCTGAGACTC 117  
Qy 61 TCCTGTGCAGTGTGGAGTGTGGGGAGGCTTGGTAAAGCCGGGGGCTCCCTTAGACTC 120  
Db 118 TCCTGTGCAGTGTGGAGTGTGGGGAGGTTTGTAGTGAGGTTTCCATGCTTGGGTGGCAGGCT 177  
Qy 121 CCAGGGAAGGGGCTCGAGTGTGGTGTGCAAAATAGATTGAATCTGATAATTATGCAACA 180  
Db 178 CCAGGGAAGGGGCTCGAGTGTGGTGTGCAAAATAGATTGAATCTGATAATTATGCAACA 231  
Qy 181 CATATCGGAGTGTGGAGGGGAAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240  
Db 232 TACTATCCAGACACTGTAAAGGGCGGATTCACATCTCCAGAGACAATGCCAAGAACACC 291  
Qy 241 CTGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCCGTGTATTACTGTACAGAT 300  
Db 292 CTGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCCGTGTATTACTGTGCAAGC 351  
Qy 301 TTCATAGACTGGGGCCAGGGAACACTAGTCACTGTCTCTCAGCTCCCAAGGGGCCCA 360  
Db 352 GGAGACTACTGGGGCCAGGCAACCTGTGTGACGTCTCTCAGCTCCCAAGGGGCCCA 411  
Qy 361 TCGGTCTTCCCTTGGACCCCTCTCCCAAGAGCACCTCTGGGGGCAAGGGGCCCTGGGC 420  
Db 412 TCGGTCTTCCCTTGGACCCCTCTCCCAAGAGCACCTCTGGGGGCAAGGGGCCCTGGGC 471  
Qy 421 TGGCTGTCAAGGACTACTTCCCGAACCCTGTGAGCGGTGTGCGGAACTCAGGGGCCCTG 480  
Db 472 TGGCTGTCAAGGACTACTTCCCGAACCCTGTGAGCGGTGTGCGGAACTCAGGGGCCCTG 531  
Qy 481 ACCAGCGGCTGCACACTTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGC 540  
Db 532 ACCAGCGGCTGCACACTTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGC 591  
Qy 541 AGCGTGTGACCGTGTCCCTCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAAGCTGAAT 600

Db 592 AGCGTGTGACCGTGTCCCTCAGCAGCTTGGGCAACCCAGACCTACATCTCAACGTAAT 651  
Qy 601 CACAAGCCAGCAACACCAAGGTGGCAAGAAAGTGGAGCCCAAACTCTTGACAAACT 660  
Db 652 CACAAGCCAGCAACACCAAGGTGGCAAGAAAGTGGAGCCCAAACTCTTGACAAACT 711  
Qy 661 CACACATGCCACCGTGTCCAGCAACCTGAACTCGCGGGGACCGTCAGTCTTCTCTTC 720  
Db 712 CACACATGCCACCGTGTCCAGCAACCTGAACTCTCTGGGGGACCGTCAGTCTTCTCTTC 771  
Qy 721 CCCCCAAAACCCAAAGACACCTCATGATCTCCGGACCCCTGAGTCAATGCGTGTG 780  
Db 772 CCCCCAAAACCCAAAGACACCTCATGATCTCCGGACCCCTGAGTCAATGCGTGTG 831  
Qy 781 GTGAGCTGAGCCACCAAGACCCCTGAGTCAAGTTCAACTGGTACGTGGACGCGTGGAG 840  
Db 832 GTGAGCTGAGCCACCAAGACCCCTGAGTCAAGTTCAACTGGTACGTGGACGCGTGGAG 891  
Qy 841 GTGCATAATGCCAAGACAAAGCCCGGGAGGACAGTACAAAGACAGTACCGTGTGGTC 900  
Db 892 GTGCATAATGCCAAGACAAAGCCCGGGAGGACAGTACAAAGACAGTACCGTGTGGTC 951  
Qy 901 AGCGTCTCACCCTCTGTGCACAGGACTGCTGAATGGCAAGGAGTACAAGTGAAGTGC 960  
Db 952 AGCGTCTCACCCTCTGTGCACAGGACTGCTGAATGGCAAGGAGTACAAGTGAAGTGC 1011  
Qy 961 TCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC 1020  
Db 1012 TCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC 1071  
Qy 1021 CGAGAAACCAAGGTGTACACCTGCCCCCATCCCGGGATGAGTGAACAAAGAACCCAGGTC 1080  
Db 1072 CGAGAAACCAAGGTGTACACCTGCCCCCATCCCGGGATGAGTGAACAAAGAACCCAGGTC 1131  
Qy 1081 AGCGTCACTGCTGTGTCAAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGC 1140  
Db 1132 AGCGTCACTGCTGTGTCAAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGC 1191  
Qy 1141 AATGGGCGAGCGGAGAACAACTACAAGACCCACGCTCCCGTGTGGAATCCGAGCGCTCC 1200  
Db 1192 AATGGGCGAGCGGAGAACAACTACAAGACCCACGCTCCCGTGTGGAATCCGAGCGCTCC 1251  
Qy 1201 TTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGGGAACGTCCTTC 1260  
Db 1252 TTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGGGAACGTCCTTC 1311  
Qy 1261 TCATGTCCGTGTATGAGGCTCTGCAACCACTACACGCAAGAGGCTCTCCCTG 1320  
Db 1312 TCATGTCCGTGTATGAGGCTCTGCAACCACTACACGCAAGAGGCTCTCCCTG 1371  
Qy 1321 TCTCCGGTAAATGA 1335  
Db 1372 TCTCCGGTAAATGA 1386  
XX  
XX RESULT 3  
XX ID ACC47232 standard; cDNA; 1386 BP.  
XX AC ACC47232;  
XX AC ACC47232;  
XX 18-AUG-2003 (first entry)  
XX Hu266 N56T heavy chain encoding cDNA.  
XX Amyloid-beta; Abeta; antibody 266; nontropic; neuroprotective; CDR;  
XX Immunostimulant; gene; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 1..1386



Transposon-based vector pTnMCS (CMV-prepro-HCPro-CPA).  
ds; multimeric protein; egg-laying; avian; milk producing animal;  
transgenic; transposase; cancer; immunotherapy; infectious disease;  
pTnMCS; CMV-prepro-HCPro-CPA; cecropia moth; chicken; gene; CMV;  
chimeric; RM2 antibody.

Hyalophora cecropia.

Cytomegalovirus.

Gallus gallus.

Synthetic.

Unidentified.

Key Location/Qualifiers

FT misc\_feature

FT 1..3715

FT /\*tag= a

FT /note= "From vector pTnMCS"

FT 3721..5364

FT /\*tag= b

FT /note= "CMV promoter/enhancer"

FT 5371..5541

FT /\*tag= c

FT /note= "Capsite/prepro from cecropia moth"

FT 5548..6912

FT /\*tag= d

FT /note= "Heavy chain gene construct from RM2 antibody"

FT 6913..6924

FT /\*tag= e

FT /note= "Pro sequence from cecropia moth"

FT 6931..7575

FT /\*tag= f

FT /note= "Light chain gene construct from RM2 antibody"

FT 7582..7989

FT /\*tag= g

FT /note= "Chicken conalbumin"

FT 7991..11590

FT /\*tag= h

FT /note= "This portion of the sequence is from cloning vector pTnMCS."

XX W02004067706-A2.

XX 12-AUG-2004.

XX 24-DEC-2003; 2003WO-US041261.

XX 21-JAN-2003; 2003US-0441377P.

XX 21-JAN-2003; 2003US-0441381P.

XX 21-JAN-2003; 2003US-0441392P.

XX 21-JAN-2003; 2003US-0441405P.

XX 21-JAN-2003; 2003US-0441447P.

XX 21-JAN-2003; 2003US-0441502P.

XX 26-JUN-2003; 2003US-00609019.

XX (TRAN-) TRANSENX INC.

XX (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.

XX Cooper RK, Fioretti WC, Cadd GG;

XX WPI; 2004-580985/56.

XX New isolated polynucleotide having two or more genes of interest and pro

XX nucleotide sequences, for use in pharmaceutical, diagnostic and

XX industrial uses, such as in treating and diagnosing cancer.

XX Example 4; SEQ ID NO 100; 119pp; English.

XX The present invention provides a new, effective and efficient method for

XX producing multimeric proteins in the egg-laying (avian) or milk producing

XX animals. The multimeric proteins include associated multimeric proteins

XX (two or more associated polypeptides) and multivalent multimeric proteins

XX (a single polypeptide is encoded by multiple genes). The expression and

XX formation of a multimeric protein is achieved by administering a

CC polynucleotide cassette containing genes of interest (for example  
CC proinsulin, antibodies, cytokines, etc.). The polynucleotide cassettes  
CC are administered to egg-laying or milk producing animals to create the  
CC transgenic animals. Several different signal sequences and promoters can  
CC be used to achieve the deposition of the multimeric protein in the egg or  
CC milk. The transposon based vector has been used for the incorporation of  
CC polynucleotide cassettes into the genomic DNA. The polynucleotide  
CC cassettes may additionally contain multiple pro sequences, prepro  
CC sequences, cecropin prepro sequences and cleavage sites. Each gene  
CC encodes a polypeptide which forms part of a multimeric protein. The pro  
CC portion of the sequences has been used to facilitate appropriate  
CC processing, expression and formation of multimeric proteins. These  
CC multimeric proteins can be produced much more efficiently and  
CC economically by this method than earlier conventional methods. This  
CC improved method can produce the multimeric proteins on a large scale. The  
CC transposon-based vectors of the invention produce high integration  
CC frequencies compared to the earlier vectors. The intratesticular  
CC injections with the novel transposon based vector produces 77 % sperm  
CC positive rosters (compared to 41% of a previous method). The transposon-  
CC based vectors of the invention include a transposase gene linked to a  
CC first promoter and a coding sequence of a desired protein linked to a  
CC second promoter. The coding sequence for the desired protein and its  
CC promoter are flanked by transposase insertion sequences recognised by the  
CC transposase. The transposon based vectors also include multiple Kozak  
CC sequences (which enhance the expression of the transposase gene),  
CC modified multiple codons at the N-terminal end (to facilitate the  
CC transcription of the transposase gene), an effective polyA sequence (to  
CC further enhance the expression of the transposase gene) and an additional  
CC stop codon (to enhance the termination of the transposase gene) and the  
CC method of the invention can be used to produce antibodies for cancer  
CC immunotherapy, infectious disease and toxic agents. The methods and  
CC compositions of producing multimeric proteins are useful in  
CC pharmaceutical, diagnostic and industrial uses (treatment and diagnosis  
CC of cancer). The polypeptide cassettes also include one or more epitopes  
CC or domains for facilitating purification of a desired protein. The  
CC presented nucleotide sequence is the transposon-based vector pTnMCS (CMV-  
CC prepro-HCPro-CPA).

XX SQ Sequence 11590 BP; 2999 A; 2984 C; 2722 G; 2885 T; 0 U; 0 Other;

Query Match 87.5%; Score 1168; DB 13; Length 11590;  
Best Local Similarity 92.1%; Pred. No. 1.8e-233;  
Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

QY 2 AGGTGAGCTGGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCTCTTAGACTCT 61  
DB 5549 AGGTGAGCTGGAGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCTCTTAGACTCT 5608

QY 62 CTGTGAGCTAGCGGATTACATTTTCAGTGGCTTACTGGATGTCTCTGGTCCGCGAGGCTC 121  
DB 5609 CTGTGAGCTCTGGATTACATTTTCAGAAACGCTGGATGAGCTGGTCCGCGAGGCTC 5668

QY 122 CAGGGAAGGGCTCGAGTGGTGTGCTGAAATTAGATTGAAATCTGTAATATTGCAACAC 181  
DB 5669 CAGGGAAGGGCTCGAGTGGTGTGCTGAAATTAGATTGAAATATTGTTGGGACACAG 5728

QY 182 ATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAGAGATGATTCAAATCTAGAC 241  
DB 5729 ACTATCTGCACCCCGTGAAGGCGAGATTACCATCTCAGAGATGATTCAAATCTAGAC 5788

QY 242 TGTATCTGAAATGAAACAGCTCGAAACCGAGGACACAGCCGTGTTATCTGTAC----- 296  
DB 5789 TATATCTGAAATGAAATGAAACCGAGGACACAGCCGTGTTATCTGTACACCG 5848

QY 297 -----AGATTTCATAGCTGGGCGGCGGCAACTAG 328  
DB 5849 GGATTATGATAACATTTGGGGAGTTATCCCTCCCGGAATTGGGGCGAGGAAACCTGG 5908

QY 329 TCACCGTCTCTCAGCTCCACCAAGGGCCCATCGTCTTCCCGTGGACCTCTCTCCA 388  
DB 5909 TCACCGTCTCTCAGCTCCACCAAGGGCCCATCGTCTTCCCGTGGACCTCTCTCCA 5968

QY 389 AGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGGAC 448

[illegible]

XX	Transposon-based vector; transposon; transgenic; vaccine;
KW	immune response; anthrax; botulism; brucellosis; glands; Q fever;
KW	plague; shigellosis; small pox; tularemia; viral encephalitis;
KW	typhus fever; viral hemorrhagic fever; bird; mammal; egg; milk;
KW	antibacterial; anti viral; antimicrobial; anti-inflammatory;
KW	neuroprotective; transposase; ptnMCS; CMV-prepro-HCPro-CPA; ds;
KW	cecropia moth.
XX	
XX	Cytomegalovirus.
OS	Hyalophora cecropia.
OS	Chimeric.
XX	
FH	Key
FT	promoter
FT	Location/Qualifiers
FT	3721..5364
FT	/tag= a
FT	/note= "CMV promoter/enhancer"
FT	5371..5541
FT	/tag= b
FT	/note= "Capsite prepro sequence"
FT	5548..6912
FT	/tag= c
FT	/note= "Heavy Chain gene construct taken from antibody
FT	RM2."
FT	6913..6924
FT	/tag= d
FT	/note= "Pro sequence"
FT	6931..7575
FT	/tag= e
FT	/note= "Light Chain gene construct taken from antibody
FT	RM2"
FT	7582..7989
FT	/tag= f
FT	/note= "Conalbumin polyA sequence"
XX	
PN	W02004067743-A1.
XX	
XX	12-AUG-2004.
XX	
XX	24-DEC-2003; 2003WO-US041269.
XX	
XX	21-JAN-2003; 2003US-0441377P.
PR	21-JAN-2003; 2003US-0441381P.
PR	21-JAN-2003; 2003US-0441392P.
PR	21-JAN-2003; 2003US-0441405P.
PR	21-JAN-2003; 2003US-0441447P.
PR	21-JAN-2003; 2003US-0441502P.
PR	26-JUN-2003; 2003US-00609019.
XX	
PA	(TRAN-) TRANSGENRX INC.
PA	(LOUT ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX	
PI	Cooper RK, Fioretti WC, Cadd GG;
XX	
DR	WPI; 2004-581003/56.
XX	
XX	New polynucleotide (transposon-based vector) cassette comprising gene
PT	interest operably linked to a cecropin prepro sequence, is useful in
PT	producing vaccines to protect an individual against infectious diseases
XX	
PS	Example 4; SEQ ID NO 100; 155pp; English.
XX	
CC	The patent discloses novel, effective and efficient method of producing
CC	multimeric proteins, antibodies using transposon-based vectors, in
CC	transgenic individuals. These proteins can be used as a vaccine.
CC	Immunising individuals with such compositions, comprising vaccines is
CC	capable of generating an immune response, to prevent or ameliorate the
CC	severity of a disease. The invention provides polynucleotide cassettes
CC	containing at least one gene of interest and one or more pro
CC	polynucleotide sequence, where in each gene of interest are operably-
CC	linked to a pro nucleotide sequence of at least one gene of interest.
CC	Transposon-based vector comprises the polynucleotide and further
CC	comprises a transposase gene operably linked to a first promoter and
CC	

CC where the first promoter comprises a modified Kozak sequence, two or more  
 CC genes of interest are each operably-linked to one or more additional  
 CC promoters, and two or more genes of interest and their operably-linked  
 CC promoters are flanked by transposase insertion sequences recognized by a  
 CC transposase encoded by the transposase gene. Many diseases and disease  
 CC causing organisms can be targets of the vaccine of the present invention.  
 CC Some of these include, anthrax, botulism, brucellosis, glanders, Q fever,  
 CC plague, shigellosis, small pox, tularemia, viral encephalitis, typhus  
 CC fever, viral hemorrhagic fever, etc. The preferred animal for production  
 CC of protein is a bird or a mammal. The egg or milk of these animals  
 CC comprises the multimeric protein encoded by the isolated polynucleotide  
 CC of the invention. Hence, these proteins are endowed with varied  
 CC properties and are antibacterial, anti viral, antimicrobial, anti-  
 CC inflammatory, and neuroprotective in nature. The sequence presented here  
 CC is the transposon based vector pTnMCS (CMV-prepro-HCPro-CPA).  
 XX

SQ Sequence 11590 BP; 2999 A; 2984 C; 2722 G; 2885 T; 0 U; 0 Other;

Query Match 87.5%; Score 1168; DB 13; Length 11590;  
 Best Local Similarity 92.1%; Pred. No. 1.8e-233;  
 Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

QY 2 AGGTGACGCTGCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61  
 DB 5549 AGGTGACGCTGACGAGTTCGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 5608  
 QY 62 CCTGTGACGCTAGCGGATTCACCTTTCAGTGGCTACTGATGCTCCTGGGTCCGCCAGGCTC 121  
 DB 5609 CCTGTGACGCTCTGGATTCACCTTTCAGAACGCTGATGAGTGGTTCGCCAGGCTC 5668  
 QY 122 CAGGGAAGGGCTCGAGTGGGTCTGCTGAAATAGATTGAAATCTGATTAATATGCAACAC 181  
 DB 5669 CAGGGAAGGGCTCGAGTGGGTCTGCTGAAATAGATTGAAATCTGATTAATATGCAACAC 5728  
 QY 182 ATTATGCGAGTCTGTAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241  
 DB 5729 ACTATGTGACCCGTGAAAGGCGAGATTACCATCTCAAGAGATGATTCAAAATCTAGAC 5788  
 QY 242 TGTATCTGCAAAATGAACAGCTGAAACCCGAGGACACAGCGTGTATTACTGTAC----- 296  
 DB 5789 TATATCTGCAAAATGAATGCTGAAAGCCGNGGACACAGCGGTATATATCTGTACACGG 5848  
 QY 297 -----AGATTTTCATAGACTGGGGCCAGCGGAACACTAG 328  
 DB 5849 GGATTATGATAACATTTGGGGAGTTATCCCTCCCGCAATTTGGGGCCAGGGAACCTCG 5908  
 QY 329 TCACCGTCTCTAGCCTCCACCAAGGGCCCATCGCTTCCCGCTGGACACCTCTCTCCA 388  
 DB 5909 TCACCGTCTCTAGCCTCCACCAAGGGCCCATCGCTTCCCGCTGGACACCTCTCTCCA 5968  
 QY 389 AGACACCTCTGGGGCACAGCGGCCCTGGGCTGCTCAAGGACTACTTCCCGGAAC 448  
 DB 5969 AGACACCTCTGGGGCACAGCGGCCCTGGGCTGCTCAAGGACTACTTCCCGGAAC 6028  
 QY 449 CGGTGACGGTGTCTGGAATCTCAGCGCCCTTGACAGCGGGCTGCACACCTTCCCGGCTG 508  
 DB 6029 CGGTGACGGTGTCTGGAATCTCAGCGCCCTTGACAGCGGGCTGCACACCTTCCCGGCTG 6088  
 QY 509 TCCTACAGTCTCAGGACTCTATCTCCTCAGACAGCGTGTGACCGTGCCTCTCAGCAGCT 568  
 DB 6089 TCCTACAGTCTCAGGACTCTATCTCCTTAGCAACGTTGGTACCGTGCCTCTCAGCAGCT 6148  
 QY 569 TGGGCCCCCAGACCTACATCTGCAACCTGGAATCAACAGCCCGACCAACCAAGGTGGACA 628  
 DB 6149 TGGGCCCCCAGACCTACATCTGCAACCTGGAATCAACAGCCCGACCAACCAAGGTGGACA 6208  
 QY 629 AGAAAGTGGAGCCCAATCTTTGTGACAAAATCTACACATGCCACCGTGCCTCCAGCCTG 688  
 DB 6209 AGAAAGTGGAGCCCAATCTTTGTGACAAAATCTACACATGCCACCGTGCCTCCAGCCTG 6268  
 QY 689 AACTCGGGGGGACCGGTCACTCTTCTTCTTCCCGGCAAAACCAAGGACACCTCTATGA 748  
 DB 6269 AACTCGGGGGGACCGGTCACTCTTCTTCTTCTTCCCGGCAAAACCAAGGACACCTCTATGA 6328

QY 749 TCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAAGCCAGAACCCCTGAGG 808  
 DB 6329 TCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAAGCCAGAACCCCTGAGG 6388  
 QY 809 TCAAGTTCAACTGGTACGTGGAGCGGCGTGGAGTGCATTAATGCGCAGACAAAAGCGCGGG 869  
 DB 6389 TCAAGTTCAACTGGTACGTGGAGCGGCGTGGAGTGCATTAATGCGCAGACAAAAGCGCGGG 6448  
 QY 869 AGCAGCAGTACAACAGCAGCTACCGTGGTGGTCAAGCTCTCAAGCTCTCCTCCACAGGACT 928  
 DB 6449 AGCAGCAGTACAACAGCAGCTACCGTGGTGGTCAAGCTCTCCTCCACAGGACT 6508  
 QY 929 GGCTGAATGGCAAGGAGTACAAGTGAAGGTCTTCCAAACAAAGCCCTCCACAGCCCCCATCG 988  
 DB 6509 GGCTGAATGGCAAGGAGTACAAGTGAAGGTCTTCCAAACAAAGCCCTCCACAGCCCCCATCG 6568  
 QY 989 AGAAAACCATCTCCAAAGCCAAAGGGGAGCCCCCGAGAACACACAGGTGTACACCTTGCCCC 1048  
 DB 6569 AGAAAACCATCTCCAAAGCCAAAGGGGAGCCCCCGAGAACACACAGGTGTACACCTTGCCCC 6628  
 QY 1049 CATCCCGGATGAGCTGACCAAGAACAGGTCAAGCTCTGCTGCTGCTCAAGGGCTTCT 1108  
 DB 6629 CATCCCGGATGAGCTGACCAAGAACAGGTCAAGCTCTGCTGCTGCTCAAGGGCTTCT 6688  
 QY 1109 ATCCCGAGCAGCATCGCGCTGGAGTGGGAGAGCAATGGCGAGCCGAGAACAACTACAAGA 1168  
 DB 6689 ATCCCGAGCAGCATCGCGCTGGAGTGGGAGAGCAATGGCGAGCCGAGAACAACTACAAGA 6748  
 QY 1169 CACAGCTCCCGTGTGGACTCCGAGCGGTCTTCTTCTCTTACAGCAAGCTCAACCGTGG 1228  
 DB 6749 CACAGCTCCCGTGTGGACTCCGAGCGGTCTTCTTCTCTTACAGCAAGCTCAACCGTGG 6808  
 QY 1229 ACAAGAGCAGGTGGGAGCGGGAAGCTTCTCATGCTCCGTGATGATGAGGCTCTGC 1288  
 DB 6809 ACAAGAGCAGGTGGGAGCGGGAAGCTTCTCATGCTCCGTGATGATGAGGCTCTGC 6868  
 QY 1289 ACAACCACTACACGCAAGAGAGCTCTCCCTGCTCTCCGGGTAAA 1332  
 DB 6869 ACAACCACTACACGCAAGAGAGCTCTCCCTGCTCTCCGGGTAAA 6912

## RESULT 6

ADS91477

ID ADS91477 standard; DNA; 11593 BP.

AC ADS91477;  
 XX

DT 02-DEC-2004 (first entry)

XX Transposon-based vector pTnMCS (CMV-prepro-HCPro-Lys-CPA).

XX ds, multimeric protein; egg-laying; avian; milk producing animal;  
 KW transgenic; transposase; cancer; immunotherapy; infectious disease;  
 KW pTnMCS; CMV-prepro-HCPro-Lys-CPA; cecropia moth; chicken; gene; CMV;  
 KW chimeric; RM2 antibody.

XX Hyalophora cecropia.

OS Gallus gallus.

OS Cytomegalovirus.

OS Synthetic.

XX Unidentified.

Key Location/Qualifiers

FT misc\_feature 1..3715

FT /tag= a

FT /note= "From vector pTnMCS"

FT promoter 3721..5364

FT /tag= b

FT /note= "CMV promoter/enhancer"

FT misc\_feature 5371..5541

FT /tag= c

FT /note= "Capsite/prepro from cecropia moth"

FT misc\_feature 5548. .6912  
 FT /\*tag= d  
 FT /note= "Heavy chain gene construct from RM2 antibody"  
 FT 6913. .6927  
 FT misc\_feature  
 FT /\*tag= e  
 FT /note= "Pro sequence from cecropia moth"  
 FT 6934. .7578  
 FT misc\_feature  
 FT /\*tag= f  
 FT /note= "light chain gene construct from RM2 antibody"  
 FT 7585. .7992  
 FT polyA\_site  
 FT /\*tag= g  
 FT /note= "Chicken conalbumin"  
 FT 7994. .11593  
 FT misc\_feature  
 FT /\*tag= h  
 FT /note= "this portion of the sequence is from cloning  
 FT vector pTnMCS."  
 FT  
 XX  
 PN  
 XX  
 XX WO2004067706-A2.  
 PD 12-AUG-2004.  
 XX  
 XX 24-DEC-2003; 2003WO-US041261.  
 XX  
 XX 21-JAN-2003; 2003US-0441377P.  
 PR 21-JAN-2003; 2003US-0441381P.  
 PR 21-JAN-2003; 2003US-0441392P.  
 PR 21-JAN-2003; 2003US-0441405P.  
 PR 21-JAN-2003; 2003US-0441477P.  
 PR 21-JAN-2003; 2003US-0441502P.  
 PR 26-JUN-2003; 2003US-00609019.  
 XX  
 XX (TRAN-) TRANSGENRX INC.  
 PA (LOU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.  
 PA  
 PA  
 PI Cooper RK, Fioretti WC, Cadd GG;  
 XX WPI; 2004-580985/56.  
 DR  
 XX  
 XX New isolated polynucleotide having two or more genes of interest and pro  
 PT nucleotide sequences, for use in pharmaceutical, diagnostic and  
 PT industrial uses, such as in treating and diagnosing cancer.  
 XX  
 XX Example 4; SEQ ID NO 101; 119pp; English.  
 PS  
 XX  
 CC The present invention provides a new, effective and efficient method for  
 CC producing multimeric proteins in the egg-laying (avian) or milk producing  
 CC animals. The multimeric proteins include associated multimeric proteins  
 CC (two or more associated polypeptides) and multivalent multimeric proteins  
 CC (a single polypeptide is encoded by multiple genes). The expression and  
 CC formation of a multimeric protein is achieved by administering a  
 CC polynucleotide cassette containing genes of interest (for example  
 CC proinsulin, antibodies, cytokines, etc.). The polynucleotide cassettes  
 CC are administered to egg-laying or milk producing animals to create the  
 CC transgenic animals. Several different signal sequences and promoters can  
 CC be used to achieve the deposition of the multimeric protein in the egg or  
 CC milk. The transposon based vector has been used for the incorporation of  
 CC polynucleotide cassettes into the genomic DNA. The polynucleotide  
 CC cassette may additionally contain multiple pro sequences, prepro  
 CC sequences, cecropin prepro sequences and cleavage sites. Each gene  
 CC encodes a polypeptide which forms part of a multimeric protein. The pro  
 CC portion of the sequences has been used to facilitate appropriate  
 CC processing, expression and formation of multimeric proteins. These  
 CC multimeric proteins can be produced much more efficiently and  
 CC economically by this method than earlier conventional methods. This  
 CC improved method can produce the multimeric proteins on a large scale. The  
 CC transposon-based vectors of the invention produce high integration  
 CC frequencies compared to the earlier vectors. The intratesticular  
 CC injections with the novel transposon based vector produces 77 % sperm  
 CC positive roosters (compared to 41 % of a previous method). The transposon-  
 CC based vectors of the invention include a transposase gene linked to a  
 CC first promoter and a coding sequence of a desired protein linked to a  
 CC second promoter. The coding sequence for the desired protein and its  
 CC promoter are flanked by transposase insertion sequences recognised by the

CC transposase. The transposon based vectors also include multiple kozak  
 CC sequences (which enhance the expression of the transposase gene),  
 CC modified multiple codons at the N-terminal end (to facilitate the  
 CC transcription of the transposase gene), an effective polyA sequence (to  
 CC further enhance the expression of the transposase gene) and an additional  
 CC stop codon (to enhance the termination of transposon synthesis). The  
 CC method of the invention can be used to produce antibodies for cancer  
 CC immunotherapy, infectious disease and toxic agents. The methods and  
 CC compositions of producing multimeric proteins are useful in  
 CC pharmaceutical, diagnostic and industrial uses (treatment and diagnosis  
 CC of cancer). The polypeptide cassettes also include one or more epitopes  
 CC or domains for facilitating purification of a desired protein. The  
 CC presented nucleotide sequence is the transposon-based vector pTnMCS (CMV-  
 CC prepro-NCPro-Lys-CPA).

XX Sequence 11593 BP; 3004 A; 2983 C; 2719 G; 2887 T; 0 U; 0 Other;  
 SQ

Query Match 87.5%; Score 1168; DB 13; Length 11593;  
 Best Local Similarity 92.1%; Pred. No. 1.8e-233;  
 Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

QY 2 AGGTGACGCTGTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGGTCCCTTAGACTCT 61  
 DB 5549 AGGTGACGCTGCAGGAGTCGGGGGAGGCTTGGTAAAGCCCGGGGGGTCCCTTAGACTCT 5608  
 QY 62 CCGTGTGACGTAGCGGATTCACTTTTCAGTGGCTACTTGGATGTCCTGGGTCCGCCAGGCTC 121  
 DB 5609 CCGTGTGACGCTCTGGATTCACTTTTCAGAAACGCCCTGGATGAGTGGGTCCGCCAGGCTC 5668  
 QY 122 CAGGGAAGGGGCTCGAGTGGGTTCGTAATTTAGATTGAAATCTGTATAATTTATGCAACAC 181  
 DB 5669 CAGGGAAGGGGCTGGAGTGGGTTCGTAATTTAGATTGAAATTTATGTTGGGACAAACAG 5728  
 QY 182 ATTATCGCGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCTAGAC 241  
 DB 5729 ACTATGCTGCACCCGCTGAAGGCAGATTTCACCATCTCAAGAGATGATTCAAATTCACACGT 5788  
 QY 242 TGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGTGTATTACTGTAC----- 296  
 DB 5789 TATATCTGCAATGAATAGTACCTGAAACCGAGGACACAGCCGTGTATTACTGTACACCG 5848  
 QY 297 -----AGATTTTCATAGACTGGGGCCAGGGAACACTAG 328  
 DB 5849 GGATTTATGATAACATTTGGGGGAGTTATCCCTCCCGGAATTTGGGGCCAGGGAACCTCG 5908  
 QY 329 TCACCGTCTCCTCAGGCTCCACCAAGGGCCCATCGGTCTTCCCTCCCTGGCAACCTCTCTCA 388  
 DB 5909 TCACCGTCTCCTCAGGCTCCACCAAGGGCCCATCGGTCTTCCCTCCCTGGCAACCTCTCTCA 5968  
 QY 389 AGAGCACCTCTCGGGGACAGCGGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCGAAC 448  
 DB 5969 AGAGCACCTCTCGGGGACAGCGGCCCTGGGCTGCTGCTCAAGGACTACTTCCCCGAAC 6028  
 QY 449 CGGTGACGCTGTCTGTGAACTCAGGCGCCCTGACAGCGCGGTGCAACACTTCCCGGCTG 508  
 DB 6029 CGGTGACGCTGTCTGTGAACTCAGGCGCCCTGACAGCGCGGTGCAACACTTTCGCGCTG 6088  
 QY 509 TCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTCACCGTCCCTCCAGCAGCT 568  
 DB 6089 TCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTCACCGTCCCTCCAGCAGCT 6148  
 QY 569 TGGGACCCAGACCTACATCTGCAACGTGAATCAAAAGCCCGAGCAACACCAAGGTGGACA 628  
 DB 6149 TGGGACCCAGACCTACATCTGCAACGTGAATCAAAAGCCCGAGCAACACCAAGGTGGACA 6208  
 QY 629 AGAAGTGGAGCCCAAACTTTGTGCAAACTCAACATCATGATGCGCCACCGTCCCGACGACT 688  
 DB 6209 AGAAGTGGAGCCCAAACTTTGTGCAAACTCAACATCATGATGCGCCACCGTCCCGACGACT 6268  
 QY 689 AACTCGCGGGGACCGTCAAGTCTTCTTCCCCCAAAACCCCAAGGACACCTCATGA 748  
 DB 6269 AACTCTCGGGGACCGTCAAGTCTTCTTCCCCCAAAACCCCAAGGACACCTCATGA 6328





Db 5549 AGTGCAGCTGCAGAGTGGGGGAGGCTTGGTAAAGCGGGGGGTCCCTTAGAGTCT 5608  
Qy 62 CTTGTGAGCTAGCGATTCACTTTCACTGAGTGTCTGAGTGTCTGGGTCCGCGAGGCTC 121  
Db CTTGTGAGCTAGCGATTCACTTTCACTGAGTGTCTGAGTGTCTGGGTCCGCGAGGCTC 5668  
Qy 122 CAGGGAAGGGCTCGAGTGGGTGCTGAAATTAGATTGAAATCTGATTAATTATGCAACAC 181  
Db CAGGGAAGGGCTCGAGTGGGTGCTGAAATTAGATTGAAATCTGATTAATTATGCAACAC 5728  
Qy 182 ATTATCGGAGTCTGTGAAGGGGAAATTCACATCTCAAGAGATGATTCAAAATCTTAGAC 241  
Db ACTATGCTGCACCGTGAAGGCAGATTCAACATCTCAAGAGATGATTCAAAATCTTAGAC 5788  
Qy 242 TGTATCTGCAATGAAACAGCTGAAACCGAGGACACAGCCGTTGTTACTGTAC----- 296  
Db TATATCTGCAATGAAATAGCTGAAAGCGGAGGACACAGCCGTTATATTACTGTACACGG 5848  
Qy 297 -----AGATTTTCATAGACTGGGGCCAGGGAACACTAG 328  
Db 5849 GSATTATGATAAATTGGGGGAGTTATCCCTCCCCCGAATTGGGGCCAGGGAACCCCTGG 5908  
Qy 329 TCACCGTCTCTCAGAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGCAGCCCTCTCTCCA 388  
Db TCACCGTCTCTCAGAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGCAGCCCTCTCTCCA 5968  
Qy 389 AGAGCACTCTGGGGGACAGCGCCCTGGGTGCTCTGCTCAAGGACTACTTCCCGGAAAC 448  
Db 5969 AGAGCACTCTGGGGGACAGCGCCCTGGGTGCTCTGCTCAAGGACTACTTCCCGGAAAC 6028  
Qy 449 CGGTGACGGTCTGTGAACTCAGGCGCCCTGACAGCGCGTGACACCTTCCCGGCTG 508  
Db 6029 CGGTGACGGTCTGTGAACTCAGGCGCCCTGACAGCGCGTGACACCTTCCCGGCTG 6088  
Qy 509 TCCTACAGTCTCAGGACTCTACTCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCT 568  
Db 6089 TCCTACAGTCTCAGGACTCTACTCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCT 6148  
Qy 569 TGGGCAACCCAGACTTACATCTGAACTGAACTCAAGCCGAGCAACCAAGGTTGGACA 628  
Db 6149 TGGGCAACCCAGACTTACATCTGAACTGAACTCAAGCCGAGCAACCAAGGTTGGACA 6208  
Qy 629 AGAAGTGGAGCCCAATCTTGTGACAAACTCACAATGCAAGCCGAGCAACCAAGGTTGGACA 688  
Db 6209 AGAAGTGGAGCCCAATCTTGTGACAAACTCACAATGCAAGCCGAGCAACCAAGGTTGGACA 6268  
Qy 689 AACTCGCGGGGACCGTCACTCTCTCTTCCCGCCCAAAACCAAGGACACCTCATGA 748  
Db 6269 AACTCTGGGGGACCGTCACTCTCTCTTCCCGCCCAAAACCAAGGACACCTCATGA 6328  
Qy 749 TCTCCCGGACCCCTGAGGTCAATGCGTGTGTGAGCGTGTGAGCGACGAAGACCCCTGAGG 808  
Db 6329 TCTCCCGGACCCCTGAGGTCAATGCGTGTGTGAGCGTGTGAGCGACGAAGACCCCTGAGG 6388  
Qy 809 TCAAGTTCACTGTGTAGTGTGAGCGTGTGAGTGTGATATGCAAGACAAAGCCCGGG 868  
Db 6389 TCAAGTTCACTGTGTAGTGTGAGCGTGTGAGTGTGATATGCAAGACAAAGCCCGGG 6448  
Qy 869 AGGAGCAGTACAAAGCAGCAGTACCGTGTGTGAGCGTCTCAGCGTCTGACCGAGGACT 928  
Db 6449 AGGAGCAGTACAAAGCAGCAGTACCGTGTGTGAGCGTCTCAGCGTCTGACCGAGGACT 6508  
Qy 929 GGCTGAATGGCAGGAGTACAGTGTGAAGTGTCTCAACAAAGCCCTCCAGCCCCCATCG 988  
Db 6509 GGCTGAATGGCAGGAGTACAGTGTGAAGTGTCTCAACAAAGCCCTCCAGCCCCCATCG 6568  
Qy 989 AGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAAGGTTGTACACCTTGCCCC 1048  
Db 6569 AGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAAGGTTGTACACCTTGCCCC 6628  
Qy 1049 CATCCCGGGATGAGTCAACCAAGAACAGGTGACCTGCTGCTGCTCAAAAGGCTTCT 1108  
Db 6629 CATCCCGGGATGAGTCAACCAAGAACAGGTGACCTGCTGCTGCTCAAAAGGCTTCT 6688

## RESULT 8

ADS91474

ID ADS91474 standard; DNA; 11964 BP.

XX ADS91474;

XX AC ADS91474;

XX DT 02-DEC-2004 (first entry)

XX DE Transposon-based vector pTnMCS (CHOVep-prepro-HCPro-CPA).

XX ds; multimeric protein; egg-laying; avian; milk producing animal;

XX KW transgenic; transposase; cancer; immunotherapy; infectious disease;

XX KW pTnMCS; CHOVep-prepro-HCPro-CPA; cecropia moth; chicken; gene; chimeric;

XX KW RM2 antibody.

XX OS Hyalophora cecropia.

XX OS Gallus gallus.

XX OS Synthetic.

XX OS Unidentified.

XX Key Location/Qualifiers

FT misc\_feature 1..3715

FT /tag= a

FT /note= "Vector pTnMCS"

FT enhancer 3721..4395

FT /tag= b

FT /note= "Chicken ovalbumin enhancer"

FT promoter 4402..5738

FT /tag= c

FT /note= "Chicken ovalbumin promoter"

FT misc\_feature 5745..5915

FT /tag= d

FT /note= "Capsite prepro from cecropia moth"

FT misc\_feature 5922..7286

FT /tag= e

FT /note= "Heavy chain gene construct from antibody RM2"

FT misc\_feature 7287..7298

FT /tag= f

FT /note= "Pro sequence from cecropia moth"

FT misc\_feature 7305..7949

FT /tag= g

FT /note= "Light chain gene construct from antibody RM2"

FT polyA\_site 7956..8363

FT /tag= h

FT /note= "Chicken conalbumin poly A"

FT misc\_feature 8365..11964

FT /tag= i

FT /note= "This portion is from cloning vector pTnMCS."

XX WO2004067706-A2.

XX 12-AUG-2004.

XX 24-DEC-2003; 2003WO-US041261.

XX









Example 4; SEQ ID NO 99; 119pp; English.

PS The present invention provides a new, effective and efficient method for  
 XX producing multimeric proteins in the egg-laying (avian) or milk producing  
 CC animals. The multimeric proteins include associated multimeric proteins  
 CC (two or more associated polypeptides) and multivalent multimeric proteins  
 CC (a single polypeptide is encoded by multiple genes). The expression and  
 CC formation of a multimeric protein is achieved by administering a  
 CC polynucleotide cassette containing genes of interest (for example  
 CC proinsulin, antibodies, cytokines, etc.). The polynucleotide cassettes  
 CC are administered to egg-laying or milk producing animals to create the  
 CC transgenic animals. Several different signal sequences and promoters can  
 CC be used to achieve the deposition of the multimeric protein in the egg or  
 CC milk. The transposon based vector has been used for the incorporation of  
 CC polynucleotide cassettes into the genomic DNA. The polynucleotide  
 CC cassette may additionally contain multiple pro sequences, prepro  
 CC sequences, cecropin prepro sequences and cleavage sites. Each gene  
 CC encodes a polypeptide which forms part of a multimeric protein. The pro  
 CC portion of the sequences has been used to facilitate appropriate  
 CC processing, expression and formation of multimeric proteins. These  
 CC multimeric proteins can be produced much more efficiently and  
 CC economically by this method than earlier conventional methods. This  
 CC improved method can produce the multimeric proteins on a large scale. The  
 CC transposon-based vectors of the invention produce high integration  
 CC frequencies compared to the earlier vectors. The intratesticular  
 CC injections with the novel transposon based vector produces 77 % sperm  
 CC positive rosters (compared to 41% of a previous method). The transposon-  
 CC based vectors of the invention include a transposase gene linked to a  
 CC first promoter and a coding sequence of a desired protein linked to a  
 CC second promoter. The coding sequence of the desired protein and its  
 CC promoter are flanked by transposase insertion sequences recognised by the  
 CC transposase. The transposon based vectors also include multiple Kozak  
 CC sequences (which enhance the expression of the transposase gene),  
 CC modified multiple codons at the N-terminal end (to facilitate the  
 CC transcription of the transposase gene), an effective polyA sequence (to  
 CC further enhance the expression of the transposase gene) and an additional  
 CC stop codon (to enhance the termination of transposon synthesis). The  
 CC method of the invention can be used to produce antibodies for cancer  
 CC immunotherapy, infectious disease and toxic agents. The methods and  
 CC compositions of producing multimeric proteins are useful in  
 CC pharmaceutical, diagnostic and industrial uses (treatment and diagnosis  
 CC of cancer). The polypeptide cassettes also include one or more epitopes  
 CC or domains for facilitating purification of a desired protein. The  
 CC presented nucleotide sequence is the transposon-based vector pTnMS  
 CC (CHOVep-prepro-HCPro-Lys-CPA).

XX SQ Sequence 11967 BP; 3263 A; 2975 C; 2686 G; 3043 T; 0 U; 0 Other;

Query Match 87.5%; Score 1168; DB 13; Length 11967;  
 Best Local Similarity 92.1%; Pred. No. 1.8e-233;  
 Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;  
 QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTCT 61  
 DB 5923 AGTGCAGCTGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTCT 5982  
 QY 62 CCTGTCCAGCTACGGATTCACTTTCAGTGGCTACTGGATGTCTGGGTCCGCGAGCTC 121  
 DB 5983 CCTGTCCAGCTCTGGATTCACTTTCAGAAACCCCTGGATGAGTGGGTCCGCGAGCTC 6042  
 QY 122 CAGGGAAGGGGCTCGAGTGGTGTGCTGAATTAGATTGAATCTGATAATTATGCAACAC 181  
 DB 6043 CAGGGAAGGGGCTGGAGTGGTTCGGCGTATTAAAGCAAAATTGATGTGGGACAAACAG 6102  
 QY 182 ATTATGCGGAGTCTGTGAAGGGGAAATTACCACTCTCAAGAGATGATTCAAAATCTTAGAC 241  
 DB 6103 ACTATGTGCACCCGTGAAGGGGAGATTACCACTCTCAAGAGATGATTCAAAAAACACGT 6162  
 QY 242 TGTATCTGCAATGACAGCCTGAAACCCGAGGACACGCCGTGTTACTGTAC----- 296  
 DB 6163 TATATCTGCAATGAAATAGCCTGAAAGCCGAGGACACAGCCGTATTATTACTGTACCACGG 6222  
 QY 297 -----AGATTTCATAGACTGGGGCCAGGGAACACTAG 328

DB 6223 GGATTATGATAACATTGGGGAGTTATCCCTCCCCGAATTGGGGCCAGGGAACCTCG 6282  
 QY 329 TCACCGTCTCTCAGCTCCACCAAGGGCCATCGGTCTTCCCTTGGCAGCCCTCTCTCCA 388  
 DB 6283 TCACCGTCTCTCAGCTCCACCAAGGGCCATCGGTCTTCCCTTGGCAGCCCTCTCTCCA 6342  
 QY 389 AGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGACTACTTCCCGGAC 448  
 DB 6343 AGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGACTACTTCCCGGAC 6402  
 QY 449 CGGTGACCGTGTCTGGGAACCTCAGCGGCCCTCACCAGCGGGCTGCACACCTTCCCGGCTG 508  
 DB 6403 CGGTGACCGTGTCTGGGAACCTCAGCGGCCCTCACCAGCGGGCTGCACACCTTCCCGGCTG 6462  
 QY 509 TCTTACAGTCTCAGGACTCTACTCTCTCAGAGCGTGTGACCGTGCCTCCTCAGAGCT 568  
 DB 6463 TCTTACAGTCTCAGGACTCTACTCTCTTAGCAAGCTGTGACCGTGCCTCCTCAGAGCT 6522  
 QY 569 TGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGAGTGGACA 628  
 DB 6523 TGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGAGTGGACA 6582  
 QY 629 AGAAGTGGAGGCCCAAACTCTGTGACAAAACCTCACACATGCCACCGTGCCTCAGCACCTG 688  
 DB 6583 AGAAGTGGAGGCCCAAACTCTGTGACAAAACCTCACACATGCCACCGTGCCTCAGCACCTG 6642  
 QY 689 AACTCGGGGGGACCGTCACTCTTCTTCTTCCCTCCAAAACCCCAAGAGACCTCTCATGA 748  
 DB 6643 AACTCTCGGGGGGACCGTCACTCTTCTTCTTCTTCCCTCCAAAACCCCAAGAGACCTCTCATGA 6702  
 QY 749 TCTCCCGGACCCCTCAGGTCAATCGGTGTGGTGGAGCTGAGCCACGAAGACCTCTGAGG 808  
 DB 6703 TCTCCCGGACCCCTCAGGTCAATCGGTGTGGTGGAGCTGAGCCACGAAGACCTCTGAGG 6762  
 QY 809 TCAAGTTCAACTGTGTCAGTGGACGGCTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 868  
 DB 6763 TCAAGTTCAACTGTGTCAGTGGACGGCTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 6822  
 QY 869 AGGAGAGTCAACAGACGTACCTGTGTGTGAGCTCTTCACTCTCTGTCGACAGGACT 928  
 DB 6823 AGGAGAGTCAACAGACGTACCTGTGTGTGAGCTCTTCACTCTCTGTCGACAGGACT 6882  
 QY 929 GGTCTGAATGGCAAGAGTACAAGTCAAGTCTCCAAACAAAGCCCTCCAGCCGCCCATCG 988  
 DB 6883 GGTCTGAATGGCAAGAGTACAAGTCAAGTCTCCAAACAAAGCCCTCCAGCCGCCCATCG 6942  
 QY 989 AGAAAACCATCTTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCTCGCCCC 1048  
 DB 6943 AGAAAACCATCTTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCTCGCCCC 7002  
 QY 1049 CATCCGGGATGAGTGCACCAAGAACCGAGGTGAGCTGACCTGCTGTGTCAAGGCTTCT 1108  
 DB 7003 CATCCGGGATGAGTGCACCAAGAACCGAGGTGAGCTGACCTGCTGTGTCAAGGCTTCT 7062  
 QY 1109 ATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGCGAGCCGAGAACCAACTACAAGA 1168  
 DB 7063 ATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGCGAGCCGAGAACCAACTACAAGA 7122  
 QY 1169 CCACGCTCCCGTGTGTGACTCCGACGGCTCTTCTTCTCTTACAGCAAGCTCACCGTGG 1228  
 DB 7123 CCACGCTCCCGTGTGTGACTCCGACGGCTCTTCTTCTCTTACAGCAAGCTCACCGTGG 7182  
 QY 1229 ACAAGAGCGGTGGGAGCGAGGAAAGCTTCTCATGTCTCGTGTATGATGAGGCTCTGC 1288  
 DB 7183 ACAAGAGCGGTGGGAGCGAGGAAAGCTTCTCATGTCTCGTGTATGATGAGGCTCTGC 7242  
 QY 1289 ACAACCACTTACACGAGAGAGGCTCTCCCTCTCTCCGGGTAAA 1332  
 DB 7243 ACAACCACTTACACGAGAGAGGCTCTCCCTCTCTCCGGGTAAA 7286

RESULT 11

ADT62604  
 ID ADT62604 standard; DNA; 11967 BP.  
 AC ADT62604;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 DE Transposon based vector pTnMCS (CMV-prepro-HCPro-Lys-CPA).  
 XX  
 KW Transposon-based vector; transposon; transgenic; vaccine;  
 KW immune response; anthrax; botulism; brucellosis; glanders; Q fever;  
 KW plague; shigellosis; small pox; tularemia; viral encephalitis;  
 KW typhus fever; viral hemorrhagic fever; bird; mammal; egg; milk;  
 KW antibacterial; anti viral; antimicrobial; anti-inflammatory;  
 KW neuroprotective; transposase; pTnMCS; CMV-prepro-HCPro-Lys-CPA; ds;  
 KW cecropia moth.  
 XX  
 OS Gallus gallus.  
 OS Hyalophora cecropia.  
 OS Chimeric.  
 XX  
 PH Key Location/Qualifiers  
 FT enhancer 3721..4395  
 FT /tag= a  
 FT /note= "Ovalbumin enhancer. This region of the sequence is  
 FT not identical to the GenBank sequence (Bos taurus) as  
 FT mentioned in the specification."  
 FT 4402..5738  
 FT promoter /tag= b  
 FT /note= "Ovalbumin promoter"  
 FT 5745..5915  
 FT misc\_feature /tag= c  
 FT 5922..7286  
 FT misc\_feature /tag= d  
 FT /note= "Heavy chain gene construct taken from antibody  
 FT RM2"  
 FT 7287..7301  
 FT misc\_feature /tag= e  
 FT /note= "Pro sequence"  
 FT 7308..7952  
 FT misc\_feature /tag= f  
 FT /note= "Light chain gene construct"  
 FT 7959..8366  
 FT polyA\_signal /tag= g  
 FT /note= "Conalbumin PolyA sequence"  
 XX  
 PN WO2004067743-A1.  
 XX  
 PD 12-AUG-2004.  
 XX  
 PP 24-DEC-2003; 2003WO-US041269.  
 XX  
 PR 21-JAN-2003; 2003US-0441377P.  
 PR 21-JAN-2003; 2003US-0441381P.  
 PR 21-JAN-2003; 2003US-0441392P.  
 PR 21-JAN-2003; 2003US-0441405P.  
 PR 21-JAN-2003; 2003US-0441447P.  
 PR 21-JAN-2003; 2003US-0441502P.  
 PR 26-JUN-2003; 2003US-00609019.  
 XX  
 PA (TRAN-) TRANSGENIX INC.  
 PA (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.  
 XX  
 PI Cooper RK, Fioretti WC, Cadd GG;  
 XX  
 DR WPI; 2004-581003/56.  
 XX  
 PT New polynucleotide (transposon-based vector) cassette comprising gene of  
 PT interest operably linked to a cecropin prepro sequence, is useful in  
 PT producing vaccines to protect an individual against infectious diseases.  
 XX  
 PS Example 4; SEQ ID NO 99; 155pp; English.

XX The patent discloses novel, effective and efficient method of producing  
 CC multimeric proteins, antibodies using transposon-based vectors, in  
 CC transgenic individuals. These proteins can be used as a vaccine.  
 CC Immunising individuals with such compositions, comprising vaccines is  
 CC capable of generating an immune response, to prevent or ameliorate the  
 CC severity of a disease. The invention provides polynucleotide cassettes  
 CC containing at least one gene of interest and one or more pro  
 CC polynucleotide sequence, where in each gene of interest are operably-  
 CC linked to a pro nucleotide sequence of at least one gene of interest. The  
 CC transposon-based vector comprises the polynucleotide and further  
 CC comprises a transposase gene operably linked to a first promoter and  
 CC where the first promoter comprises a modified kozak sequence, two or more  
 CC genes of interest are each operably-linked to one or more additional  
 CC promoters, and two or more genes of interest and their operably-linked  
 CC promoters are flanked by transposase insertion sequences recognized by a  
 CC transposase encoded by the transposase gene. Many diseases and disease  
 CC causing organisms can be targets of the vaccine of the present invention.  
 CC Some of these include, anthrax, botulism, brucellosis, glanders, Q fever,  
 CC plague, shigellosis, small pox, tularemia, viral encephalitis, typhus  
 CC fever, viral hemorrhagic fever, etc. The preferred animal for production  
 CC of protein is a bird or a mammal. The egg or milk of these animals  
 CC comprises the multimeric protein encoded by the isolated polynucleotide  
 CC of the invention. Hence, these proteins are endowed with varied  
 CC properties and are antibacterial, anti viral, antimicrobial, anti-  
 CC inflammatory, and neuroprotective in nature. The sequence presented here  
 CC is the transposon based vector pTnMCS (CMV-prepro-HCPro-Lys-CPA).  
 XX  
 SQ Sequence 11967 BP; 3263 A; 2975 C; 2686 G; 3043 T; 0 U; 0 Other;  
 Query Match 87.5%; Score 1168; DB 13; Length 11967;  
 Best Local Similarity 92.1%; Pred. No. 1.8e-233;  
 Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;  
 QY 2 AGGTGACGTGGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTCT 61  
 DB 5923 AGGTGACGTGGAGGAGTGGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGAGTCT 5982  
 QY 62 CCTGTGACGTAGCGGATTCACTTTTCAGTGGCTTACTGGATGTCTGGTCCGCCAGGCTC 121  
 DB 5983 CCTGTGACGCTCTGGATTCACTTTTCAGAAACGCTGGATGAGTGGTCCGCCAGGCTC 6042  
 QY 122 CAGGGAAGGGGCTCGAGTGGTGGTGAATAAGATTAGATTGAAATCTGATAATATTGCAACAC 181  
 DB 6043 CAGGGAAGGGGCTGGAGTGGTGGTGAATAAGAAATTTGATGGTGGGACAAACAG 6102  
 QY 182 ATTATCGGAGTCTGTGAAGGGAATTCACCATCTCAGAGATGATTCAAATCTAGAC 241  
 DB 6103 ACTATGCTGCACCCGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAATAACACGT 6162  
 QY 242 TGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCCGTGTATTACTGTAC----- 296  
 DB 6163 TATATCTGCAATGAATAGCTGAAAGCCGAGGACACAGCCGTATATTACTGTACCAAGG 6222  
 QY 297 -----AGATTTCAATAGCTGGGGCCAGGGAACTAG 328  
 DB 6223 GGATTATGATAACATTTGGGGAGATTATCCCTCCCGGAATTGGGGCCAGGAAACCTTGG 6282  
 QY 329 TCACCGTCTCTCAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGACCTCTCTCCA 388  
 DB 6283 TCACCGTCTCTCAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGACCTCTCTCCA 6342  
 QY 389 AGAGCACCTCTGGGGGCACAGCGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGGAAC 448  
 DB 6343 AGAGCACCTCTGGGGGCACAGCGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGGAAC 6402  
 QY 449 CGGTGACGCTGTGCTGGAACCTCAGGGCCCTGACACAGCGCGTGCACACCTTCCCGGCTG 508  
 DB 6403 CGGTGACGCTGTGCTGGAACCTCAGGGCCCTGACACAGCGCGTGCACACCTTCCCGGCTG 6462  
 QY 509 TCCTACAGTCTCAGGACTCTACTCCCTGACGAGCGTGGTGGCGCTCCCTCAGGAGCT 568  
 DB 6463 TCCTACAGTCTCAGGACTCTACTCCCTGACGAGCGTGGTGGCGCTCCCTCAGGAGCT 6522

QY 569 TGGCACCAGACCTACATCTGAACTGTAATCACAGCCAGCAACACCAAGGTGACA 628  
 DB 6523 TGGCACCAGACCTACATCTGAACTGTAATCACAGCCAGCAACACCAAGGTGACA 6582  
 QY 629 AGAAGTGGAGCCCAATCTTTGTGACAAAATCTCACACATGCCACCGTGCCACGACCTG 688  
 DB 6583 AGAAGTTGAGCCCAATCTTTGTGACAAAATCTCACACATGCCACCGTGCCACGACCTG 6642  
 QY 689 AACTCGGGGGGACCGTCACTGCTTCTCTTCCCTCCCAAAACCCAGGACACCTCATGA 748  
 DB 6643 AACTCTCTGGGGGACCGTCACTGCTTCTCTTCCCTCCCAAAACCCAGGACACCTCATGA 6702  
 QY 749 TCTCCCGGACCCCTGAGGTCACTGCTGCTGCTGAGCGTGCAGCCAGAGACCTTGAGG 808  
 DB 6703 TCTCCCGGACCCCTGAGGTCACTGCTGCTGAGCGTGCAGCCAGAGACCTTGAGG 6762  
 QY 809 TCAAGTTCAACTGTTACGTGAGCGGTGAGGTGATATGTCACAGCAAAAGCCGCGGG 868  
 DB 6763 TCAAGTTCAACTGTTACGTGAGCGGTGAGGTGATATGTCACAGCAAAAGCCGCGGG 6822  
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 QY 929 GGCTGAATGCAAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCG 988  
 DB 6883 GGCTGAATGCAAGGAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCG 6942  
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 DB 7063 ATCCAGCAGCATCGCGGTGAGTGGAGAGCAATGGCGAGCGGAGAACCACTACAAGA 7122  
 QY 1169 CCAAGCTCCCGTCTGAGTCCGAGCGGTCTCTTCTCTACAGCAAGCTCACCGTGG 1228  
 DB 7123 CCAAGCTCCCGTCTGAGTCCGAGCGGTCTCTTCTCTACAGCAAGCTCACCGTGG 7182  
 QY 1229 ACAAGAGCAGTGGCAGCAGGGAAGCTTCTCTCATGCTCCGATGATGAGGCTCTGC 1288  
 DB 7183 ACAAGAGCAGTGGCAGCAGGGAAGCTTCTCTCATGCTCCGATGATGAGGCTCTGC 7242  
 QY 1289 ACAACCACTACACGAGAGAGCTCTCCCTGTCTCCGGTAAA 1332  
 DB 7243 ACAACCACTACACGAGAGAGCTCTCCCTGTCTCCGGTAAA 7286

## RESULT 12

AD591480  
 ID AD591480 standard; DNA; 11970 BP.  
 AC AD591480;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Transposon-based vector pTnMod (CMV-prepro-HCPro-CPA).  
 XX  
 KW ds, multimeric protein; egg-laying; avian; milk producing animal;  
 KW transgenic; transposase; cancer; immunotherapy; infectious disease;  
 KW pTnMod; CMV-prepro-HCPro-CPA; cecropia moth; chicken; gene; CMV;  
 KW chimeric; RM2 antibody.  
 XX  
 OS Hyalophora cecropia.  
 OS Cytomegalovirus.  
 OS Gallus gallus.  
 OS Synthetic.

## Unidentified.

XX Key Location/Qualifiers  
 PH misc\_feature 1..4090  
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 FT 4096..5739  
 FT /\*tag= b  
 FT /note= "CMV promoter/enhancer"  
 FT 5746..5916  
 FT /\*tag= c  
 FT /note= "Capsite/prepro from cecropia moth"  
 FT 5923..7287  
 FT /\*tag= d  
 FT /note= "Heavy chain gene construct from RM2 antibody"  
 FT 7288..7299  
 FT /\*tag= e  
 FT /note= "Pro sequence from cecropia moth"  
 FT 7306..7950  
 FT /\*tag= f  
 FT /note= "Light chain gene construct from RM2 antibody"  
 FT 7557..7969  
 FT /\*tag= g  
 FT /note= "Chicken conalbumin"  
 FT 7971..11970  
 FT /\*tag= h  
 FT /note= "This portion of the sequence is from cloning vector pTnMod."

WO2004067706-A2.

12-AUG-2004.

24-DEC-2003; 2003WO-US041261.

21-JAN-2003; 2003US-0441377P.

21-JAN-2003; 2003US-0441381P.

21-JAN-2003; 2003US-0441392P.

21-JAN-2003; 2003US-0441403P.

21-JAN-2003; 2003US-0441447P.

21-JAN-2003; 2003US-0441502P.

26-JUN-2003; 2003US-00609019.

(TRAN-) TRANSGENEX INC.

(LOU) UNIV LOUISIANA STATE &amp; AGRIC &amp; MECH COLL.

Cooper RK, Fioretti WC, Cadd GG;

WPI; 2004-580985/56.

New isolated polynucleotide having two or more genes of interest and pro

nucleotide sequences, for use in pharmaceutical, diagnostic and

industrial uses, such as in treating and diagnosing cancer.

Example 4; SEQ ID NO 104; 119pp; English.

The present invention provides a new, effective and efficient method for producing multimeric proteins in the egg-laying (avian) or milk producing animals. The multimeric proteins include associated multimeric proteins (two or more associated polypeptides) and multivalent multimeric proteins (a single polypeptide is encoded by multiple genes). The expression and formation of a multimeric protein is achieved by administering a polynucleotide cassette containing genes of interest (for example proinsulin, antibodies, cytokines, etc.). The polynucleotide cassettes are administered to egg-laying or milk producing animals to create the transgenic animals. Several different signal sequences and promoters can be used to achieve the deposition of the multimeric protein in the egg or milk. The transposon based vector has been used for the incorporation of polynucleotide cassettes into the genomic DNA. The polynucleotide cassette may additionally contain multiple pro sequences, pro sequences, cecropin prepro sequences and cleavage sites. Each gene encodes a polypeptide which forms part of a multimeric protein. The pro portion of the sequences has been used to facilitate appropriate



processing, expression and formation of multimeric proteins. These multimeric proteins can be produced much more efficiently and economically by this method than earlier conventional methods. This improved method can produce the multimeric proteins on a large scale. The transposon-based vectors of the invention produce high integration frequencies compared to the earlier vectors. The intratesticular injections with the novel transposon based vector produces 77 % sperm positive rosters (compared to 41% of a previous method). The transposon-based vectors of the invention include a transposase gene linked to a first promoter and a coding sequence of a desired protein linked to a second promoter. The coding sequence for the desired protein and its promoter are flanked by transposase insertion sequences recognised by the transposase. The transposon based vectors also include multiple kozak sequences (which enhance the expression of the transposase gene), modified multiple codons at the N-terminal end (to facilitate the transcription of the transposase gene), an effective polyA sequence (to further enhance the expression of the transposase gene) and an additional stop codon (to enhance the termination of transposon synthesis). The method of the invention can be used to produce antibodies for cancer immunotherapy, infectious disease and toxic agents. The methods and compositions of producing multimeric proteins are useful in pharmaceutical, diagnostic and industrial uses (treatment and diagnosis of cancer). The polypeptide cassettes also include one or more epitopes or domains for facilitating purification of a desired protein. The presented nucleotide sequence is the transposon-based vector ptnMod (CMV-prepro-HCPro-CPA).

Query Match 87.5%; Score 1168; DB 13; Length 11970; Best Local Similarity 92.1%; Pred. No. 1.8e-233; Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

2 AGGTGACAGTGGTGGGGAGGCTGGTAAAGCCGGGGGGTCCCTTAGACTCT 61  
5924 AGGTGACAGTGGTGGGGAGGCTGGTAAAGCCGGGGGGTCCCTTAGACTCT 5983  
62 CCTGTGACGTAGCGGATTCACTTTAGTGGTACTCGGATGTCTGGGTCCGGCAGGCTC 121  
5984 CCTGTGACGCTCTGGATTCACTTTAGAAAGCGCTGGATGAGCTGGGTCCGGCAGGCTC 6043  
122 CAGGGAAGGGGCTGAGTGGGTGCTGAAATTAGATTGAATCTGATAATTATGCAACAC 181  
6044 CAGGGAAGGGGCTGAGTGGGTGCTGCGCGGTATTAAGCAAAATTTGATGGGACACAG 6103  
182 ATTATGCGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241  
6104 ACTATGCTGCACCGGTGAAGGCGAGATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 6163  
242 TGTATCTGCAAAATGAACAGCTGAAACCGAGGACACAGCGCGTGTATTACTGTAC----- 296  
6164 TATATCTGCAAAATGAATAGCTGAAAGCGGAGACACAGCGGTATATTACTGTAGCAGCG 6223  
297 -----AGATTCTAGACTGGGGCCAGGGACACTAG 328  
6224 GGATTATGATAAATTTGGGGAGTATTATCCCTCCCGGAAATTTGGGGCCAGGGAACCTGG 6283  
329 TCACCGTCTCTCAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGCACCCTCTCTCCA 388  
6284 TCACCGTCTCTCAGCTCTCAACGAGGGCCATCGGTCTTCCCGCTGGCACCCTCTCTCCA 6343  
389 AGAGCACCCTCTGGGGGACACAGCGCCCTGGGCTGCGCTGGTCAAGGACTACTTCCCGGAAC 448  
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509 TCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGGTGCCCTCCAGGAGCT 568  
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569 TGGGCAACCCAGACCTATCTGCAAGCGTGAATCAAGGCCAGCAACACCAAGGTGACA 628  
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6584 AGAAGTGGAGCCCAATCTTGTGACAAACTCAGACATGCCACCGTGCAGGACCTG 6643  
689 AACTCCGGGGGACCGTCACTCTTCTTCCCCCAAAACCAAGGACACCTCATGA 748  
6644 AACTCTGGGGGACCGTCACTCTTCTTCCCCCAAAACCAAGGACACCTCATGA 6703  
749 TCTCCGGACCCCTGAGGTCAATGCGTGTGTGAGTGCAGGACCAAGAACCTTGAGG 808  
6704 TCTCCGGACCCCTGAGGTCAATGCGTGTGTGAGTGCAGGACCAAGAACCTTGAGG 6763  
809 TCAAGTTCAACTGGTGTGAGGCGGTGAGTGCATTAATGCAAGAACCAAGGACCTG 868  
6764 TCAAGTTCAACTGGTGTGAGGCGGTGAGTGCATTAATGCAAGAACCAAGGACCTG 6823  
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6824 AGGAGCAGTACAAACAGCAGTACCGTGTGTGAGTGCAGGCTCTCAGCGTCTGCACGAGCT 6883  
929 GGCTGAATGGCAAGGAGTCAAGTGCAGGCTCTCAGCGTCTCAGCGTCTGCACGAGCT 988  
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989 AGAARACCATCTCCAAAGCCCAAGGCGCGGACCAAGGACCAAGGACCAAGGACCTG 1048  
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7064 ATCCAGCAGCATCGCGGTGGAGTGCAGCAAGAACAGTGCAGGACCAAGGACCAAGGACCT 7123  
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7124 CACGCGCTCCCGTGGTGGTCCGAGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 7183  
1229 ACAAGAGCAGTGGCAGCAGGGAAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1288  
7184 ACAAGAGCAGTGGCAGCAGGGAAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 7243  
1289 ACAACCACTACAGCAGGAGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1332  
7244 ACAACCACTACAGCAGGAGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 7287

## RESULT 13

ADT62609

ID ADT62609 standard; DNA; 11970 BP.

XX AC ADT62609;

XX DT 16-DEC-2004 (first entry)

XX Transposon based vector ptnMod (CMV-prepro-HCPro-CPA).

Transposon-based vector; transposon; transgenic; vaccine;  
immune response; anthrax; botulism; brucellosis; glanders; Q fever;  
plague; shigellosis; small pox; tularemia; viral encephalitis;  
typhus fever; viral hemorrhagic fever; bird; mammal; egg; milk;  
antibacterial; anti viral; antimicrobial; anti-inflammatory;  
neuroprotective; transposase; ptnMod; CMV-prepro-HCPro-CPA; ds;  
cecropia moth.

XX Cytomegalovirus.

OS Hyalophora cecropia.





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Db 6824 AGGAGCAGTACAAACAGCACGTACCGTGTGCTGAGCGTCTCACCGTCTCTCACCAGGACT 6883
Qy 929 GGCTGAATGCAAGAGTACAAAGTCAAGTGTCCAAACAAAGCCCTCCAGCCCCCATCG 988
Db 6884 GGCTGAATGCAAGAGTACAAAGTCAAGTGTCCAAACAAAGCCCTCCAGCCCCCATCG 6943
Qy 989 AGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCC 1048
Db 6944 AGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCC 7003
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Db 7064 ATCCCGGATGAGCTGAGTGGGAGAGCAATGGCGAGCAACCACTACAAAGA 7123
Qy 1169 CCAGCCTCCCGTGTGAGTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGG 1228
Db 7124 CCAGCCTCCCGTGTGAGTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGG 7183
Qy 1229 ACAAGAGAGTGGCAGAGGGAACGTCTTCTCATGCTCCGTGATGATGAGCTCTGC 1288
Db 7184 ACAAGAGAGTGGCAGAGGGAACGTCTTCTCATGCTCCGTGATGATGAGCTCTGC 7243
Qy 1289 ACAACCACTACACGAGAGGCTCTCCCTGCTCCGGGTAA 1332
Db 7244 ACAACCACTACACGAGAGGCTCTCCCTGCTCCGGGTAA 7287

RESULT 14
ADS91473
ID ADS91473 standard; DNA; 11973 BP.
XX
AC ADS91473;
XX
DT 02-DEC-2004 (first entry)
XX
DE Transposon-based vector pTnMod (CMV-prepro-HCPro-Lys-CPA).
XX
KW ds; multimeric protein; egg-laying; avian; milk producing animal;
KW transgenic; transposase; cancer; immunotherapy; infectious disease;
KW pTnMod; CMV-prepro-HCPro-Lys-CPA; cecropia moth; CMV; chicken; gene;
KW chimeric; RM2 antibody.
XX
OS Hyalophora cecropia.
OS Cyomegalovirus.
OS Gallus gallus.
OS Synthetic.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 1..4090
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FT /note= "CMV promoter/enhancer"
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FT /note= "Capsite/prepro from cecropia moth"
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FT vector pTnMod"
XX
PN W02004067706-A2.
XX
PD 12-AUG-2004.
XX
XX 24-DEC-2003; 2003WO-US041261.
XX
PR 21-JAN-2003; 2003US-0441377P.
PR 21-JAN-2003; 2003US-0441381P.
PR 21-JAN-2003; 2003US-0441392P.
PR 21-JAN-2003; 2003US-0441405P.
PR 21-JAN-2003; 2003US-0441447P.
PR 21-JAN-2003; 2003US-0441502P.
PR 26-JUN-2003; 2003US-00609019.
XX
XX (TRAN-) TRANSGENIX INC.
XX (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX
XX Cooper RK, Fioretti WC, Cadd GG;
XX WPI; 2004-580985/56.
XX
XX New isolated polynucleotide having two or more genes of interest and pro
XX nucleotide sequences, for use in pharmaceutical, diagnostic and
XX industrial uses, such as in treating and diagnosing cancer.
XX
XX Example 3; SEQ ID NO 97; 119pp; English.
XX
CC The present invention provides a new, effective and efficient method for
CC producing multimeric proteins in the egg-laying (avian) or milk producing
CC animals. The multimeric proteins include associated multimeric proteins
CC (two or more associated polypeptides) and multivalent multimeric proteins
CC (a single polypeptide is encoded by multiple genes). The expression and
CC formation of a multimeric protein is achieved by administering a
CC polynucleotide cassette containing genes of interest (for example
CC proinsulin, antibodies, cytokines, etc.). The polynucleotide cassettes
CC are administered to egg-laying or milk producing animals to create the
CC transgenic animals. Several different signal sequences and promoters can
CC be used to achieve the deposition of the multimeric protein in the egg or
CC milk. The transposon based vector has been used for the incorporation of
CC polynucleotide cassettes into the genomic DNA. The polynucleotide
CC cassette may additionally contain multiple pro sequences, prepro
CC sequences, cecropin prepro sequences and cleavage sites. Each gene
CC encodes a polypeptide which forms part of a multimeric protein. The pro
CC portion of the sequences has been used to facilitate appropriate
CC processing, expression and formation of multimeric proteins. These
CC multimeric proteins can be produced much more efficiently and
CC economically by this method than earlier conventional methods. This
CC improved method can produce the multimeric proteins on a large scale. The
CC transposon-based vectors of the invention produce high integration
CC frequencies compared to the earlier vectors. The intratesticular
CC injections with the novel transposon based vector produces 77 % sperm
CC positive roosters (compared to 41% of a previous method). The transposon-
CC based vectors of the invention include a transposase gene linked to a
CC first promoter and a coding sequence of a desired protein linked to a
CC second promoter. The coding sequence for the desired protein and its
CC promoter are flanked by transposase insertion sequences recognised by the
CC transposase. The transposon based vectors also include multiple Kozak
CC sequences (which enhance the expression of the transposase gene),
CC modified multiple codons at the N-terminal end (to facilitate the
CC transcription of the transposase gene), an effective polyA sequence (to
CC further enhance the expression of the transposase gene) and an additional
CC stop codon (to enhance the termination of transposon synthesis). The
CC method of the invention can be used to produce antibodies for cancer
CC immunotherapy, infectious disease and toxic agents. The methods and
CC compositions of producing multimeric proteins are useful in
CC pharmaceutical, diagnostic and industrial uses (treatment and diagnosis
```

CC of cancer). The polypeptide cassettes also include one or more epitopes  
CC or domains for facilitating purification of a desired protein. The  
CC presented nucleotide sequence is the transposon-based vector pTnMod (CMV-  
XX prepro-HCPro-Lys-CPA).

SQ Sequence 11973 BP; 3063 A; 3088 C; 2807 G; 3015 T; 0 U; 0 Other;

Query Match 87.58; Score 1168; DB 13; Length 11973;  
Best Local Similarity 92.14; Pred. No. 1.8e-233;  
Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

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QY 2 AGGTGACGCTGGTGGAGCTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
DB 5924 AGGTGACGCTCGAGGAGTCCGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGAGTCT 5983
QY 62 CCTGTGACGTAGCGGATTCACITTTAGTGGCTACGTGATGTCTCTGGTCCGCCAGGCTC 121
DB 5984 CCTGTGACGCTCTGGATTCACITTTAGAAACGCTGGATGAGTGGGTCCGCCAGGCTC 6043
QY 122 CAGGAGGGGCTCGAGTGGGTTGCTGAATTTAGATTGAATCTGATATATTATGCAACAC 181
DB 6044 CAGGAGGGGCTCGAGTGGGTTGCTGAATTTAGAAATTTGATGGGACAAACAG 6103
QY 182 ATTATGCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
DB 6104 ACTATGCTGCACCGTGAAGGCGAGTTTCAACATCTCAAGAGATGATTCAAAACACAGT 6163
QY 242 TGTATCTGCAAAATGAACAGGCTGAACACCGAGACACAGCCGTGTATTACTGTAC 296
DB 6164 TATATCTGCAAAATGAATGAGCTGAAGCCCGAGGACACAGCCGTATATTACTGTACCA 6223
QY 297 -----AGATTTCTAGACTGGGCCAGGGAACACTAG 328
DB 6224 GGATTTATGATAACATTTGGGGGAGTTATCCCTCCCGCGAATTTGGGGCCAGGAACTCTGG 6283
QY 329 TCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACACCTCTCTCCA 388
DB 6284 TCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACACCTCTCTCCA 6343
QY 389 AGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAGAGACTACTTCCCGGAAC 6403
DB 6344 AGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAGAGACTACTTCCCGGAAC 6403
QY 449 CGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACACGCGCGTGCACACTTCCCGGCTG 508
DB 6404 CGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACACGCGCGTGCACACTTTCGGGCTG 5463
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DB 6464 TCCTACAGTCTCTCAGGACTCTACTCCCTTAGCAACGTGTGACCGTCCCTCCAGCAGCT 6523
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RESULT 15
ADT62602
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AC ADT62602;
XX
DT 16-DEC-2004 (first entry)
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XX
KW Transposon-based vector; transposon; transgenic; vaccine;
immune response; anthrax; botulism; brucellosis; glanders; Q fever;
plague; shigellosis; small pox; tularemia; viral encephalitis;
typhus fever; viral hemorrhagic fever; bird; mammal; egg; milk;
antibacterial; anti viral; antimicrobial; anti-inflammatory;
neuroprotective; transposase; pTnMod; CMV-prepro-HCPro-Lys-CPA; ds;
cecropia moth.
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PT XX WO2004067743-A1.  
 XX PN  
 XX PD  
 XX PF 12-AUG-2004.  
 XX PR 24-DEC-2003; 2003WO-US041269.  
 XX PR 21-JAN-2003; 2003US-0441377P.  
 XX PR 21-JAN-2003; 2003US-0441381P.  
 XX PR 21-JAN-2003; 2003US-0441392P.  
 XX PR 21-JAN-2003; 2003US-0441405P.  
 XX PR 21-JAN-2003; 2003US-0441447P.  
 XX PR 21-JAN-2003; 2003US-0441502P.  
 XX PR 26-JUN-2003; 2003US-00609019.  
 XX PA (TRAN-) TRANSENEX INC.  
 XX PA (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.  
 XX PI Cooper RK, Fioretti WC, Cadd GG;  
 XX PR WPI; 2004-581003/56.  
 XX DR  
 XX PT New polynucleotide (transposon-based vector) cassette comprising gene of  
 PT interest operably linked to a cecropin prepro sequence, is useful in  
 PT producing vaccines to protect an individual against infectious diseases.  
 XX PT  
 XX PS Example 3; SEQ ID NO 97; 155pp; English.  
 XX CC The patent discloses novel, effective and efficient method of producing  
 CC multimeric proteins, antibodies using transposon-based vectors, in  
 CC transgenic individuals. These proteins can be used as a vaccine.  
 CC Immunising individuals with such compositions, comprising vaccines is  
 CC capable of generating an immune response, to prevent or ameliorate the  
 CC severity of a disease. The invention provides polynucleotide cassettes  
 CC containing at least one gene of interest and one or more pro  
 CC polynucleotide sequence, where in each gene of interest are operably-  
 CC linked to a pro nucleotide sequence of at least one gene of interest. The  
 CC transposon-based vector comprises the polynucleotide and further  
 CC comprises a transposase gene operably linked to a first promoter and  
 CC where the first promoter comprises a modified Kozak sequence, two or more  
 CC genes of interest are each operably-linked to one or more additional  
 CC promoters, and two or more genes of interest and their operably-linked  
 CC promoters are flanked by transposase insertion sequences recognized by a  
 CC transposase encoded by the transposase gene. Many diseases and disease  
 CC causing organisms can be targets of the vaccine of the present invention.  
 CC Some of these include, anthrax, botulism, brucellosis, glanders, Q fever,  
 CC plague, shigellosis, small pox, tularemia, viral encephalitis, typhus  
 CC fever, viral hemorrhagic fever, etc. The preferred animal for production  
 CC of protein is a bird or a mammal. The egg or milk of these animals  
 CC comprises the multimeric protein encoded by the isolated polynucleotide  
 CC of the invention. Hence, these proteins are endowed with varied  
 CC properties and are antibacterial, anti viral, antimicrobial, anti-  
 CC inflammatory, and neuroprotective in nature. The sequence presented here  
 CC is the transposon based vector pTnMod (CMV-prepro-HCPro-Lys-CPA).  
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GenCore version 5.1.6  
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SUMMARIES

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4	1168	87.5	11964	18 US-10-746-943-98	Sequence 98, Appl
5	1168	87.5	11967	18 US-10-746-943-99	Sequence 99, Appl
6	1168	87.5	11970	18 US-10-746-943-104	Sequence 104, Appl
7	1168	87.5	11973	18 US-10-746-943-97	Sequence 97, Appl
8	1168	87.5	12339	18 US-10-746-943-102	Sequence 102, App
9	1168	87.5	12342	18 US-10-746-943-103	Sequence 103, App
10	1158.8	86.8	1413	19 US-10-938-353-97	Sequence 97, Appl
11	1154.6	86.5	1392	15 US-10-150-475A-7	Sequence 7, Appli

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15	1147.8	86.0	1798	10 US-09-925-299-230	Sequence 230, App
16	1147.2	85.9	1437	9 US-09-758-173-7	Sequence 7, Appli
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18	1147.2	85.9	1437	13 US-10-123-905-7	Sequence 7, Appli
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22	1145	85.8	1616	9 US-09-822-830A-572	Sequence 572, App
23	1142.2	85.6	1407	17 US-10-656-763-25	Sequence 25, Appl
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28	1141.2	85.5	19040	18 US-10-817-950-3	Sequence 3, Appli
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35	1136	85.1	1425	17 US-10-461-148-11	Sequence 11, Appl
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38	1135.4	85.0	1410	17 US-10-408-901-41	Sequence 41, Appl
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40	1135	85.0	1347	17 US-10-463-442-20	Sequence 20, Appl
41	1134	84.9	1413	17 US-10-408-901-45	Sequence 45, Appl
42	1132	84.8	1409	17 US-10-408-901-67	Sequence 67, Appl
43	1132	84.8	1409	17 US-10-656-769-51	Sequence 51, Appl
44	1131	84.7	1356	9 US-09-822-698A-27	Sequence 27, Appl
45	1129.2	84.6	2197	18 US-10-858-186-13	Sequence 13, Appl

ALIGNMENTS

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; Publication No. US20050059113A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA  
; APPLICANT: FOLTZ, IAN  
; APPLICANT: HAAR-FRENDSCHO, MARY  
; APPLICANT: KELLERMANN, SIRID-AIMSEE  
; APPLICANT: LOW, JOSEPH EDWIN  
; APPLICANT: MOBLEY, JAMES LESLIE  
; TITLE OF INVENTION: ANTIBODIES TO M-CSF  
; FILE REFERENCE: ABX-PF4  
; CURRENT APPLICATION NUMBER: US/10/938,353  
; CURRENT FILING DATE: 2004-09-09  
; PRIOR APPLICATION NUMBER: 60/502,163  
; PRIOR FILING DATE: 2003-09-10  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 101  
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; TYPE: DNA  
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US-10-938-353-101

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Db 6809 ACAAGAGCAGTGGCAGCGGGAACGTCTTCTCATGCTCCGTGATGCATGAGCTCTGC 6868

Qy 1289 ACAACCACTACACGACGAGAGGCTCTCTCTGTCTCCGGGTAA 1332  
Db 6869 ACAACCACTACACGACGAGAGGCTCTCTCTGTCTCCGGGTAA 6912

## RESULT 3

US-10-746-943-101  
; Sequence 101, Application US/10746943  
; Publication No. US20040235011A1  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Richard K.  
; APPLICANT: Fioretti, William C.  
; APPLICANT: Cadd, Gary G.  
; TITLE OF INVENTION: Production of Multimeric Proteins  
; FILE REFERENCE: 51687-0230 (51687-294924)  
; CURRENT APPLICATION NUMBER: US/10/746,943  
; CURRENT FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: US 60/392,415  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: US 60/441,381  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US 60/441,447  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US 60/441,405  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US 60/441,502  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US 60/441,377  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US 60/441,392  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US 10/609,019  
; PRIOR FILING DATE: 2003-06-26  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 101  
; LENGTH: 11593  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-10-746-943-101

Query Match 87.5%; Score 1168; DB 18; Length 11593;  
Best Local Similarity 92.1%; Pred. No. 2 5e-310;  
Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

Qy 2 AGGTGAGCTGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61  
Db 5549 AGGTGAGCTGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 5608  
Qy 62 CCTGTGAGCTAGCGGATTCACCTTCAGTGGCTACTTGGATGCTCTGGTCCGCGAGCTC 121  
Db 5609 CCTGTGAGCTGTGGATTCACCTTCAGAAACCCCTGGATGAGCTCGGCTC 5668  
Qy 122 CAGGGAAGGGGCTCGAGTGGTGTGAAATAGATTGAAATCTGATTAATTGCAACAC 181  
Db 5669 CAGGGAAGGGGCTGGATGGTGTGGCCGTATTAAAGCAAAATTTGTTGGGACAAAC 5728  
Qy 182 ATTATGCGGAGTCTGTGAAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241  
Db 5729 ACTATGCTGCAACCCGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAACACGT 5788  
Qy 242 TGTATCTGCAATGAACACCCCTGAAACCCGAGGACACAGCCGTGTATTACTGTAC----- 296  
Db 5789 TATATCTGCAATGAATAGCTTGAACCCCTGAAAGCCGAGGACACAGCCGTATATTACTGTACACCG 5848  
Qy 297 -----AGATTTTCATAGACTGGGCGCAGGGAACACTAG 328  
Db 5849 GGATTTATGATAACATTTGGGGAGTATCCCTCCCGGAAATTTGGGCGCAGGGAACCCCTGG 5908  
Qy 329 TCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTCGGACACCTCTCTCCA 388









QY 689 AACTCGCGGGGACCGTCACTCTTCTTCCCGGAGGACCAAGGACACCTCATGA 748  
Db 6643 AACTCTGGGGGACCGTCACTCTTCTTCCCGGAGGACCAAGGACACCTCATGA 6702  
QY 749 TCTCCCGGACCCCTGAGGTCAATGCGTGTGTGTGAGCGTGAAGCCGAGCCCTGAGG 808  
Db 6703 TCTCCCGGACCCCTGAGGTCAATGCGTGTGTGTGAGCGTGAAGCCGAGCCCTGAGG 6762  
QY 809 TCAAGTTCACTGCTGAGGTGAGCGGCGTGTGAGTGCATATGCAAGCAAAAGCCGCGG 868  
Db 6763 TCAAGTTCACTGCTGAGGTGAGCGGCGTGTGAGTGCATATGCAAGCAAAAGCCGCGG 6822  
QY 869 AGGAGCAGTACAACAGCAGCAGTACCGTGTGTGTGAGCGTGAAGCCGAGCCCTGAGG 928  
Db 6823 AGGAGCAGTACAACAGCAGTACCGTGTGTGTGAGCGTGAAGCCGAGCCCTGAGG 6882  
QY 929 GGCTGAATGCAAGGAGTACAAGTGCAGGTCTTCCAAAGGCGCTTCCAGCCCGCCATCG 988  
Db 6883 GGCTGAATGCAAGGAGTACAAGTGCAGGTCTTCCAAAGGCGCTTCCAGCCCGCCATCG 6942  
QY 989 AGAAGACCTCTCCAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1048  
Db 6943 AGAAGACCTCTCCAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7002  
QY 1049 CATCCCGGGATGAGTCAACAGAACCCAGGTGAGCGTCAAGTCTTCCAAAGGCGCTTCC 1108  
Db 7003 CATCCCGGGATGAGTCAACAGAACCCAGGTGAGCGTCAAGTCTTCCAAAGGCGCTT 7062  
QY 1109 ATCCAGCAGCATCGCGTGTGAGTGGAGGAGCAATGGGAGCGGAGGAGGAGGAGGAGG 1168  
Db 7063 ATCCAGCAGCATCGCGTGTGAGTGGAGGAGCAATGGGAGCGGAGGAGGAGGAGGAGG 7122  
QY 1169 CCAGCCTCCCGTGTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1228  
Db 7123 CCAGCCTCCCGTGTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7182  
QY 1229 ACAAGCAGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1288  
Db 7183 ACAAGCAGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7242  
QY 1289 ACAACCACTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1332  
Db 7243 ACAACCACTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7286

## RESULT 6

US-10-746-943-104  
; Sequence 104, Application US/10746943  
; Publication No. US20040235011A1  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Richard K.  
; APPLICANT: Fioretti, William C.  
; TITLE OF INVENTION: Production of Multimeric Proteins  
; FILE REFERENCE: 51687-0230 (51687-294924)  
; CURRENT APPLICATION NUMBER: US/10746, 943  
; CURRENT FILING DATE: 2003-12-24  
; PRIORITY APPLICATION NUMBER: US 60/392,415  
; PRIORITY FILING DATE: 2002-06-26  
; PRIORITY APPLICATION NUMBER: US 60/441,381  
; PRIORITY FILING DATE: 2003-01-21  
; PRIORITY APPLICATION NUMBER: US 60/441,447  
; PRIORITY FILING DATE: 2003-01-21  
; PRIORITY APPLICATION NUMBER: US 60/441,405  
; PRIORITY FILING DATE: 2003-01-21  
; PRIORITY APPLICATION NUMBER: US 60/441,502  
; PRIORITY FILING DATE: 2003-01-21  
; PRIORITY APPLICATION NUMBER: US 60/441,377  
; PRIORITY FILING DATE: 2003-01-21  
; PRIORITY APPLICATION NUMBER: US 60/441,392  
; PRIORITY FILING DATE: 2003-01-21  
; PRIORITY APPLICATION NUMBER: US 10/609,019  
; PRIORITY FILING DATE: 2003-06-26

; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 104  
; LENGTH: 11970  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-746-943-104  
  
Query Match 87.5%; Score 1168; DB 18; Length 11970;  
Best Local Similarity 92.1%; Pred. No. 2,5e-310;  
Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;  
  
QY 2 AGGTGAGCTGTGTGAGTCTGGGAGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61  
Db 5924 AGGTGAGCTGTGTGAGTCTGGGAGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 5983  
QY 62 CCGTGTGAGCTAGCGGATTCACCTTTCAGTGGCTACTTGGATGTCTTGGGTCCGCCAGGCTC 121  
Db 5984 CCGTGTGAGCTAGCGGATTCACCTTTCAGTGGCTACTTGGATGTCTTGGGTCCGCCAGGCTC 6043  
QY 122 CAGGGAAGGGGCTCGAGTGGGTGTGAAATTTAGATTTGAAATCTGATTAATTAACAACAC 181  
Db 6044 CAGGGAAGGGGCTCGAGTGGGTGTGAAATTTAGATTTGAAATCTGATTAATTAACAACAC 6103  
QY 182 ATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGAC 241  
Db 6104 ACTATGTGACCGCTGTGAAGGGGAGATTCACCATCTCAAGAGATGATTCAAATCTAGAC 6163  
QY 242 TGTATCTGCAATTAAGTAAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 296  
Db 6164 TGTATCTGCAATTAAGTAAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6223  
QY 297 -----AGATTTCATAGACTGGGGCCAGGGAACACTAG 328  
Db 6224 GGATTATGATAACATTTGGGGGAGTTATCTCTCCCGGAAATTTGGGGCCAGGGAACCTTGG 6283  
QY 329 TCACCGTCTCTCAGCGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCAGCCCTCCTCCA 388  
Db 6284 TCACCGTCTCTCAGCGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCAGCCCTCCTCCA 6343  
QY 389 AGAGCACCTCTGGGGGCGACAGCGGCCCTGGGTCTGCTCAAGGAGTACTTTCGCCGAGAC 448  
Db 6344 AGAGCACCTCTGGGGGCGACAGCGGCCCTGGGTCTGCTCAAGGAGTACTTTCGCCGAGAC 6403  
QY 449 CGGTGACGGTGTGTGGAATCTCAGCGGCCCTGGAACAGCGGGGTGACACCTTTCGCCGCTG 508  
Db 6404 CGGTGACGGTGTGTGGAATCTCAGCGGCCCTGGAACAGCGGGGTGACACCTTTCGCCGCTG 6463  
QY 509 TCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGTCCCTCCAGCAGCT 568  
Db 6464 TCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGTCCCTCCAGCAGCT 6523  
QY 569 TGGGCAACCCAGACCTACATCTGCAACGTGAATCAAGCCAGCAGCAGCAGCAGCAGCAGCAG 628  
Db 6524 TGGGCAACCCAGACCTACATCTGCAACGTGAATCAAGCCAGCAGCAGCAGCAGCAGCAGCAG 6583  
QY 629 AGAAGTGGAGCCCAAAATCTTGTGACAAAATCTCAACATGCCCCACCGTCCCGAGCAGCTG 688  
Db 6584 AGAAGTGGAGCCCAAAATCTTGTGACAAAATCTCAACATGCCCCACCGTCCCGAGCAGCTG 6643  
QY 689 AACTCGGGGGGACCGTCACTCTTCTTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 748  
Db 6644 AACTCGGGGGGACCGTCACTCTTCTTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6703  
QY 749 TCTCCCGGAGCCCTGAGGTCAATCGGTGGTGGAGCGTGAAGCCAGCAGCAGCAGCAGCAGG 808  
Db 6704 TCTCCCGGAGCCCTGAGGTCAATCGGTGGTGGAGCGTGAAGCCAGCAGCAGCAGCAGGAGG 6763  
QY 809 TCAAGTTCACTGCTGAGTGTGAGCGGCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 868  
Db 6764 TCAAGTTCACTGCTGAGTGTGAGCGGCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6823

Qy	869	AGGAGCAGTACAA	CAGCAGCCTACCGTGTGGT	CAGGCTCCTCACCGTCTCTGCACCAGACT	928
Db	6824	AGGAGCAGTACAA	CAGCAGCCTACCGTGTGGT	CAGGCTCCTCACCGTCTCTGCACCAGACT	6883
Qy	929	GGCTGAATGGCA	AGGAGTACAAGTGC	AAGGTTCTCAAACAAAGCCCTCCACAGCCCCCATCG	988
Db	6884	GGCTGAATGGCA	AGGAGTACAAGTGC	AAGGTTCTCAAACAAAGCCCTCCACAGCCCCCATCG	6943
Qy	989	AGAAAAACATCT	CCAAAGCCAAAGGGCAGCCCG	CAGAACCAACAGGTGTACACCTGCCCC	1048
Db	6944	AGAAAAACATCT	CCAAAGCCAAAGGGCAGCCCG	CAGAACCAACAGGTGTACACCTGCCCC	7003
Qy	1049	CATCCCGGATAG	CTGCTCAACGAACAGGT	CAGCCTGACCTGCTGGTCAAAAGGCTTCT	1108
Db	7004	CATCCCGGATAG	CTGCTCAACGAACAGGT	CAGCCTGACCTGCTGGTCAAAAGGCTTCT	7063
Qy	1109	ATCCACGCGATC	CGCGTGGAGTGGGAGCAGT	ATGGCAGCCGGAGAACACTTACAGA	1168
Db	7064	ATCCACGCGATC	CGCGTGGAGTGGGAGCAGT	ATGGCAGCCGGAGAACACTTACAGA	7123
Qy	1169	CCACGCTCCCGT	GCTGGACTCGACGGCTCT	TTCTTCTCTACAGCAAGCTCACCGTGG	1228
Db	7124	CCACGCTCCCGT	GCTGGACTCGACGGCTCT	TTCTTCTCTACAGCAAGCTCACCGTGG	7183
Qy	1229	ACAAGCAGGTGG	CACACAGGGAACTCTTCTCAT	GCTCCGTGATGCATGGGCTCTGC	1288
Db	7184	ACAAGCAGGTGG	CACACAGGGAACTCTTCTCAT	GCTCCGTGATGCATGGGCTCTGC	7243
Qy	1289	ACAACCACTACA	CACAGAAGCCTCTCCCTGT	CTCCGGGTAA	1332
Db	7244	ACAACCACTACA	CACAGAAGCCTCTCCCTGT	CTCCGGGTAA	7287

## RESULT 7

```

US-10-746-943-97
; Sequence 97, Application US/10746943
; Publication No. US20040235011A1
; GENERAL INFORMATION:
; APPLICANT: Cooper, Richard K.
; APPLICANT: Fioretti, William C.
; APPLICANT: Cadd, Gary G.
; TITLE OF INVENTION: Production of Multimeric Proteins
; FILE REFERENCE: 51687-0230 (51687-294324)
; CURRENT APPLICATION NUMBER: US/10/746,943
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/392,415
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/441,381
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,447
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,405
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,502
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,377
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,392
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 10/609,019
; PRIOR FILING DATE: 2003-06-26
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 11973
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-746-943-97

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Query Match 87.5%; Score 1168; DB 18; Length 11973;

[illegible]





RESULT 10  
US-10-938-353-97  
; Sequence 97, Application US/10938353  
; Publication No. US20050059113A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA  
; APPLICANT: FOLTZ, IAN  
; APPLICANT: HAAK-FRENDSCHO, MARY  
; APPLICANT: KELLERMANN, SIRID-AIMEE  
; APPLICANT: LOW, JOSEPH EDWIN  
; APPLICANT: MOBLEY, JAMES LESLIE  
; TITLE OF INVENTION: ANTIBODIES TO M-CSF  
; FILE REFERENCE: ABX-PF4  
; CURRENT APPLICATION NUMBER: US/10/938,353  
; CURRENT FILING DATE: 2004-09-09  
; PRIOR APPLICATION NUMBER: 60/502,163  
; PRIOR FILING DATE: 2003-09-10  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 97  
; LENGTH: 1413  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-938-353-97

Query Match 86.8%; Score 1158.8; DB 19; Length 1413;  
Best Local Similarity 92.3%; Pred. No. 4.9e-308;  
Matches 1255; Conservative 0; Mismatches 72; Indels 33; Gaps 2;

QY 1 GAGGTGAGCTGTGGAGTCTGGGGAGGCTTGTAAAGCCGGGGGTCCTTAGACTC 60  
DB 58 GAGGTGAGCTGTGGAGTCTGGGGAGGCTTGTACAGCTGGGGGTCCTTAGACTC 117  
QY 61 TCCTGTGACGTAGCGGATTCACCTTCAGTGGCTACTGGATGTCTGGGTCCGCCAGGCT 120  
DB 118 TCCTGTGACGCTCTGGATTCACCTTCAGTGGCTACTGGATGTCTGGGTCCGCCAGGCT 177  
QY 121 CAGGGNAGGGCTCGATGGTGTCTGAAATAGATTGAATCTGATTAATGCAACA 180  
DB 178 CAGGGNAGGGCTCGATGGTGTCTGAAATAGATTGAATCTGATTAATGCAACA 231  
QY 181 CATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCATAAATCTAGA 240  
DB 232 TCCTACGACACTCTGTGAAGGGCCGATTCACCATCTCCAGAGCAATGCGCAAGACTCA 291  
QY 241 CTGTATCTGCAATGAACAGCCTGAAACCCGAGGACAAGCCGTGTATTACTG----- 293  
DB 292 CTGTATCTGCAATGAACAGCCTGAGAGAGGAGGACAGGCTGTGTATTACTGTGCGAGA 351  
QY 294 -----TACAGATTTTCATAGCTGGGGCCAGGGAACACTAGTCAAC 333  
DB 352 GATCTCTTTCTAGCGGAGTACTCTTTTGTACTCTGGGGCCAGGGAACCCCTGGTCAAC 411  
QY 334 GTCTCTCAGCCTCCACCAAGGCGCATCGGTCTTCCCTCGCACCTCTCCCAAGAGC 393  
DB 412 GTCTCTCAGCCTCCACCAAGGCGCATCGGTCTTCCCTCGCACCTCTCCCAAGAGC 471  
QY 394 ACCTCTGGGGGCA CAGCGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGCAACCGGTG 453  
DB 472 ACCTCTGGGGGCA CAGCGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGCAACCGGTG 531  
QY 454 ACGGTGTCTGGAACTCAGCGGCCCTGACAGCGGGGTGACACCTTCCGGGTGCTCTTA 513  
DB 532 ACGGTGTCTGGAACTCAGCGGCCCTGACAGCGGGGTGACACCTTCCGGGTGCTCTTA 591  
QY 514 CAGTCTCTCAGACTCTACTCTCTCAGCAGCGGTGTGACCGTGCCTCCAGCAGCTTGGGC 573  
DB 592 CAGTCTCTCAGACTCTACTCTCTCAGCAGCGGTGTGACCGTGCCTCCAGCAGCTTGGGC 651  
QY 574 ACCCAGACCTTACTGTGCAACGTGAATCAAGGCCCGAGCAACCAAGGTGGCAAGAAA 633

## RESULT 11

US-10-150-475A-7  
; Sequence 7, Application US/10150475A  
; Publication No. US20030103985A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, G. et al.  
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates  
; FILE REFERENCE: 1/1211  
; CURRENT APPLICATION NUMBER: US/10/150,475A  
; CURRENT FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: US 60/307,451  
; PRIOR FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 1392  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Humanised  
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 7  
US-10-150-475A-7

652 ACCCAGACCTACATCTGCAACCGTGAATCACAAGCCAGCAACACAAGGTGGACAAGAA 711  
QY 634 GTGGAGCCCAATCTTGTGACAAAACACTCACATGCCACCGTCCCGACGACCTGAATC 693  
DB 712 GTTGAAGCCCAATCTTGTGACAAAACACTCACATGCCACCGTCCCGACGACCTGAATC 771  
QY 694 GCGGGGGCACCGTCAAGTCTTCTTCCCGCCCAAAACCAAGGACACCCCTCATGTCTCC 753  
DB 772 CTGGGGGGACCGTCAAGTCTTCTTCCCGCCCAAAACCAAGGACACCCCTCATGTCTCC 831  
QY 754 CCGACCCCTGAGGTCAATGCTGTGTGGAGCGTGAAGCAAGAACCCCTGAGGTCAAG 813  
DB 832 CCGACCCCTGAGGTCAATGCTGTGTGGAGCGTGAAGCAAGAACCCCTGAGGTCAAG 891  
QY 814 TTCAACTGTGTAGTGGAGCGGTGAGTGCATATGCAAGCAAGAACCCCGGGAGGAG 873  
DB 892 TTCAACTGTGTAGTGGAGCGGTGAGTGCATATGCAAGCAAGAACCCCGGGAGGAG 951  
QY 874 CAGTACAAACAGCACGCTACCGTGTGTGCTCAGCGTCTCACCCTCTGACCAAGACTGGCTG 933  
DB 952 CAGTACAAACAGCACGCTACCGTGTGTGCTCAGCGTCTCACCCTCTGACCAAGACTGGCTG 1011  
QY 934 AATGCAAGGAGTACAAGTGAAGTCTCAACAAAGCCCTCCAGCCCGCCCATCGAGAAA 993  
DB 1012 AATGCAAGGAGTACAAGTGAAGTCTCAACAAAGCCCTCCAGCCCGCCCATCGAGAAA 1071  
QY 994 ACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCTGCCCCATCC 1053  
DB 1072 ACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCTGCCCCATCC 1131  
QY 1054 CGGGATGAGTCAACCAAGAACACAGTCAAGCTCTGCTGCTCAAGGGCTTCTATCC 1113  
DB 1132 CGGGATGAGTCAACCAAGAACACAGTCAAGCTCTGCTGCTCAAGGGCTTCTATCC 1191  
QY 1114 AGCGACATCGCGTGGAGTGGAGAGCAATGGGACCGCGAGAAACAATCAAGACCAAG 1173  
DB 1192 AGCGACATCGCGTGGAGTGGAGAGCAATGGGACCGCGAGAAACAATCAAGACCAAG 1251  
QY 1174 CTTCCGCTGTGAGTCCGAGCGGTCTTCTCTCTACAGCAAGCTCACCGTGGACAAG 1233  
DB 1252 CTTCCGCTGTGAGTCCGAGCGGTCTTCTCTCTACAGCAAGCTCACCGTGGACAAG 1311  
QY 1234 AGCAGTGGCAGCAGCGGGAACGCTCTTCTCATCTCTCGTATCATGAGGCTCTGCACAC 1293  
DB 1312 AGCAGTGGCAGCAGCGGGAACGCTCTTCTCATCTCTCGTATCATGAGGCTCTGCACAC 1371  
QY 1294 CACTACAGCAGAGAGGCTCTTCTCTGCTCCGGGTAAAT 1333  
DB 1372 CACTACAGCAGAGAGGCTCTTCTCTGCTCCGGGTAAAT 1411



Query Match 86.5%; Score 1154.6; DB 15; Length 1392;  
Best Local Similarity 92.5%; Pred. No. 7e-307;  
Matches 1240; Conservative 0; Mismatches 89; Indels 12; Gaps 2;

QY 1 GAGGTGAGCTGGTGGAGTCTGGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60  
DB 58 GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 117  
QY 61 TCCTGTGCAGCTAGCGGATTCATTTTCAGTGGCTTACTGGGTCCCGCCAGGCT 120  
DB 118 TCCTGTGCAGCTTGTGATTCATTTTCAGTGGCTTACTGGGTCCCGCCAGGCT 177  
QY 121 CCAGGGAAGGGGCTCGAGTGGTGTGAAATTTAGATTGAAATCTGATAATTTAGCAACA 180  
DB 178 CCGGGGAAGGGGCTGGAGTGGTCTCAACCAATTAG-----TAGTGGTGGTAGTTACACC 231  
QY 181 CATTTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGTTCAAAATCTAGA 240  
DB 232 TACTATCTAGACAGTATAAAGGGCCGATTCAACATCTCCAGACAAATGCCAAGACTCC 291  
QY 241 CTGTATCTGAAATGAACAGCCTGAAACCGAGGACACAGCCGTGTATTACTGTACA--- 297  
DB 292 CTGTACTGGAATGAACAGTCTGAGGGCTGAGGACACGGCCGTGTATTACTGTGCAAGA 351  
QY 298 ---GATTTCTATAGACTGGGCGCAGGGAACACTAGTACCGTCTCTCCAGCCTCCACCAAG 354  
DB 352 CAGGGGTTGGACTACTGGGTCGAGGAACCTTAGTACCGGCTCTCTCAGCTAGCACCAAG 411  
QY 355 GGCCCATCGGTCTTCCCGCTGGACCTCTCTCAAGAGACCTCTGGGGGCAAGCGGCC 414  
DB 412 GGCCCATCGGTCTTCCCGCTGGACCTCTCTCAAGAGACCTCTGGGGGCAAGCGGCC 471  
QY 415 CTGGGCTGCTGGTCAAGGACTACTCTCCCGAACCGGTGACGGTGTCTGCGAACTCAGGC 474  
DB 472 CTGGGCTGCTGGTCAAGGACTACTCTCCCGAACCGGTGACGGTGTCTGCGAACTCAGGC 531  
QY 475 GCCCTGACAGCGGCTGCACACCTCTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCC 534  
DB 532 GCCCTGACAGCGGCTGCACACCTCTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCC 591  
QY 535 CTGAGAGCGGTGTGACCGTCCCTCAGAGAGCTTGGGCAACAGACCTACATCTGCAAC 594  
DB 592 CTGAGAGCGGTGTGACCGTCCCTCAGAGAGCTTGGGCAACAGACCTACATCTGCAAC 651  
QY 595 GTGAATCACAGCCCAAGCACAACAGGTGGAAGAAAGTGGAGCCCAATCTTGTGAC 654  
DB 652 GTGAATCACAGCCCAAGCACAACAGGTGGAAGAAAGTGGAGCCCAATCTTGTGAC 711  
QY 655 AAAAATCACATGCCCAAGCAGCAGCCTGAACTCGCGGGGCAACCGTCAAGTCTTC 714  
DB 712 AAAAATCACATGCCCAAGCAGCAGCCTGAACTCGCGGGGCAACCGTCAAGTCTTC 771  
QY 715 CTCTTCCCGCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAGGTACATGC 774  
DB 772 CTCTTCCCGCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAGGTACATGC 831  
QY 775 GTGGTGTGACGTCAGCCAGAGACCTGAGTCAAGTTCAACTGGTACGTGGAGCGC 834  
DB 832 GTGGTGTGACGTCAGCCAGAGACCTGAGTCAAGTTCAACTGGTACGTGGAGCGC 891  
QY 835 GTGGAGGTGCATAATGCAAGACAAAGCCGGGAGGAGAGTACACACAGCATCCGT 894  
DB 892 GTGGAGGTGCATAATGCAAGACAAAGCCGGGAGGAGAGTACACACAGCATCCGT 951  
QY 895 GTGGTCAAGCGTCTCAGCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAGTGC 954  
DB 952 GTGGTCAAGCGTCTCAGCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAGTGC 1011  
QY 955 AAGGTCTCCAAAGCCCTCCAGGCCCCATCGAGAAACCATCTCCAAAGCCAAAGGG 1014  
DB 1012 AAGGTCTCCAAAGCCCTCCAGGCCCCATCGAGAAACCATCTCCAAAGCCAAAGGG 1071

RESULT 12  
US-10-704-522-7  
; Sequence 7, Application US/10704522  
; Publication No. US20040120949A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, Gunther  
; APPLICANT: Baumann, Michael  
; APPLICANT: Heider, Karl-Heinz  
; TITLE OF INVENTION: Compositions and methods for treating cancer using  
; TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjugates  
; FILE REFERENCE: 1/1414  
; CURRENT APPLICATION NUMBER: US/10/704,522  
; PRIOR FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US 60/429,516  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: EP 02024881  
; PRIOR FILING DATE: 2002-11-08  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 1392  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain  
US-10-704-522-7

Query Match 86.5%; Score 1154.6; DB 18; Length 1392;  
Best Local Similarity 92.5%; Pred. No. 7e-307;  
Matches 1240; Conservative 0; Mismatches 89; Indels 12; Gaps 2;

QY 1 GAGGTGAGCTGGTGGAGTCTGGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60  
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DB 178 CCGGGGAAGGGGCTGGAGTGGTCTCAACCAATTAG-----TAGTGGTGGTAGTTACACC 231  
QY 181 CATTTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGTTCAAAATCTAGA 240  
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Db 1372 TCCCTGTCTCCGGTAAATGA 1392  
RESULT 13  
US-10-645-215-7  
; Sequence 7, Application US/10645215  
; Publication No. US20040126379A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, Guenther  
; APPLICANT: Baum, Anke  
; APPLICANT: Heider, Karl-Heinz  
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using  
; Cytotoxic CD4 Antibody Immunoconjugates and  
; TITLE OF INVENTION: Chemotherapeutic Agents  
; FILE REFERENCE: 1/1383  
; CURRENT APPLICATION NUMBER: US/10/645,215  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: EP 02 018 686.2  
; PRIOR FILING DATE: August 21, 2002  
; PRIOR APPLICATION NUMBER: US 60/405,956  
; PRIOR FILING DATE: August 26, 2002  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 1392  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanised Antibody BIWA 4 Heavy Chain  
US-10-645-215-7  
Query Match 86.5%; Score 1154.6; DB 18; Length 1392;  
Best Local Similarity 92.5%; Pred. No. 76-307; Indels 12; Gaps 2;  
Matches 1240; Conservative 0; Mismatches 89;  
QY 1 GAGGTGACAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
Db 58 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCTGGAGGGTCCCTTAGACTC 117  
QY 61 TCCGTGACAGTAGAGCGGATTCATTTCTAGTGGCTACTGGATGTCCTGGGTCCGCCAGGT 120  
Db 118 TCCGTGACAGCTCTGGATTCATTTCTAGTAGTATGACATGTCCTGGGTCCGCCAGGT 177  
QY 121 CCAGGGAGGGGCTGAGTGGGTCTGAAATAGATTGAAATCTGATAATTTATGCAACA 180  
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Db 412 GGCCCATCGGTCTTCCCGCTGGCACCTCTCTCAAGAGCACCTCTGGGGGCACAGCGGC 471  
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Qy 775 GTGGTGTGAGCTGAGCAGCAAGAACCCCTGAGTCAAGTTCAACTGGTACGTGACGGC 834  
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Db 1372 TCCCTGTCTCCGGGTAAATGA 1392

RESULT 14

US-09-925-299-230  
; Sequence 230. Application US/09925299  
; Patent No. US20020055627A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA102  
; CURRENT APPLICATION NUMBER: US/09/925,299  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05883  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1556  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 230  
; LENGTH: 1798

; TYPE: DNA  
; ORGANISM: Homo sapiens  
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; NAME/KEY: misc\_feature  
; LOCATION: (1)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc\_feature  
; LOCATION: (15)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc\_feature  
; LOCATION: (24)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc\_feature  
; LOCATION: (31)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc\_feature  
; LOCATION: (501)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc\_feature  
; LOCATION: (1798)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-299-230  
  
Query Match 86.0%; Score 1147.8; DB 9; Length 1798;  
Best Local Similarity 91.0%; Pred. No. 5.5e-305;  
Matches 1245; Conservative 10; Mismatches 73; Indels 40; Gaps 2;  
  
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Db 740 GTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGC 799  
  
Qy 568 TTGGGACCCAGACCTTACATCTCAAGCTGAATCAAGCCAGCAACCAAGGTTGGAC 627  
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US-09-925-299-230
; Sequence 230, Application US/0925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (15)
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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
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US-09-925-299-230

Query Match 86.0%; Score 1147.8; DB 10; Length 1798;
Best Local Similarity 91.0%; Pred. No. 5.5e-305;
Matches 1245; Conservative 10; Mismatches 73; Indels 40; Gaps 2;

Qy 2 AGGTGACGCTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 206 AGGTGACGCTGTGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 265
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 257.521 Seconds  
(without alignments)

8482.539 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335

Sequence: 1 gaggtgcagctggtggagtc.....ccctgtctccgggtaaatga 1335

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA.\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1147.2	85.9	1437	3	US-08-487-550-7
2	1147.2	85.9	1437	4	US-09-526-098-7
3	1147.2	85.9	1437	4	US-09-383-916-7
4	1143.6	85.7	1576	1	US-08-157-101A-6
5	1141.2	85.5	19040	3	US-09-343-485A-3
6	1140.6	85.4	1350	1	US-08-157-101A-9
7	1082.6	81.1	8120	3	US-09-027-449-68
8	1082.6	81.1	8120	3	US-09-026-985-68
9	1082.6	81.1	8120	3	US-09-121-952A-68
10	1082.6	81.1	8120	3	US-09-234-340A-68
11	1072.6	80.3	1467	4	US-08-030-175-5
12	1066.4	79.9	1655	3	US-09-049-672A-21
13	1063.4	79.7	6557	1	US-08-286-740-3
14	1063.4	79.7	6557	5	PCT-US95-09576-3
15	1060	79.4	1458	4	US-08-030-175-7
16	1058.4	79.3	1458	4	US-08-030-175-6
17	1057.6	79.2	1392	4	US-09-472-087-30
18	1057.6	79.2	1392	4	US-09-472-087-59
19	1056	79.1	1392	4	US-09-472-087-27
20	1056	79.1	1392	4	US-09-472-087-53
21	1054.6	79.0	1395	4	US-09-472-087-28
22	1054.6	79.0	1395	4	US-09-472-087-57
23	1052.8	78.9	1392	4	US-09-472-087-55
24	1044.2	78.2	1599	4	US-09-023-655-1120
25	1042.6	78.1	1617	2	US-08-378-939-9
26	1040.6	77.9	1431	3	US-08-487-550-11
27	1040.6	77.9	1431	4	US-09-526-098-11

28	1040.6	77.9	1431	4	US-09-383-916-11
29	1039.8	77.9	1418	3	US-08-793-450-7
30	1039.8	77.9	9209	1	US-08-149-099C-3
31	1039.8	77.9	9209	1	US-08-476-275-2
32	1039.8	77.9	9209	2	US-08-478-967A-3
33	1039.8	77.9	9209	3	US-08-475-815B-3
34	1039.8	77.9	9209	4	US-08-475-813-2
35	1039.8	77.9	18986	2	US-08-819-866-2
36	1039.8	77.9	18986	2	US-09-023-715-2
37	1039.8	77.9	18986	3	US-09-343-485A-2
38	1039	77.8	1567	3	US-09-049-672A-17
39	1035	77.5	1329	5	PCT-US96-13152-3
40	1035	77.5	1413	4	US-09-472-087-61
41	1021.4	76.5	1431	3	US-08-487-550-3
42	1021.4	76.5	1431	4	US-09-526-098-3
43	1021.4	76.5	1431	4	US-09-383-916-3
44	1020.6	76.4	1404	3	US-09-485-737B-66
45	1020.6	76.4	1404	4	US-10-071-485-66

ALIGNMENTS

RESULT 1  
US-08-487-550-7  
; Sequence 7, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,550  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1437 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1437  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 1..1437  
; US-08-487-550-7

Query Match 85.9%; Score 1147.2; DB 3; Length 1437;

Best Local Similarity 90.7%; Pred. No. 4.6e-262;  
Matches 1252; Conservative 0; Mismatches 83; Indels 45; Gaps 1;

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QY 1 GAGGTGAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 58 GAGGTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGCGGTCCCTGAGAGTC 117
QY 61 TCCTGTGCAGCTAGCGGATTCACCTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT 120
Db 118 TCCTGTGCAGCTCTCTGATTCACCTTCAGTGACACACTACATGATTTGGTTCCGCCAGGCT 177
QY 121 CCAGGGAAGGGGCTCGAGTGGGTGCTGAAATAGATTGAAATCTGATATTTATGCAACA 180
Db 178 CCAGGGAAGGGGCGGGAATGGTGGTTCATTAGAAAACAAACCGAACGGTGGGCAACA 237
QY 181 CATTATCGGAGTCTGTGAAGGGAATTCACCATCTCAAGAGATGATTCAMAACTAGA 240
Db 238 GAATAGCCCGCTGTGTGAAGACAGATTCCACCATCTCCAGAGATGATTTCCAAAAGCATC 297
QY 241 CTGTATCTGCAAAATGAACGCTGAAACCGAGGACACAGCGCTGTATTACTGTAC- --- 296
Db 298 GCCTATCTGCAAAATGACAGCCTGAAATTCGAGGACACGGCGCTCTATTACTGTACTACA 357
QY 297 -----AGATTTTCATAGACTGGGC 315
Db 358 TCCTACATTTACATTTGCGGGTGGTGTCTGCTATGGAGTTTACTTCGAAATTTCTGGGC 417
QY 316 CAGGGAACACTAGTACCCTGCTCTGAGCTCCACCAAGGGGCCCATCGGTCTTCCCGCTG 375
Db 418 CAGGGGCGCTGTGCTACCGCTCTCTCAGCTAGCACCAAGGGGCCCATCGGTCTTCCCGCTG 477
QY 376 GCACCTCTCTCCAAAGAGCACTCTGGGGGCACAGCGCCCTGGGCTGCTGTGTCAGGAC 435
Db 478 GCACCTCTCTCCAAAGAGCACTCTGGGGGCACAGCGCCCTGGGCTGCTGTGTCAGGAC 537
QY 436 TACTTCCCGAACCGGTGACGGTGTCTGGAATCTAGGGCCCTCGACGCGCGTGCAC 495
Db 538 TACTTCCCGAACCGGTGACGGTGTCTGGAATCTAGGGCCCTCGACGCGCGTGCAC 597
QY 496 ACCTTCCCGCTGTCTCAGTCTCTCAGGACTCTACTCCTCAGCAGCGTGTGACGGT 555
Db 598 ACCTTCCCGCTGTCTCAGTCTCTCAGGACTCTACTCCTCAGCAGCGTGTGACGGT 657
QY 556 CCTTCAGCAGCTTGGGACCCAGACCTCATCTGCAACGTGAATCACAGCCCAACCAAC 615
Db 658 CCTTCAGCAGCTTGGGACCCAGACCTCATCTGCAACGTGAATCACAGCCCAACCAAC 717
QY 616 ACCAAGGTGACAAAGTGGAGCCCAATCTTGTGACAAAACTCACACATGCCACCG 675
Db 718 ACCAAGGTGACAAAGTGGAGCCCAATCTTGTGACAAAACTCACACATGCCACCG 777
QY 766 TGCCAGCAGCTGAACCTCGGGGGGACCGTGAAGTCTTCTTCCCGCCAAACCAAG 735
Db 778 TGCCAGCAGCTGAACCTCTCGGGGGGACCGTGAAGTCTTCTTCCCGCCAAACCAAG 837
QY 736 GACACCTCATGATCTCCCGGACCCCTGAGGTGCATGCTGTGTGGAGCGTGAGCCAC 795
Db 838 GACACCTCATGATCTCCCGGACCCCTGAGGTGCATGCTGTGTGGAGCGTGAGCCAC 897
QY 796 GAAGACCTCAGGTCAAGTTCAACTGCTAGTGGAGCGGTGGAGGTGCATATGCAAG 855
Db 898 GAAGACCTCAGGTCAAGTTCAACTGCTAGTGGAGCGGTGGAGGTGCATATGCAAG 957
QY 856 ACAAGCCGGGAGGAGGAGTACACAGCAGCTAGCTGTGTGTGTCAGCTCTCAGCGTC 915
Db 958 ACAAGCCGGGAGGAGGAGTACACAGCAGCTAGCTGTGTGTGTCAGCTCTCAGCGTC 1017
QY 916 CTCGACGAGCTGGCTGAATGCAAGGAGTCAAGTGAAGTCTTCCAAAGCCCTC 975
Db 1018 CTCGACGAGCTGGCTGAATGCAAGGAGTCAAGTGAAGTCTTCCAAAGCCCTC 1077
QY 976 CCAGCCCGCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGGAGAACACAGGTG 1035
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QY 1036 TACACCTCGCCCATCCCGGATGAGCTGACCAAGAACCAAGTCCAGCTGACCTGACCTG 1095
Db 1138 TACACCTCGCCCATCCCGGATGAGCTGACCAAGAACCAAGTCCAGCTGACCTGACCTG 1197
QY 1096 GTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGCGAGCGGAG 1155
Db 1198 GTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGCGAGCGGAG 1257
QY 1156 AACAATACAAGACCAACCGCTCCCGTGGTGGACTCCGAGCGCTCTTCTTCTTCTACAGC 1215
Db 1258 AACAATACAAGACCAACCGCTCCCGTGGTGGACTCCGAGCGCTCTTCTTCTTCTACAGC 1317
QY 1216 AGCTCACCGTGGACAGAGGAGTGGCAGAGGGGAGGCTTCTTCTCATGCTCCGTGATG 1275
Db 1318 AGCTCACCGTGGACAGAGGAGTGGCAGAGGGGAGGCTTCTTCTCATGCTCCGTGATG 1377
QY 1276 CATGAGGCTTCTGCAACCACTACACGAGAGAGCTTCCCTGTCTCCGGGTAAATGA 1335
Db 1378 CATGAGGCTTCTGCAACCACTACACGAGAGAGCTTCCCTGTCTCCGGGTAAATGA 1437
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RESULT 2

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US-09-526-098-7
; Sequence 7, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1437
; FEATURE:
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NAME/KEY: mat peptide  
LOCATION: 1..1437  
US-09-526-098-7

Query Match 85.9%; Score 1147.2; DB 4; Length 1437;  
Best Local Similarity 90.7%; Pred. No. 4.6e-262;  
Matches 1252; Conservative 0; Mismatches 83; Indels 45; Gaps 1;

Qy	1	GAGTGCAGCTGTGGAGTCTGGGGAGGCTGTGTAAGCCCGGGGGTCCCTTAGACTC	60
Db	58	GAGGTGCAACTGTGTGAGTCTGGGGAGGCTTGTCCAGCTGCGGGTCCCTGAGAGTC	117
Qy	61	TCCTGTGCGCTACCGGATTCACCTTCAGTGGCTACTGGATGCTCTGGTCCGCGAGCT	120
Db	118	TCCTGTGCGCTTCGTGATTCACCTTCAGTGACCATACATGATTAATGTTCCGCGAGCT	177
Qy	121	CCAGGGAAGGGGCTCGAGTGGGTGTGTAATAGATTGAATCTGTAATATATGCAACA	180
Db	178	CCAGGGAAGGGGCGGATGGGTAGTTTCAATAGAAACAAACCGAACGGTGGGCAACA	237
Qy	181	CATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA	240
Db	238	GAATACCGCGCTCTGTGAAAGACAGATTTCACCATCTCCAGAGATGATTCAAAAGCATC	297
Qy	241	CTGTATCTGCMAATGAACAGCTGAAAACCGAGGACACAGCGGTGTTACTGTAC	296
Db	298	GCCTATCTGCAATGAGCAGCTGAAAATCGAGGACACGCGCGCTTATTACTGTACTACA	357
Qy	297	-----AGATTTTCATAGACTGGGC	315
Db	358	TCCTACATTTTCATGTCGGGGTGTGTCTGTATGGAGTTACTTCGAATTCCTGGGC	417
Qy	316	CAGGGAACACTAGTACCGTCTCTCAGCCTTCAACAAAGGGCCCATCGGTCTTCCCGCTG	375
Db	418	CAGGCGCCCTGTGTACCGTCTCTCAGTAGCACCAAGGGCCCATCGGTCTTCCCGCTG	477
Qy	376	GCACCTCTCTCAAGACACTCTGGGGGACACAGCGCCCTGGCTCCCTGGTCAAGGAC	435
Db	478	GCACCTCTCTCAAGACACTCTGGGGGACACAGCGCCCTGGCTCCCTGGTCAAGGAC	537
Qy	436	TACTTCCCGAAGCGGTGAGTGTCTGTGAACTCAGCGCCCTGACAGCGGTGCAC	495
Db	538	TACTTCCCGAAGCGGTGAGTGTCTGTGAACTCAGCGCCCTGACAGCGGTGCAC	597
Qy	496	ACCTTCCCGGTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTG	555
Db	598	ACCTTCCCGGTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTG	657
Qy	556	CCCTCCAGAGCTTTGGGACCCAGACTATACCTGCAAGTGAATCAAGCCAGCAAC	615
Db	658	CCCTCCAGAGCTTTGGGACCCAGACTATACCTGCAAGTGAATCAAGCCAGCAAC	717
Qy	616	ACCAAGGTGACAGAAAGTGGGCCCAATCTGTGACAAATCAACATGCCACCG	675
Db	718	ACCAAGGTGACAGAAAGTGGGCCCAATCTGTGACAAATCAACATGCCACCG	777
Qy	676	TGCCAGCAGCTGAACTCGGGGGGACCCGTGAGTCTTCTTCTTCCCGCCAAACCCAAAG	735
Db	778	TGCCAGCAGCTGAACTCTGGGGGACCCGTGAGTCTTCTTCTTCCCGCCAAACCCAAAG	837
Qy	736	GACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGGACGTGAGCCAC	795
Db	838	GACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGGACGTGAGCCAC	897
Qy	796	GAAGACCTGAGTCAAGTTCACTGTAAGTGAACCGGTGGAGGTGCATATGCCAAG	855
Db	898	GAAGACCTGAGTCAAGTTCACTGTAAGTGAACCGGTGGAGGTGCATATGCCAAG	957
Qy	856	ACAAAGCGGGGAGGAGAGTCAACAGCACGTGACGTGTGGTCAAGCTCCACCGTC	915
Db	958	ACAAAGCGGGGAGGAGAGTCAACAGCACGTGACGTGTGGTCAAGCTCCACCGTC	1017
Qy	916	CTGCACCGAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAAAGGCCCTC	975

RESULT 3

US-09-383-916-7  
; Sequence 7, Application US/09383916  
; Patent No. 6709654  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/383,916  
; FILING DATE: 26-AUG-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/487,550  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teekin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1437 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:

Db	1018	CTGCACGAGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAAAGGCCCTC	1077
Qy	976	CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGGAGCCCGGAGAACCAAGGTG	1035
Db	1078	CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGGAGCCCGGAGAACCAAGGTG	1137
Qy	1036	TACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGGTGAGCTGAGCTGCGCTG	1095
Db	1138	TACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGGTGAGCTGAGCTGCGCTG	1197
Qy	1096	GTCAAGAGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGAGCCGGAG	1155
Db	1198	GTCAAGAGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGAGCCGGAG	1257
Qy	1156	AACAATCTAAGAACCAAGCTCCCGTGGTGGACTCCGAGCGCTCTTCTCTCTACAGC	1215
Db	1258	AACAATCTAAGAACCAAGCTCCCGTGGTGGACTCCGAGCGCTCTTCTCTCTACAGC	1317
Qy	1216	AGCTCACCGTGACAAAGAGAGGTGGGAGAGGGGAAAGTCTTCTCATGCTCCGTGATG	1275
Db	1318	AGCTCACCGTGACAAAGAGAGGTGGGAGAGGGGAAAGTCTTCTCATGCTCCGTGATG	1377
Qy	1276	CATGAGGCTCTGCACCAACCACTACACGACAGAGGCTCTCCCTGTCTCCGGGTAAATGA	1335
Db	1378	CATGAGGCTCTGCACCAACCACTACACGACAGAGGCTCTCCCTGTCTCCGGGTAAATGA	1437

NAME/KEY: CDS  
LOCATION: 1..1437  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 1..1437  
US-09-383-916-7

Query Match 85.9%; Score 1147.2; DB 4; Length 1437;  
Best Local Similarity 90.7%; Pred. No. 4.6e-262; Indels 45; Gaps 1;  
Matches 1252; Conservative 0; Mismatches 83;

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
DB 58 GAGGTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCTCGCGGGTCCCTGAGATC 117  
QY 61 TCCTGTGCAGCTAGCGGATTCATTTTCAGTGGCTACTGATGATCTCTGGGTCCGCCAGGCT 120  
DB 118 TCCTGTGCAGTCTCTGGATTCATTTTCAGTGCACCTACATGATTTGGTTTCGCCAGGCT 177  
QY 121 CCAGGGAAGGGGCTCGAGTGGTCTGAAATAGATTGAATCTGATAATTATGCAACA 180  
DB 178 CCAGGGAAGGGGCGGAAATGGGTAGTTTCATTAGAAAACCAACCGAAGCGGTGGGCAACA 237  
QY 181 CATTATGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240  
DB 238 GAATAGCGCGCTGTGAAAGACAGATTCCACCATCTCCAGAGATGATTCCTCAAAAGCATC 297  
QY 241 CTGTATCTGAATGAACAGCCCTGAAACCGAGGACACAGCCGTGTATTTACTGTAC---- 296  
DB 298 GCCTATCTGCAATGAGCAGCTGAAATCGAGGACACGCGCGCTCTATTACTGTACTACA 357  
QY 297 -----AGATTTTCATAGACTGGGC 315  
DB 358 TCCTACATTTACATTTGCGGGTGTGTCTGATATGGAGTTACTTCGAATTTCTGGGC 417  
QY 316 CAGGGAACACTAGTACCGCTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCCCTG 375  
DB 418 CAGGGCGCCCTGTGTACCGTCTCTCAGCTAGCAACCAAGGGCCCATCGGTCTTCCCCCTG 477  
QY 376 GCACCTCTCCAAAGACACCTCTGGGGGACAGCGCCCTGGGCTGCCCTGTGTCAGGAC 435  
DB 478 GCACCTCTCCAAAGACACCTCTGGGGGACAGCGCCCTGGGCTGCCCTGTGTCAGGAC 537  
QY 436 TACTTCCCGAAACCGGTGACGGTGTGTGAACTCAGGCGCCCTGACAGCGCGCTGAC 495  
DB 538 TACTTCCCGAAACCGGTGACGGTGTGTGAACTCAGGCGCCCTGACAGCGCGCTGAC 597  
QY 496 ACCTTCCCGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTG 555  
DB 598 ACCTTCCCGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTG 657  
QY 556 CCCTCCAGCAGCTGGGACCCAGCCTACATCTGCAAGTGAATCAAGCCCAAC 615  
DB 658 CCCTCCAGCAGCTGGGACCCAGCCTACATCTGCAAGTGAATCAAGCCCAAC 717  
QY 616 ACCAAGTGCAGAAAGTGGAGCCCAATCTTTGTGACAAAACCTCACAATGCCCAACG 675  
DB 718 ACCAAGTGCAGAAAGTGGAGCCCAATCTTTGTGACAAAACCTCACAATGCCCAACG 777  
QY 676 TGCCCAAGCCTGAACTTCGCGGGGACCGTCACTTCTTCTTCCCCCAAAACCAAG 735  
DB 778 TGCCCAAGCCTGAACTTCGCGGGGACCGTCACTTCTTCTTCCCCCAAAACCAAG 837  
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DB 838 GACACCTCATGATCTCCCGGACCCCTGAGTTCACATGGTGTGGTGGAGCGGAC 897  
QY 796 GAAGACCTCAGGTCAAGTTCACTGTGAGTGGAGCGGCTGGAGTGCATATGCAAG 855  
DB 898 GAAGACCTCAGGTCAAGTTCACTGTGAGTGGAGCGGCTGGAGTGCATATGCAAG 957  
QY 856 ACAAGCGCGGAGGAGAGTGAACAACAGCACCTGACCGTGTGTGACCGTCTCACCGTC 915

DB 958 ACAAGCCGCGGAGGAGCAGTACAAACAGCACCTACCGTGTGGTCAAGCGTCTCACCGTC 1017  
QY 916 CTGCAACCAAGTGGCTGAATGGCAAGAGTACAGTGCAGGTCTTCAACAAAGCCCTC 975  
DB 1018 CTGCAACCAAGTGGCTGAATGGCAAGAGTACAGTGCAGGTCTTCAACAAAGCCCTC 1077  
QY 976 CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTG 1035  
DB 1078 CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTG 1137  
QY 1036 TACACCTCTGCCCATCCCGGATGAGTGCACCAAGAACCAAGGTGAGCTGACCTGCTGCTG 1095  
DB 1138 TACACCTCTGCCCATCCCGGATGAGTGCACCAAGAACCAAGGTGAGCTGACCTGCTGCTG 1197  
QY 1096 GTCAAGGCTTATATCCAGCGACATCCCGTGGAGTGGAGCAATGGGCGAGCGGAG 1155  
DB 1198 GTCAAGGCTTATATCCAGCGACATCCCGTGGAGTGGAGCAATGGGCGAGCGGAG 1257  
QY 1156 AACAACCTACAGAACCAAGCTCCCGTGGTGGTCCGACGGCTCTTCTTCTTCTTCTACAGC 1215  
DB 1258 AACAACCTACAGAACCAAGCTCCCGTGGTGGTCCGACGGCTCTTCTTCTTCTTCTACAGC 1317  
QY 1216 AAGCTCACCGTGGCAAGAGCAGGTGGGAGGAGGAAAGTCTTCTCATGCTCCGTGATG 1275  
DB 1318 AAGCTCACCGTGGCAAGAGCAGGTGGGAGGAGGAAAGTCTTCTCATGCTCCGTGATG 1377  
QY 1276 CATGAGGCTCTGCAACCAACCTACAGCGAGAGAGCCTTCCCTCTCCGGGTAAATGA 1335  
DB 1378 CATGAGGCTCTGCAACCAACCTACAGCGAGAGAGCCTTCCCTCTCCGGGTAAATGA 1437

## RESULT 4

US-08-157-101A-6  
; Sequence 6, Application US/08157101A  
; Patent No. 5808032  
; GENERAL INFORMATION:  
; APPLICANT: KURIHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU  
; APPLICANT: TSURUOKA, NOBUO  
; APPLICANT: ARIMA, KENJI  
; APPLICANT: NISHIHARA, TATSURO  
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION  
; TITLE OF INVENTION: PLASMIDS THEREFOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/157,101A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TITUS, MARLANA K  
; REGISTRATION NUMBER: 35843  
; REFERENCE/DOCKET NUMBER: 9437/204199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3711  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 CUCH  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1576 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single





Qy	175	GC	AACACATTTATGGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTTCAAAA	234
Db	9667	CCCACATGGTACG	CAGACTCCGTTGAAGGGCAGATTCACCATCTCCAGAGAGAAACGCCAAG	9726
Qy	235	TCTAGACTGTATCTGCAATATGAACAGCCTGMAAACCGAGGACACAGCCGTGTATTACTGT	294	
Db	9727	AACACACTGTTCTTCAAAATGAACACGCTTGAGAGCTGAGGACACCGCTGTCTATTACTGT	9786	
Qy	295	AC-----AGATTTCTATAGACTGGGGCCAGGGAAACA	341	
Db	9787	GGGAGCTTGACTACAGGGTCTGACTCCCTGGGGCCAGGGAGTCTCTGTCA	9846	
Qy	342	AGCCTCCACCAAGGGGCCATCGGTCTTCCCTCTGGCACCCCTCCTCCAAAGACACCTCTGG	401	
Db	9847	AGCTAGCACCAAGGGGCCATCGGTCTTCCCTCTGGCACCCCTCCTCCAAAGACACCTCTGG	9906	
Qy	402	GGGACAGCGCGCCCTGGGCTGCCGTGTCAAGNACTACTTCCCGGAAACCGGTGA	461	
Db	9907	GGGACAGCGCGCCCTGGGCTGCCGTGTCAAGGACTACTTCCCGGAAACCGGTGA	9966	
Qy	462	GTGGAACTCAGGCGCCCTGACACAGCGCGCTGACACCTTCCCGGCTGTCTTACAGTCCCTC	521	
Db	9967	GTGGAACTCAGGCGCCCTGACACAGCGCGCTGACACCTTCCCGGCTGTCTTACAGTCCCTC	10026	
Qy	522	AGGACTTACTCCCTCAGCAGCGTGTGACCGGTGCCCTCCAGCAGCTTGGGCACCCAGAC	581	
Db	10027	AGGACTTACTCCCTCAGCAGCGTGTGACCGGTGCCCTCCAGCAGCTTGGGCACCCAGAC	10086	
Qy	582	CTACATCTGCAACGCTGAATCAAAAGCCCAAGCAACCAAGGTGGACAGAAAGTGGAGCC	641	
Db	10087	CTACATCTGCAACGCTGAATCAAAAGCCCAAGCAACCAAGGTGGACAGAAAGTGGAGCC	10146	
Qy	642	CAAACTCTGTGACAAAACACTCACACATGCCACCGTGCCCGAGCACCTGAACCTCGCGGGGC	701	
Db	10147	CAAACTCTGTGACAAAACACTCACACATGCCACCGTGCCCGAGCACCTGAACCTCGCGGGGC	10206	
Qy	702	ACCGTCAGTCTTCTCTTCCCGCAAAACCCAAAGCACCCCTCATGTATCCCGGACCCC	761	
Db	10207	ACCGTCAGTCTTCTCTTCCCGCAAAACCCAAAGCACCCCTCATGTATCCCGGACCCC	10266	
Qy	762	TGAGGTCACATGCGTGGTGGAGCTGAGGCCACGAAAGACCCCTGAGGTCAAGTTCAACTG	821	
Db	10267	TGAGGTCACATGCGTGGTGGAGCTGAGGCCACGAAAGACCCCTGAGGTCAAGTTCAACTG	10326	
Qy	822	GTACGTGGACGGCGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAA	881	
Db	10327	GTACGTGGACGGCGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAA	10386	
Qy	882	CAGCAGTACCGTGTGGTCAGCGTCTCTACCGTCTCTGCACACGAGCTGGCTGAATGGCAA	941	
Db	10387	CAGCAGTACCGTGTGGTCAGCGTCTCTACCGTCTCTGCACACGAGCTGGCTGAATGGCAA	10446	
Qy	942	GGAGTACAAGTGAAGGTCTCCAAAGACCCCTCCAGCCCCCATCGAGAAACCAATCTC	1001	
Db	10447	GGAGTACAAGTGAAGGTCTCCAAAGACCCCTCCAGCCCCCATCGAGAAACCAATCTC	10506	
Qy	1002	CAAAGCCAAAGGCGACGCCGAGAACACAGGTGTACCCCTGCCCCCATCCCGGGATGA	1061	
Db	10507	CAAAGCCAAAGGCGACGCCGAGAACACAGGTGTACCCCTGCCCCCATCCCGGGATGA	10566	
Qy	1062	GCTGACCAAGAACGAGCTCAGCTGCCTTGGTCAAAGGCTTCTATCCAGCGACAT	1121	
Db	10567	GCTGACCAAGAACGAGCTCAGCTGCCTTGGTCAAAGGCTTCTATCCAGCGACAT	10626	
Qy	1122	CGCCGTGGAGTGGAGAGCAATGGGAGCCGGAGAACAACTACAGAACCGCTCCCGT	1181	
Db	10627	CGCCGTGGAGTGGAGAGCAATGGGAGCCGGAGAACAACTACAGAACCGCTCCCGT	10686	
Qy	1182	GCTTGGACTCCGACGGCTCTTCTTCTTACAGAGCTCAACGCTGGACAGACAGGTG	1241	
Db	10687	GCTTGGACTCCGACGGCTCTTCTTCTTACAGAGCTCAACGCTGGACAGACAGGTG	10746	
Qy	1242	GCAGCAGGGGAAACGCTTCTTCTATGCTCCGCTGATGATGAGGCTCTGTCACCAACCTACAC	1301	

RESIT.T 6

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US-08-157-101A-9
; Sequence 9, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARINA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PC-DOS/MS-DOS
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-157-101A-9

Query Match      85.4%; Score 1140.6; DB 1; Length 1350;
Best Local Similarity 91.8%; Pred. No. 1.7e-260;
Matches 1241; Conservative 0; Mismatches 84; Indels 30; Gaps 2;

Qy      2      AGGTGCAGCTGGTGGAGTCTGGGGGAGGCTGTGTAAGCCCGGGGGTCCCTTAGACTCT 61
Db      2      AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
Qy      62      CCTGTGCAGCTAGCGGATTCATTTTCAGTGGCTACTTGGATGTCTCTGGGTCCGCGAGGCTC 121
Db      62      CCTGTGCAGCTCTGGATTCACCTTCAGTAGCAATTCATATGACCTGGTCCGCGAGGCTC 121
Qy      122     CAGGGAAGGGCTCGAGTGGTGTCTGGAATTAGATTGAAATCTGATAATTATGCAACAC 181
Db      122     CAGGCAAGGGTGGAGTGGTGGTGGAGTTA-----TATTATATGATGGAATCATAAAT 175
Qy      182     ATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGAC 241
Db      176     TCTACGCAGACTCCGTGAAGGGCCGATTCACATTTCCAGAGCAATTCAGAGAACACAC 235

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Qy 242 TGTATCTGCAAAATGAACAGCCTGAAAAACCGAGGACACAGCGGTGTATTACTGTACA----- 297  
Db 236 TGTATCTGGAAGTGAAGAGCCTGCAAACTGAGGACACCGGTGTCTATTCTGTATTAAGAG 295  
Qy 298 -----GATTTTCATAGCTGGGGCCAGGGNAACACTAGTCACTGCT 337  
Db 296 ATCAAACTTAGGAGTCCACAGATTTTGACTCTCTGGGGCCAGGGAACTCTGGTCACTGCT 355  
Qy 338 CCTCAGCTCTCACCAGGGCCATCGGTCTTCCCTCTGGCACCTCTCTCCAAGAGCACCT 397  
Db 356 CCTCAGCTCTCACCAGGGCCATCGGTCTTCCCTCTGGCACCTCTCTCCAAGAGCACCT 415  
Qy 398 CTGGGGCACAGCGGCCCTGGGCTGCTCTGCTCAAGGACTACTTCTCCCGAACCCTGACGG 457  
Db 416 CTGGGGCACAGCGGCCCTGGGCTGCTCTGCTCAAGGACTACTTCTCCCGAACCCTGACGG 475  
Qy 458 TGTCTGGAACCTAGGGCCCTCTGACAGCGCGGTGACACCTTCCCGGCTGTCTACAGT 517  
Db 476 TGTCTGGAACCTAGGGCCCTCTGACAGCGCGGTGACACCTTCCCGGCTGTCTACAGT 535  
Qy 518 CCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCACCC 577  
Db 536 CCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCACCC 595  
Qy 578 AGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCCAGCAACACCAAGGTGGACAAGTGG 637  
Db 596 AGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCCAGCAACACCAAGGTGGACAAGTGG 655  
Qy 638 AGCCCAAACTTGTGACAAAACCTCACAATGCTCCACCGTCCAGCGCTGCTGAACCTCGCGG 697  
Db 656 AGCCCAAACTTGTGACAAAACCTCACAATGCTCCACCGTCCAGCGCTGCTGAACCTCGCGG 715  
Qy 698 GGGCACGCTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTCCCGGA 757  
Db 716 GGGCACGCTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTCCCGGA 775  
Qy 758 CCCCTGAGGTACATGCTGTGTGGACGTGAGCCACGAAGACCTCTGAGGTCAAAGTTCA 817  
Db 776 CCCCTGAGGTACATGCTGTGTGGACGTGAGCCACGAAGACCTCTGAGGTCAAAGTTCA 835  
Qy 818 ACTGCTGAGTGAACGGGTGAGGTGCATATGCAAGACAAAGCCCGGGAGGAGCAGT 877  
Db 836 ACTGCTGAGTGAACGGGTGAGGTGCATATGCAAGACAAAGCCCGGGAGGAGCAGT 895  
Qy 878 ACACAGCAGTACCGTGTGTGAGCTCTCCTCAGCTCTGACAGGACTGCTGTAATG 937  
Db 896 ACAACAGCAGTACCGGTGTGTGAGCTCTCCTCAGCTCTGACAGGACTGCTGTAATG 955  
Qy 938 GCAAGGAGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCAGCCCTCATCGAGAAACCA 997  
Db 956 GCAAGGAGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCAGCCCTCATCGAGAAACCA 1015  
Qy 998 TCTCCAAAGCAAGGGAGCGCCCGAGAACACAGGTGTACACCTGCCCTCCATCCCGGG 1057  
Db 1016 TCTCCAAAGCAAGGGAGCGCCCGAGAACACAGGTGTACACCTGCCCTCCATCCCGGG 1075  
Qy 1058 ATGAGCTGACCAAGAACAGGTGAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGCG 1117  
Db 1076 ATGAGCTGACCAAGAACAGGTGAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGCG 1135  
Qy 1118 ACATCGCGTGGAGTGGAGAGCAATGGGAGCGCGAGAACCACTACAAGACCAACGCTC 1177  
Db 1136 ACATCGCGTGGAGTGGAGAGCAATGGGAGCGCGAGAACCACTACAAGACCAACGCTC 1195  
Qy 1178 CCGTCTGAGTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCCTGGGAGCAAGACCA 1237  
Db 1196 CCGTCTGAGTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCCTGGGAGCAAGACCA 1255  
Qy 1238 GGTGGCAGCAGGGAAAGTCTTCTCTCATGCTCCGTGATGATGAGGCTCTGCAACACCACT 1297  
Db 1256 GGTGGCAGCAGGGAAAGTCTTCTCTCATGCTCCGTGATGATGAGGCTCTGCAACACCACT 1315

Qy 1298 ACACGCAAGAGCCTCTCCCTGTCTCTCCGGGTAAA 1332  
Db 1316 ACACGCAAGAGCCTCTCCCTGTCTCTCCGGGTAAA 1350  
RESULT 7  
US-09-027-449-68  
; Sequence 68, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027,449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,664  
; FILING DATE: 21-Feb-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8120 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
US-09-027-449-68

Query Match 81.1%; Score 1082.6; DB 3; Length 8120;  
Best Local Similarity 88.6%; Pred. No. 1.6e-246;  
Matches 1210; Conservative 0; Mismatches 119; Indels 36; Gaps 2;

Qy 1 GAGGTGACGTGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
Db 1363 GAAGTTTCAGCTAGTCAGTCTGGCGGTGGCTGGTGCAGCCAGGGGGCTCACTCCGTTTG 1422  
Qy 61 TCCTGTGCAGTAGCGGATTCACCTTTCAGTGGCTACTTGGATGTCTGGGTCCGCGAGGCT 120  
Db 1423 TCCTGTGCAGTCTTGGTACTCTCTTCGAGTCATATATGACTGGTCCGTCAGGCC 1482  
Qy 121 CCAGGAAGGGGCTCGAGTGGGTGTGAAATAGATGAAATCTGATAAATATGCAACA 180  
Db 1483 CCGGGTAAGGGCTGGAATGGTGGATATATT-----GATCTTCAATGGTGAAT 1536  
Qy 181 CATATGCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240  
Db 1537 ACGTATAATCAAAAGTTTCAGGGCCGTTTTCATCTTTATCTCGCAGACACTCCAAAAACACA 1596

Qy	241	CTGTATCTGCAAAATGAAACAGCCTTGAAACCGAGGACACAGCGTGTATTA	297
Dy	1597	GCATACCTGCAGATGAACAGCCTCGTGTCTGAGGACATGCGTCTATTACTGTGCAAGA	1656
Qy	298	-----GATTTTATAGACTGTGGGCCAAGGAAACACTAGTC	330
Dy	1657	GGGGATTATCGCTACAATGTGTACTTGACGTCTGGGTCAAGGAACCCCTGGTC	1716
Qy	331	ACCGTCTCCTCAGCCTCACCAAGGGCCCATCGTCTTCCCTCGGCACACCTCCTCCAAG	390
Dy	1717	ACCGTCTCCTGGGCTCCACNAGGGCCCATCGTCTTCCCTTGGCACCTCTCTCCNAG	1776
Qy	391	AGCACCTCTGGGGCACAGCGGCCCTGGGCTCGCTGTCAAGGACTACTTCCCGGAACCG	450
Dy	1777	AGCACCTCTGGGGCACAGCGGCCCTGGGCTCGCTGTCAAGGACTACTTCCCGGAACCG	1836
Qy	451	GTGACGCTGTCTGGAACCTCAGGCGCCCTGACNAGCGGCGTGCACACTTCCCGGCTGTC	510
Dy	1837	GTGACGCTGTCTGGAACCTCAGGCGCCCTGACNAGCGGCGTGCACACTTCCCGGCTGTC	1896
Qy	511	CTACAGTCTCAGGACTCTACTCCTCCTCAGCAGCGTGTGTGACCGTGCCTCCAGCAGCTTG	570
Dy	1897	CTACAGTCTCAGGACTCTACTCCTCCTCAGCAGCGTGTGTGACTGTGCTCTTAGCAGCTTG	1956
Qy	571	GGCACCCAGACCTACATCTGCAACGCTGAATCACAAGCCCAAGCAACCAAGGTGGACAAG	630
Dy	1957	GGCACCCAGACCTACATCTGCAACGCTGAATCACAAGCCCAAGCAACCAAGGTGGACAAG	2016
Qy	631	AAAGTGAAGCCCAAAATCTTGACAAAACTCACACATGCCGACCGTGCCAGACACTGAA	690
Dy	2017	AAAGTGAAGCCCAAAATCTTGACAAAACTCACACATGCCGACCGTGCCAGACACTGAA	2076
Qy	691	CTCGCGGGGCACCGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATC	750
Dy	2077	CTCTGCGGGGACCGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATC	2136
Qy	751	TCCCGGACCCCTGAGGTCACATGCGTGGTGTGGACGTGAGCCACGAAGACCTCTGAGTC	810
Dy	2137	TCCCGGACCCCTGAGGTCACATGCGTGGTGTGGACGTGAGCCACGAAGACCTCTGAGTC	2196
Qy	811	AAGTTCAACTGGTTACGTGGAACGGCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAG	870
Dy	2197	AAGTTCAACTGGTTACGTGGAACGGCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAG	2256
Qy	871	GAGCAGTACACACGACGTACCGTGTGGTGTGAGTCTCACCGTCTGCAACCGAGTGG	930
Dy	2257	GAGCAGTACACACGACGTACCGTGTGGTGTGAGTCTCACCGTCTGCAACCGAGTGG	2316
Qy	931	CTGAATGGCAAGGAGTACAAGTGCAGAGTCTTCCAAACAAGCCCTCCAGGCCCCATCGAG	990
Dy	2317	CTGAATGGCAAGGAGTACAAGTGCAGAGTCTTCCAAACAAGCCCTCCAGGCCCCATCGAG	2376
Qy	991	AAAACCATCTCAAAGCCAAAGGGACGCCCGAGAACCAAGGTGTACAACCTGCCCCCA	1050
Dy	2377	AAAACCATCTCAAAGCCAAAGGGACGCCCGAGAACCAAGGTGTACAACCTGCCCCCA	2436
Qy	1051	TCCCGGATCAGCTGACCAAGAACCGGTGAGCTGACCTGCTGCTCAAGGCTTCTAT	1110
Dy	2437	TCCCGGAAAGAGATGACCAAGAACCGGTGAGCTGACCTGCTGCTCAAGGCTTCTAT	2496
Qy	1111	CCCAGCACATCGCCGTGGAGTGGGAGCAATGGGCAGCGGAGAACAACTACAAGACC	1170
Dy	2497	CCCAGCACATCGCCGTGGAGTGGGAGCAATGGGCAGCGGAGAACAACTACAAGACC	2556
Qy	1171	ACGCTCCCGTGTGGAATCCGACGGCTCTTCTTCTTCTTACGAAGACTCAACGTGGAC	1230
Dy	2557	ACGCTCCCGTGTGGAATCCGACGGCTCTTCTTCTTCTTACGAAGACTCAACGTGGAC	2616
Qy	1231	AAGAGCAGGTGGCAGCAGGGGACGTCTTCTCATGTCTCGTGTGATGATGAGGCTCTGCAC	1290
Dy	2617	AAGAGCAGGTGGCAGCAGGGGACGTCTTCTCATGTCTCGTGTGATGATGAGGCTCTGCAC	2676
Qy	1291	AACCACTACACGCAAGAGAGCCTCTCCGTGTCTCCGGGTAATGCA	1335

Db 2677 AACCACTACACGAGAGAGCCTCTCCCTGCTCCGGGTAATGA 2721

RESULT 8

US-09-026-985-68

; Sequence 68, Application US/09026985

; Patent No. 6133426

; GENERAL INFORMATION:

; APPLICANT: Gonzalez, Tania R.

; APPLICANT: Leong, Steven R.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and

; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA: US/09/026,985

; APPLICATION NUMBER: US/09/026,985

; FILING DATE: 20-Feb-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: PI085R3-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5530

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8120 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

US-09-026-985-68

Query Match 81.1%; Score 1082.6; DB 3; Length 8120;

Best Local Similarity 88.6%; Pred. No. 1.6e-246;

Matches 1210; Conservative 0; Mismatches 119; Indels 36; Gaps 2;

Qy 1 GAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTCGTAAGCCGGGGGTCCTTAGACTC 60

Db 1363 GAAGTTCAGCTAGTGCAGTCTGGCGTGGCTGGTGAGCCAGGGGGCTCACTCCGTTG 1422

Qy 61 TCCTGTGCAGTAGCGGATTCATTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT 120

Db 1423 TCCTGTGCAGCTTCTGCTACTCTTCTCGAGTCATATATGACTGGGTCCGTAGGCC 1482

Qy 121 CCAGGGAAGGGGCTCGAGTGGTGTCTGAAATTAGATGAAATCTGATAATATGCAACA 180

Db 1483 CCGGGTAAGGGCCCTGGAAATGGGTGGATATATT-----GATCCTTCCAATGGTGAAC 1536

Qy 181 CATTAATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCARAACTAGA 240

Db 1537 ACGTATTAATCAAAAGTTCAAGGGCCGTTTCACATTTATCTCGGACAACTCCAAAAACACA 1596

Qy 241 CTGTATCTGCAAAATGAACAGCCTCGAAAAACCGAGGACACAGCCCGTGTATTACTGTACA--- 297

Db 1597 GCATACCTGCAGATGAACAGCCTCGGTGCTGAGGACACTGCCGTCTATTACTGTGCAAGA 1656

Qy 298 -----GATTTCAATAGCTGGGGCCAGGAAACACTAGTC 330

Db 1657 GGGGATTATCGCTACAAATGGTGAAGTGGTCTTCGAGCTCTCTGGGTCAAGGAAACCTGGTC 1716



Db 1657 GGGGATTATCGCTACAAATGGTGACTGGTCTTCGACGTCTGGGGTCAAGGAACCCCTGGTC 1716  
QY 331 ACCGTCTCTCGACCTCCACCAAGGGCCCATCGGTCTTCCCTCCCTGGACCCCTCTCTCAAG 390  
Db 1717 ACCGTCTCTCGGCGCTCCACCAAGGGCCCATCGGTCTTCCCTCCCTGGACCCCTCTCTCAAG 1776  
QY 391 AGCACCTCTGGGGGACACGGGCGCTGGCTGGTCAAGGACTACTTCCCGGAACCG 450  
Db 1777 AGCACCTCTGGGGGACACGGGCGCTGGCTGGTCAAGGACTACTTCCCGGAACCG 1836  
QY 451 GTGACGCTGTCTGGAACTCAGCGCCCTGACCAAGGGGGTGCACACCTTCCCGGCTGTC 510  
Db 1837 GTGACGCTGTCTGGAACTCAGCGCCCTGACCAAGGGGGTGCACACCTTCCCGGCTGTC 1896  
QY 511 CTAAGTCTCTGAGACTCTACTCTCCCTCAGAGGGTGTGACCGTCCCTCCAGCACTTGG 570  
Db 1897 CTAAGTCTCTGAGACTCTACTCTCCCTCAGAGGGTGTGACCGTCCCTCCAGCACTTGG 1956  
QY 571 GGCACCCAGACCTACATCTGACAGCTGAATCAAGCCCGACCAACCAAGGTGGACAAG 630  
Db 1957 GGCACCCAGACCTACATCTGACAGCTGAATCAAGCCCGACCAACCAAGGTGGACAAG 2016  
QY 631 AAGTGGAGCCCAAACTTGTGACAAAATCTCACATGCCCCACCGTCCCGACCACTGAA 690  
Db 2017 AAGTGGAGCCCAAACTTGTGACAAAATCTCACATGCCCCACCGTCCCGACCACTGAA 2076  
QY 691 CTCGGGGGGCACCGTCAAGTCTTCTCTTCCCCCCCCAAACCCCAAGACACCTCTCATGATC 750  
Db 2077 CTCGGGGGGCACCGTCAAGTCTTCTCTTCCCCCCCCAAACCCCAAGACACCTCTCATGATC 2136  
QY 751 TCCCGGACCCCTGAGCTCACTGCGGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 810  
Db 2137 TCCCGGACCCCTGAGCTCACTGCGGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 2196  
QY 811 AAGTCAACTGGTACGTGGAGCGGTGGAGTGCATAATGCCAAGACAAAGCCCGGGGAG 870  
Db 2197 AAGTCAACTGGTACGTGGAGCGGTGGAGTGCATAATGCCAAGACAAAGCCCGGGGAG 2256  
QY 871 GAGCAGTACAAAGCAGTACCGTGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 930  
Db 2257 GAGCAGTACAAAGCAGTACCGTGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 2316  
QY 931 CTGAATGGCAAGAGTACAGTCAAGTCAAGTCTCAACAAAGCCCTCCAGCCGCCATCGAG 990  
Db 2317 CTGAATGGCAAGAGTACAGTCAAGTCAAGTCTCAACAAAGCCCTCCAGCCGCCATCGAG 2376  
QY 991 AAAACCATCTCCAAAGCCAAAGGGCAGCCCGGAGAACCAAGGTGTACACCCCTGCCCCCA 1050  
Db 2377 AAAACCATCTCCAAAGCCAAAGGGCAGCCCGGAGAACCAAGGTGTACACCCCTGCCCCCA 2436  
QY 1051 TCCCGGATGAGTGAACCAAGAACCAAGGTGAGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1110  
Db 2437 TCCCGGATGAGTGAACCAAGAACCAAGGTGAGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 2496  
QY 1111 CCAGCGCATCCCGTGGAGTGGAGCAATGGCGCCGAGAACCAAGTGGAGTGGAGTGGAGTGGAG 1170  
Db 2497 CCAGCGCATCCCGTGGAGTGGAGCAATGGCGCCGAGAACCAAGTGGAGTGGAGTGGAGTGGAG 2556  
QY 1171 ACSCCTCCCGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1230  
Db 2557 ACSCCTCCCGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 2616  
QY 1231 AAGAGCGTGGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1290  
Db 2617 AAGAGCGTGGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 2676  
QY 1291 AACCATCTACCGCAGAGAGCTCTCCCTGTCTCCGGTAAATGA 1335  
Db 2677 AACCATCTACCGCAGAGAGCTCTCCCTGTCTCCGGTAAATGA 2721

US-09-234-340A-68  
; Sequence 68, Application US/09234340A  
; Patent No. 648552  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Hsei, Vanessa  
; APPLICANT: Koumenis, Iphigenia  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/234,340A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/121,952  
; FILING DATE: 24-Jul-1998  
; APPLICATION NUMBER: 60/074330  
; FILING DATE: 22-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/075467  
; FILING DATE: 20-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8120 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
US-09-234-340A-68  
Query Match 81.1%; Score 1082.6; DB 3; Length 8120;  
Best Local Similarity 88.6%; Pred. No. 1.6e-246;  
Matches 1210; Conservative 0; Mismatches 119; Indels 36; Gaps 2;  
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
Db 1363 GAAGTTACGTAGTGCAGTCTGGCGGTGGCTGGTGCAGCCAGGGGGCTCACTCCGGTTTG 1422  
QY 61 TCCTGTGACGTAGCGGATTCTTTCAGTGGCTACTGGATGCTCTGGGTCCGCCAGGCT 120  
Db 1423 TCCTGTGACGTCTTGGTACTCTTCTCGAGTCACTATATGCACTGGTCCGTGAGGCC 1482  
QY 121 CCAGGGAAGGGGCTCGAGTGGTGTCTGAAATAGATTGAAATCTGATTAATTATGCAACA 180  
Db 1483 CCGGGTAAGGGCTGGAATGGGTGGATATTT-----GATCCTTCCCAATGGTGAACCT 1536  
QY 181 CATTATCGGAGTCTGTGAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240  
Db 1537 ACGTATATCAAAAGTTCAAGGGGCGGTTTCACTTTTATCTCGCGACACACTCCAAAACA 1596  
QY 241 CTGTATCTGCAAAATGAACAGCCTGAAACCCGAGGACACAGCGGTGTATTACTGTACA --- 297





298 -----GATTTCATAGACTGGGGCCAGGGAACACTAGTCCACGCTCTCT 340  
394 AGGCCACACTGCTGCTCTCTTTGATTACTTGGGTCAGGACGCTCTGTCACAGTCTCT 453  
341 CAGCCTCCACAAAGGGCCCATCGGTCTTCCCTTGGCACCTCTCTCCAAAGACACTCTG 400  
454 CAGCCTCCACAAAGGGCCCATCGGTCTTCCCTTGGCACCTCTCTCCAAAGACACTCTG 513  
401 GGGGCACAGCGGCGCTGGGCTGCTGGTCAAGACTACTTCCCGAACCGGTGACGGTGT 460  
514 GGGGCACAGCGGCGCTGGGCTGCTGGTCAAGACTACTTCCCGAACCGGTGACGGTGT 573  
461 CGTGGAACTCAGCGCGCTCACCAGCGGCTGCACACCTTCCCGGTGCTCTACAGTCT 520  
574 CGTGGAACTCAGCGGCGCTGACAGCGGCTGCACACCTTCCCGGTGCTCTACAGTCT 633  
521 CAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGCCTCAGCAGCTTGGGCACCCAGA 580  
634 CAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGCCTCAGCAGCTTGGGCACCCAGA 693  
581 CTTACATCTCTCAAGCTGAATCAAGCCCGACGACCAACCAAGGTGGACAGAAAGTGGAGC 640  
694 CTTACATCTCTCAAGCTGAATCAAGCCCGACGACCAACCAAGGTGGACAGAAAGTGGAGC 753  
641 CCAAACTTTGTGACAAAACCTCACACATGCCACCGTGCACGACCTGAACCTCGCGGGG 700  
754 CCAAACTTTGTGACAAAACCTCACACATGCCACCGTGCACGACCTGAACCTCGCGGGG 813  
701 CACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTCCCGAACCC 760  
814 GACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTCCCGAACCC 873  
761 CTGAGGTCAATCGGTGGTGGAGCGTGAGCCACGAGACCTGTAGGTCAGTTCAACT 820  
874 CTGAGGTCAATCGGTGGTGGAGCGTGAGCCACGAGACCTGTAGGTCAGTTCAACT 933  
821 GGTACGTGGACGGGTGGAGGTGATAATGCCAAGCAAAAGCCGCGGAGGACGACGTACA 880  
934 GGTACGTGGACGGGTGGAGGTGATAATGCCAAGCAAAAGCCGCGGAGGACGACGTACA 993  
881 ACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 940  
994 ACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1053  
941 AGGAGTACAGTACAGTCTCAACAAAGCCCTCCCGACCCCTCGAGAAACCATCT 1000  
1054 AGGAGTACAGTACAGTCTCAACAAAGCCCTCCCGACCCCTCGAGAAACCATCT 1113  
1001 CCAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGGATG 1060  
1114 CCAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGGATG 1173  
1061 AGCTGACCAAGAACCAAGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1120  
1174 AGCTGACCAAGAACCAAGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1233  
1121 TCSCCGTGGAGTGGAGAGCAATGGGAGCGGAGGACCACTACAGAGCACGCTCCCG 1180  
1234 TCSCCGTGGAGTGGAGAGCAATGGGAGCGGAGGACCACTACAGAGCACGCTCCCG 1293  
1181 TGCTGAGCTCCGAGCGGCTCTCTTCTCTACAGCAAGCTCAACGCTGGAGCAAGAGCAGGT 1240  
1294 TGCTGAGCTCCGAGCGGCTCTCTTCTCTACAGCAAGCTCAACGCTGGAGCAAGAGCAGGT 1353  
1241 GGACAGAGGGGAACGCTCTCTATGCTCGTGTGATGATGAGGTCTGTGCAACCACTACA 1300  
1354 GGACAGAGGGGAACGCTCTCTATGCTCGTGTGATGATGAGGTCTGTGCAACCACTACA 1413  
1301 CGCAGAGAGCGCTCTCCCTGCTCTCCGGTAAATGA 1335  
1414 CGCAGAGAGCGCTCTCCCTGCTCTCCGGTAAATGA 1448

RESULT 12  
US-09-049-672A-21  
; Sequence 21, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,672A  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cerrone, Michael C  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0497 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1655 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNGUT11  
; CLONE: 2747531  
US-09-049-672A-21  
  
Query Match 79.9%; Score 1066.4; DB 3; Length 1655;  
Best Local Similarity 88.2%; Pred. No. 6.6e-243;  
Matches 1192; Conservative 0; Mismatches 136; Indels 24; Gaps 2;  
  
QY 2 AGGTGACGTGTGTGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61  
DB 105 AGGTCCAGTTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCTCAGTGCAGGTCT 164  
QY 62 CTGTGTGACGTAGCGGATTTCACTTTTCAGTGGCTACTGGATGTCCTGGGTCCCGCAGGGCTC 121  
DB 165 CTGTGACCGTTTCCGGATTCACCTCAGTGATTTATCCGTGACATGGGTGGCAGGGCTC 224  
QY 122 CAGGGAAGGGCTCGAGTGGGTGCTGAAATTTAGATTTGAAATCTGATTAATATGCAACAC 181  
DB 225 CTGGAACAAGGCTTGTGATGGATGGAG-----GTTAGCTCTCGAAATATGAGAGGCAG 278  
QY 182 ATTATGCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCTAGAC 241  
DB 279 TCTAGCACAGAAATTTCTGGGCGACTCACCTTGTCCGAGGACACATCTGCAGACACAG 338



QY 242 TGTATCTGCAATGAACAGCTGAAACCCGAGGACACAGCGGTGATTACTGTACA----- 297  
Db 339 CCTACATGTTCTTGAACAACCTAGGATCTGAGGACTCGGCATCTATTACTGTGCAAGAC 398  
QY 298 -----GATTTATAGACTGGGCGCAGGGAACACTAGTCACCGTCTCTCTCAG 343  
Db 399 AACATTAGGATTTTCTTTCGACTTCTGGGGCCAGGGGACAAATGGTCACCGTCTCTTCAG 458  
QY 344 CTTCCACCAAGGGCCCATCGGTCTTCCCTGGCACCCCTCTCTCAAGAGCACCTCTGGGG 403  
Db 459 CTTCCACCAAGGGCCCATCGGTCTTCCCTGGCACCCCTCTCTCAAGAGCACCTCTGGGG 518  
QY 404 GCACAGCGGCGCTGGGTGCTGCTGCTCAAGACTATCTTCCCGAACCGGTGACGGTGTCT 463  
Db 519 GCACAGCGGCGCTGGGTGCTGCTGCTCAAGACTATCTTCCCGAACCGGTGACGGTGTCT 578  
QY 464 GGAACCTCAGGCGCTCAGCAGCGGCTGCACACTTTCGGGCTGCTCTACAGCTCTCAG 523  
Db 579 GGAACCTCAGGCGCTCAGCAGCGGCTGCACACTTTCGGGCTGCTCTACAGCTCTCAG 638  
QY 524 GACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGACCT 583  
Db 639 GACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGACCT 698  
QY 584 ACATCTGCAAGTGAATCAAGCCCAAGCAACCAAGGTGGACAAGAAAGTGGAGCCCA 643  
Db 699 ACATCTGCAAGTGAATCAAGCCCAAGCAACCAAGGTGGACAAGAAAGTGGAGCCCA 758  
QY 644 AATCTTGTGAAAACTCACAATGACCGGCTGACCGTGCCTGACCTGAACTCTGGGGGGAC 703  
Db 759 AATCTTGTGAAAACTCACAATGACCGGCTGACCGTGCCTGACCTGAACTCTGGGGGGAC 818  
QY 704 CGTCAGTCTTCTTCTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGACCCCTG 763  
Db 819 CGTCAGTCTTCTTCTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGACCCCTG 878  
QY 764 AGTTCATGCTGGTGGTGGAGCGTAGCAAGAGACCTTGAGGTCAAGTTCAACTGGT 823  
Db 879 AGTTCATGCTGGTGGTGGAGCGTAGCAAGAGACCTTGAGGTCAAGTTCAACTGGT 938  
QY 824 ACGTGGACGGGTGGAGTGCATATGCCAAGACAAAGCCCGGAGGAGCAGTACACA 883  
Db 939 ACGTGGACGGGTGGAGTGCATATGCCAAGACAAAGCCCGGAGGAGCAGTACACA 998  
QY 884 GCAGTACCGTGTGCTCAGCGTCTCACCCTGCTGACACAGGACTGCTGAATGGCAAG 943  
Db 999 GCAGTACCGTGTGCTCAGCGTCTCACCCTGCTGACACAGGACTGCTGAATGGCAAG 1058  
QY 944 AGTACAAAGTGAAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAAGAACCATCTCCA 1003  
Db 1059 AGTACAAAGTGAAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAAGAACCATCTCCA 1118  
QY 1004 AAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACCTGCTGCCCTCCATCCCGGGATGAGC 1063  
Db 1119 AAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACCTGCTGCCCTCCATCCCGGGAGGAGA 1178  
QY 1064 TGACCAAGAACCAAGTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123  
Db 1179 TGACCAAGAACCAAGTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1238  
QY 1124 CCGTGGAGTGGAGAGCAATGGGCGAGCGGAGAACCAACTACAGACCAACCCCTCCCGTGC 1183  
Db 1239 CCGTGGAGTGGAGAGCAATGGGCGAGCGGAGAACCAACTACAGACCAACCCCTCCCGTGC 1298  
QY 1184 TGAGCTCCGAGCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1243  
Db 1299 TGGACTCCGAGCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1358  
QY 1244 AGCAGGGGAGCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1303  
Db 1359 AGCAGGGGAGCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1418  
QY 1304 AGAAGAGCCTCTCCCTGCTCTCCGGGTAATGA 1335

Db 1419 AGAAGAGCCTCTCCCTGCTCCCGGTAATGA 1450

## RESULT 13

US-08-286-740-3  
; Sequence 3, Application US/08286740  
; Patent No. 5561053  
; GENERAL INFORMATION:  
; APPLICANT: Crowley, Craig W.  
; TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING  
; TITLE OF INVENTION: HOST CELLS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,740  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 798  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6557 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-286-740-3

Query Match 79.7%; Score 1063.4; DB 1; Length 6557;  
Best Local Similarity 88.3%; Pred. No. 5.2e-242;  
Matches 1205; Conservative 0; Mismatches 121; Indels 39; Gaps 3;  
QY 1 GAGTGCAGCTGTGTGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
Db 1363 GAAGTTTCAGCTGTGTGAGTCTGGCGGTGGCTGTGCAGCAGCGGGGCTCACTCCGTTG 1422  
QY 61 TCTGTGCACTAGCGGATTCATTTCAC---GTGGCTACTGGATGTCTCGGTCCGCCAG 117  
Db 1423 TCTGTGCACTTCTTCTGGTACTCCATCACCTCCGATATAGCTGGAACTCGATCCGTCAG 1482  
QY 118 GCTCCAGGAAGGGGCTCGAGTGGTGTGAAATTTAGATTGAAATCTGATAATTATGCA 177  
Db 1483 GCCTCCGGTAAAGGCTTGGATGGGTTC-----ATCGATTAGTATGCCGATCG 1533  
QY 178 ACACATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATCAAAATCT 237  
Db 1534 ACTAATATAAACCCTAGCGTCAAGGGCCGTATCACTATAAGTCCGACGATTCGAAAC 1593  
QY 238 AGACTTACTGCAATGAACAGCTGAAACCGAGGACACAGCCGCTGTATTACTGTAC- 296  
Db 1594 ACATTCTACGTGAGTGAACAGCCCTGCGTGTGAGGACACTCCGCTCTATTATTGTCT 1653  
QY 297 -----AGATTTTCATAGACTGGGGCCAGGGAACACTAGTC 330

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Db 1654 CGAGGAGCACCATTATTCGGCGCTCGCAGCTTCGGGTCAAGAACCTCGTC 1713
QY 331 ACCGTCTCTCAGCTCCACAAAGGCCATCGGTCTTCCCTCGCACCTCTCCAAAG 390
Db 1714 ACCGTCTCTCGGCTCCACAAAGGCCATCGGTCTTCCCTCGCACCTCTCCAAAG 1773
QY 391 AGCACTCTGGGGGACAGGGGCTGGGTGCTGTCAGGACTACTTCCCGAACCG 450
Db 1774 AGCACTCTGGGGGACAGGGGCTGGGTGCTGTCAGGACTACTTCCCGAACCG 1833
QY 451 GTACGGGTCTGGGAACTCAGGCGCTGACAGCGGCTGCACACCTTCCCGGTGTC 510
Db 1834 GTACGGGTCTGGGAACTCAGGCGCTGACAGCGGCTGCACACCTTCCCGGTGTC 1893
QY 511 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGTTC 570
Db 1894 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACTGTGCTCTAGCAGCTTC 1953
QY 571 GGCACCCAGACCTACATCTGACAGTGAATCAAGCCAGCAACCAAGGTGGACAAG 630
Db 1954 GGCACCCAGACCTACATCTGACAGTGAATCAAGCCAGCAACCAAGGTGGACAAG 2013
QY 631 AAAGTGGAGCCCAATCTTGTGACAAATCTCACACATGCCACCGTCCCGACCTGAA 690
Db 2014 AAAGTGGAGCCCAATCTTGTGACAAATCTCACACATGCCACCGTCCCGACCTGAA 2073
QY 691 CTCGGGGGACACCGTCAGTCTTCTTCCCTCCCAAAACCCAAAGACACCTCATGATC 750
Db 2074 CTCGGGGGACACCGTCAGTCTTCTTCCCTCCCAAAACCCAAAGACACCTCATGATC 2133
QY 751 TCCCGGACCTCAGGTGCATCGTGGTGGTGGAGCTGAGCCACCAAGACCTGAGTTC 810
Db 2134 TCCCGGACCTCAGGTGCATCGTGGTGGTGGAGCTGAGCCACCAAGACCTGAGTTC 2193
QY 811 AAGTTCAAATGCTGACGCGGTGGAGTGCATAATGCCAAAGCAAGCCGCGGGAG 870
Db 2194 AAGTTCAAATGCTGACGCGGTGGAGTGCATAATGCCAAAGCAAGCCGCGGGAG 2253
QY 871 GAGCAGTACAAAGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 930
Db 2254 GAGCAGTACAAAGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2313
QY 931 CTGAATGGCAAGAGTACAGTCAAGTCTCAACAAAGCCCTCCAGCCCTCCATCGAG 990
Db 2314 CTGAATGGCAAGAGTACAGTCAAGTCTCAACAAAGCCCTCCAGCCCTCCATCGAG 2373
QY 991 AAAACCATCTCAAAGCCAAAGGCGAGCCCGAGAAACCAAGGTGTACACCTGCCCCA 1050
Db 2374 AAAACCATCTCAAAGCCAAAGGCGAGCCCGAGAAACCAAGGTGTACACCTGCCCCA 2433
QY 1051 TCCCGGATGAGTGCACCAAGAACAGGTGAGCTGACCTGCTGCTGCTGCTGCTGCT 1110
Db 2434 TCCCGGATGAGTGCACCAAGAACAGGTGAGCTGACCTGCTGCTGCTGCTGCTGCT 2493
QY 1111 CCCAGCGCATCCCGTGGAGTGGAGCAATGGGCGAGCCGAGAGCAACTACAAGACC 1170
Db 2494 CCCAGCGCATCCCGTGGAGTGGAGCAATGGGCGAGCCGAGAGCAACTACAAGACC 2553
QY 1171 ACGCTCTCCGTGTGATCTCCGAGGCTCTTCTTCTCTACAGCAAGTCTACCGTGGAC 1230
Db 2554 ACGCTCTCCGTGTGATCTCCGAGGCTCTTCTTCTCTACAGCAAGTCTACCGTGGAC 2613
QY 1231 AAGAGCGTGGGAGCGAGGGAAGTCTTCTCATGCTCGTGTGATGATGAGGCTCTGCAC 1290
Db 2614 AAGAGCGTGGGAGCGAGGGAAGTCTTCTCATGCTCGTGTGATGATGAGGCTCTGCAC 2673
QY 1291 AACCACTACAGCAGAGAGCCCTCTCCCTGCTCCGGTAAATGA 1335
Db 2674 AACCACTACAGCAGAGAGCCCTCTCCCTGCTCCGGTAAATGA 2718
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RESULT 14

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PCT-US95-09576-3
; Sequence 3, Application PC/TUS9509576
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
; TITLE OF INVENTION: HOST CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09576
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286740
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 798PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6557 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US95-09576-3
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Query Match 79.7%; Score 1063.4; DB 5; Length 6557;
Best Local Similarity 88.3%; Pred. No. 5.2e-242;
Matches 1205; Conservative 0; Mismatches 121; Indels 39; Gaps 3;

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1363 GAAGTTACGCTGGTGGAGTCTGGCGTGGCTGGTGCAGCCAGGGGGCTCACTCCGTTTG 1422
QY 61 TCCTGTGCAGCTAGCGGATTCACCTTCA---GTGGCTACTGGATGTCCTGGGTCCGCCAG 117
Db 1423 TCCTGTGCAGTTCCTGGCTACTCCATCACCTCCGGATATAGCTGGAATCGGTTCAG 1482
QY 118 GCTCCAGGAAGGGGCTCGAGTGGGTGCTGAAATTAGATTGAAATCTGATAATTATGCA 177
Db 1483 GCCCGGGTAAAGGCTCGAATGGTTCG-----ATCGATTACGTATCCGGATCG 1533
QY 178 ACACATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCT 237
Db 1534 ACTAATATAAACCCCTAGCGTCAAGGGCCGTATCACTATAAGTCGCGACGATTCCAAAC 1593
QY 238 AGACTGTATCTCAATGAACAGCTGAAACCCGAGGACACAGCGTGTATTACTGTAC- 296
Db 1594 ACATTCTACCTGAGATGAACAGCTTGGCTGTGAGGACACTGCGCTCTATTATTGTCT 1653
QY 297 -----AGATTTTCATAGACTGGGGCCAGGAAACACTAGTGC 330
Db 1654 CGAGGAGCCACTATTTCGGCGCTGGGCACTTCGCGCTGGGTCAAGGAACCTCGTTC 1713
QY 331 ACCGTCTCTCAGCTCCACAAAGGCCATCGGTCTTCCCTCGCACCTCTCCAAAG 390
Db 1714 ACCGTCTCTCGGCTCCACCAAGGGGCCATCGGTCTTCCCTCGCACCTCTCCAAAG 1773
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QY 391 AGCACTCTGGGGGACAGCGGCGCTGGGCTGCTCAAGGACTACTTCCCGAACCG 450  
DB 1774 AGCACTCTGGGGGACAGCGGCGCTGGGCTGCTCAAGGACTACTTCCCGAACCG 1833  
QY 451 GTGACGGTGTGCTGGAACCTAGGCGGCTGACAGCGGCTGACACTTCCCGGCTGTC 510  
DB 1834 GTGACGGTGTGCTGGAACCTAGGCGGCTGACAGCGGCTGACACTTCCCGGCTGTC 1893  
QY 511 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACGCGTCCAGCAGCTTG 570  
DB 1894 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACGCGTCCAGCAGCTTG 1953  
QY 571 GGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCAACCAAGGTGGAAG 630  
DB 1954 GGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCAACCAAGGTGGAAG 2013  
QY 631 AAGTGAGGCCAAATCTTGTGACAAATCTACATGCTCCAGCGCTGCCAGCAGCTGAA 690  
DB 2014 AAGTTGAGGCCAAATCTTGTGACAAATCTACATGCTCCAGCGCTGCCAGCAGCTGAA 2073  
QY 691 CTCGCGGGGACCGCTCAGTCTTCTCTTCCCGGCAAAACCCAGGACACCTCATGATC 750  
DB 2074 CTCGCGGGGACCGCTCAGTCTTCTCTTCCCGGCAAAACCCAGGACACCTCATGATC 2133  
QY 751 TCCCGGACCCCTGAGGTTCATGCTGCTGCTGCTGAGCCAGCAAGACCCCTGAGGTC 810  
DB 2134 TCCCGGACCCCTGAGGTTCATGCTGCTGCTGAGCCAGCAAGACCCCTGAGGTC 2193  
QY 811 AAGTTCACTGTTAGTGGACGCGCTGGAATGATGCTGCAAGCAAGCGCGGAG 870  
DB 2194 AAGTTCACTGTTAGTGGACGCGCTGGAATGATGCTGCAAGCAAGCGCGGAG 2253  
QY 871 GAGCAGTACACAGCAGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930  
DB 2254 GAGCAGTACACAGCAGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2313  
QY 931 CTGAATGGCAAGGAGTCAAGTCAAGTCTTCCAAAGGCGCTTCCAGCGCCCATCGAG 990  
DB 2314 CTGAATGGCAAGGAGTCAAGTCAAGTCTTCCAAAGGCGCTTCCAGCGCCCATCGAG 2373  
QY 991 AAAACCATCTCCAAAGGCAAGGCGCGCGGAGCAAGCAAGGCTGACACCTGCCCCCA 1050  
DB 2374 AAAACCATCTCCAAAGGCAAGGCGCGCGGAGCAAGCAAGGCTGACACCTGCCCCCA 2433  
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QY 1111 CCCAGCGACATCGCGGTGGAGTGGAGCAATGGGCGAGCGGAGCAACTACAGACC 1170  
DB 2494 CCCAGCGACATCGCGGTGGAGTGGAGCAATGGGCGAGCGGAGCAACTACAGACC 2553  
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DB 2674 AACCACTACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2718

## RESULT 15

US-08-030-175-7

; Sequence 7, Application US/08030175  
; Patent No. 6767996  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Scott D.  
; APPLICANT: Clark, Michael R.

APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Hexman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington  
STATE: D. C.  
COUNTRY: U. S.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage  
COMPUTER: IBM AT compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
SOFTWARE: WordPerfect 5.0 (Dos Text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,175  
FILING DATE: 17-MAY-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB91/01578  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ernst, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1768-113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1458 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEetical: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 36..1439  
US-08-030-175-7

Query Match 79.4%; Score 1060; DB 4; Length 1458;

Best Local Similarity 87.9%; Pred. No. 2.1e-241;

Matches 1188; Conservative 0; Mismatches 140; Indels 24; Gaps 2;

QY 2 AGGTGCGAGTGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGCTCCCTTAGACTCT 61  
DB 94 AGGTCCAACTGCAGGAGAGCGGTCAGGCTTTGTGAGACCTAGCCAGACCTGAGGCTGA 153  
QY 62 CTTGTCCAGTACGCGATTCACTTTTCAGTGGTACTTGGATGTCTCTGGGTCGCCAGGCTC 121  
DB 154 CTTGCACCGTGTCTGGCTTCACTTCAGCAACTATGCGATGGCTGGTGAGACAGCCAC 213  
QY 122 CAGGGAAGGGCTCGAGTGGTGTGCTGAAATAGATTGAAATCTGATAATTATGCAACAC 181  
DB 214 CTGACGAGGCTTGTAGTGGATTGGAACCACTTAG-----TCATGATGGTAGTGA 267  
QY 182 ATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241  
DB 268 ACTTTCGAGACTCTGTGAAGGGGAGAGTGAATGCTGGTAGACACAGCAAGAACAGT 327  
QY 242 TGTATCTGCAAAATGAACAGCCTGAAACCGAGGACACAGCGGTGTATTACTGTACA----- 297  
DB 328 TCAGCCTGAGACTCAGCAGCGTGAACAGCCGCGCACACCGCGGTCTATTATTGTGCAAGAC 387  
QY 298 -----GATTTTCATAGACTGGGGCCAGGGAAACATAGTACCGTCTCTCTCAG 343  
DB 388 AAGGCACATATAGCTGTGTATACGTCACCTGGGGTCAAGGCGAGCCTCGTACAGTCTCTCAG 447  
QY 344 CCTCCACCAAGGCCCATCGGTCTTCCCTTGGCACCCTCTCCACAGACACCTCTCTGGG 403

Db 448 CCTCCACCAAGGCCCCCTCGGCTCTCCCTGSCACCTCTCCCAAGAGCACCTCTGGGG 507  
QY 404 GCACAGGGCCCTGGGGCTGCTGGTCAAGACTACTTCCCGGAACCGGTGACGCTGTCGT 463  
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QY 464 GGAACCTCAGGCGCCCTGACACAGGGGGTGCACACCTTCCGGGCTGCTACAGTCCCTCAG 523  
Db 568 GGAACCTCAGGCGCCCTGACACAGGGGGTGCACACCTTCCGGGCTGCTACAGTCCCTCAG 627  
QY 524 GACTTACTCCCTCAGCAGCGGTGACCGTGGCCCTCCAGCAGCTTGGGCACCCAGACCT 583  
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Db 688 ACATCTGCAACGTGAATCAACAGCCCGAGCAACACCAAGGTGGACAAAGTGGAGCCCA 747  
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QY 704 CGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCTCTCATGATCTCCCGGACCCCTG 763  
Db 808 CGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCTCTCATGATCTCCCGGACCCCTG 867  
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Db 928 ACCTGACCGGTGGAGGTGCATANTGCCAAGCAACCGCGGGAGGAGCAGTACAACA 987  
QY 884 GCACGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 943  
Db 988 GCACGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1047  
QY 944 AGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCAGCCGCCATCGAGAAACCATCTCCA 1003  
Db 1048 AGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCAGCCGCCATCGAGAAACCATCTCCA 1107  
QY 1004 AGCCAAAGGGAGCGCCCGAGACACAGGTGTACACCTGCCCCCATCCCGGGATGAGC 1063  
Db 1108 AGCCAAAGGGAGCGCCCGAGACACAGGTGTACACCTGCCCCCATCCCGGGATGAGC 1167  
QY 1064 TGACCAAGAACCAAGGTGACCTGACCTGGTCAAGGCTTCTATCCAGCGACATCG 1123  
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QY 1124 CCGTGGAGTGGGAGAGCAATGGGAGCGCGGAGAAACAACTACAAGACAACGCTCCCGTGC 1183  
Db 1228 CCGTGGAGTGGGAGAGCAATGGGAGCGCGGAGAAACAACTACAAGACAACGCTCCCGTGC 1287  
QY 1184 TGGACTCCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGGC 1243  
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QY 1244 AGCAGGGGAACGTCTTCTCTATGCTCCGTGATGATGAGGTCTGACACCACTACACGC 1303  
Db 1348 AGCAGGGGAACGTCTTCTCTATGCTCCGTGATGATGAGGTCTGACACCACTACACGC 1407  
QY 1304 AGAAGACCTCTCCCTGTCTCCGGTAAATGA 1335  
Db 1408 AGAAGACCTCTCCCTGTCTCCGGTAAATGA 1439